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(54) HỆ PHÂN CẮT GLYXIN, VI SINH VẬT TÁI TỔ HỢP CHỨA HỆ PHÂN CẮT GLYXIN NÀY VÀ PHƯƠNG PHÁP SẢN XUẤT LƯỢNG LỚN AXIT L-AMIN

(57) Sáng chế đề cập đến hệ phân cắt glyxin, polypeptit cấu thành hoặc polynucleotit mã hoá enzym của hệ phân cắt glyxin này, vectơ chứa polynucleotit này, vi sinh vật tái tổ hợp chứa hệ phân cắt glyxin này và phương pháp sản xuất lượng lớn axit L-amin.

Lĩnh vực kỹ thuật được đề cập

Sáng chế đề cập đến phương pháp sản xuất axit L-amin trong *Corynebacteria*, trong đó hệ phân cắt glyxin được sử dụng.

Tình trạng kỹ thuật của sáng chế

Người có hiểu biết trung bình trong lĩnh vực này đã biết các phương pháp sản xuất axit L-amin sử dụng vi khuẩn từ chi *Corynebacterium*.

Mặc dù đã biết nhiều loài *Corynebacterium*, các vi khuẩn thuộc loài *Corynebacterium glutamicum* thường được sử dụng trong các phương pháp này, do các loài này đã được phát hiện ra đặc biệt có lợi để sản sinh các axit L-amin.

Đã biết rằng rằng hiệu suất axit L-amin có thể tiếp tục được gia tăng hơn bằng cách sử dụng hệ phân cắt glyxin (glycine cleavage-GCV), do sự tạo ra sản phẩm phụ L-glyxin không mong muốn có thể được ngăn ngừa ở mức độ lớn bởi hệ phân cắt glyxin này. Đặc biệt là, việc ngăn ngừa hình thành L-glyxin hoặc phân huỷ L-glyxin với lượng lớn là đặc biệt quan trọng trong sản xuất L-methionin, do L-glyxin đã được tạo ra này là sản phẩm phụ đẳng mol.

Hệ phân cắt glyxin cấu thành bởi hai hoặc nhiều tiểu đơn vị, cụ thể là các tiểu đơn vị GcvP, GcvT và GcvH. Nó có dạng phức đa enzym, xúc tác quá trình tách nhóm carboxyl oxy-hoá và tách nhóm amin của glyxin thành cacbon dioxit, ion amoni và N^{5-10}-metylentetrahydrofolat.

Glyxin dehydrogenaza GcvP là decarboxylaza chứa pyridoxal phosphat giải phóng cacbon dioxit và tạo ra hợp chất aminometyl gắn kết với pyridoxal phosphat.

H-protein GcvH là aminometyltransferaza chứa lipoamit.

Enzym GcvT xúc tác sự gắn nhóm ưa nhân vào aminometyllipoamit bởi tetrahydrofolat để tạo ra N^{5-10}-metylentetrahydrofolat và giải phóng ion amoni, trong đó lipoamit được khử hoàn toàn vẫn được gắn kết với GcvH.

Các hệ phân cắt glyxin không có mặt trong tất cả *Corynebacteria*, nhưng đến nay chỉ rất ít *Corynebacteria* được mô tả. Ví dụ, chủng sản sinh *C. glutamicum* được đặc biệt ưu tiên để sản sinh axit amin, ví dụ không có hệ phân cắt glyxin vốn có. Để sử dụng các ưu điểm của hệ phân cắt glyxin đối với *C. glutamicum*, hệ này phải được đưa vào *C. glutamicum* từ *Corynebacterium* khác và được biểu hiện theo cách không tương đồng. Hệ phân cắt glyxin từ *C. jeikeium* (WO2008/101857) được sử dụng đến nay nhằm mục đích này. Trong trường hợp này, các nhược điểm trầm trọng là ở chỗ C. *jeikeium* là sinh vật gây bệnh. Các nhược điểm khác ở chỗ, đối với mục đích phân huỷ sản phẩm phụ glyxin không mong muốn, cấu trúc không tương đồng phải được tạo ra.

Do đó, mục đích quan trọng nhất của sáng chế là đề xuất hệ phân cắt glyxin mới, tốt hơn nếu hệ phân cắt glyxin không thu được từ sinh vật gây bệnh, trong đó tốt hơn nếu hệ phân cắt glyxin là thích hợp để đưa vào Corynebacteria khác, cụ thể là *C. glutamicum*.

Sáng chế cũng đề xuất Corynebacterium mà thực chất có khả năng sản sinh các axit L-amin và có hệ phân cắt glyxin vốn có sao cho việc tạo ra cấu trúc không tương đồng - như trong trường hợp *C. glutamicum* - là không cần thiết.

Các tác giả sáng chế đã ngạc nhiên phát hiện thấy rằng các loài *Corynebacterium humireducens*, không gây bệnh, có hệ phân cắt glyxin vốn có khác nhau đáng kể về mặt cấu trúc với hệ phân cắt glyxin đã được mô tả đến nay.

Các tác giả sáng chế cũng đã ngạc nhiên phát hiện thấy rằng hệ phân cắt glyxin của Corynebacterium humireducens là rất hữu hiệu, sao cho glyxin, là sản phẩm phụ không mong muốn trong quá trình tổng hợp axit amin, chỉ tích tụ trong tế bào với lượng tương đối thấp, nếu không phải tất cả, trong chủng thể dại. Bằng cách khuếch đại hệ phân cắt glyxin theo sáng chế, cụ thể là bằng cách biểu hiện quá mức, việc ngăn chặn sự tạo ra sản phẩm phụ glyxin có thể được cải thiện hơn nữa một cách tương ứng. Cụ thể là, sự tạo ra sản phẩm phụ glyxin còn có thể được ngăn chặn một cách hữu hiệu nhờ sự biểu hiện quá mức của hệ phân cắt glyxin theo sáng chế ở các vi sinh vật khác, cụ thể là trong *C. glutamicum*.

Hơn nữa, các tác giả sáng chế đã ngạc nhiên phát hiện thấy rằng *C. humireducens* thực chất còn có khả năng sản sinh axit L-amino, cụ thể là L-alanin, L-

valin và axit L-glutamic, thông qua nhu cầu vốn có của nó, sao cho C. *humireducens* là chủng sản sinh axit L-amin có hệ phân cắt glyxin tương đồng có thể được dùng đặc biệt là làm điểm khởi đầu để phát triển các chủng sản sinh khác có hệ phân cắt glyxin của vật chủ.

Chủng *C. humireducens* được mô tả lần đầu tiên bởi Wu et al. (International Journal of Systematic and Evolutionary Microbiology (2011), 61, 882-887). Chủng này được lưu trữ ở DSMZ dưới mã lưu trữ DSM 45392 và ARN ribosom 16S của nó được lưu trữ ở EMBL và có mã lưu trữ GQ421281. Chủng gốc là vi khuẩn chịu mặn, ưa kiềm, khử axit humic.

Các thông tin khác liên quan đến C. *humireducens* được tìm thấy trong các tài liệu công bố sau của Wu et al. (Microb.Biotechnol. (2013), 6(2), 141-149), Lin et al. (Bioresour. Technol. (2013), 136, 302-308).

Bản chất kỹ thuật của sáng chế

Do đó, mục đích thứ nhất của sáng chế là đề xuất các enzym của hệ phân cắt glyxin được chọn từ nhóm bao gồm:

a) enzym GcvP có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.40,

b) enzym GcvT có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.42,

c) enzym GcvH có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.38.

Do đó, sáng chế cũng đề xuất hệ phân cắt glyxin chứa các enzym GcvP, GcvT và GcvH, khác biệt ở chỗ, hệ này chứa ít nhất một polypeptit trong số các polypeptit sau:

a) enzym GcvP có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.40,

b) enzym GcvT có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.42,

c) enzym GcvH có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.38.

Trong trường hợp này, tốt hơn nếu hệ phân cắt glyxin theo sáng chế chứa ít nhất hai, tốt hơn nếu tất cả ba polypeptit từ (a) đến (c) nêu trên.

Tốt hơn nếu hệ phân cắt glyxin theo sáng chế chứa ba polypeptit sau:

a) enzym GcvP có độ tương đồng trình tự ít nhất bằng 95% hoặc 98% so với trình tự nêu trong SEQ ID NO.40,

b) enzym GcvT có độ tương đồng trình tự ít nhất bằng 95% hoặc 98% so với trình tự nêu trong SEQ ID NO.42,

c) enzym GcvH có độ tương đồng trình tự ít nhất bằng 95% hoặc 98% so với trình tự nêu trong SEQ ID NO.38.

Theo nghĩa rộng hơn, các enzym LpdA, LplA, LipA, LipB và GcvH cũng thuộc hệ phân cắt glyxin.

Dihydrolipoamit dehydrogenaza (LpdA) oxy hoá lại lipoamit gắn kết với GcvH.

Lipoat-protein ligaza A (LplA) xúc tác quá trình lipoyl hoá GcvH.

Axit lipoic synthaza (LipA) xúc tác quá trình tổng hợp axit lipoic.

Lipoyl-[protein mang axyl]-protein N-lipoyltransferaza (LipB) xúc tác quá trình vận chuyển axit lipoic vào GcvH.

GcvL là dihydrolipoyl dehydrogenaza.

Theo phương án ưu tiên, hệ phân cắt glyxin theo sáng chế còn chứa ít nhất một enzym bổ sung được chọn từ nhóm bao gồm:

a) enzym LipA, tốt hơn nếu enzym LipA có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.48,

b) enzym LipB, tốt hơn nếu enzym LipB có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.50,

c) enzym Lpd, tốt hơn nếu enzym Lpd có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.52,

d) enzym LplA, tốt hơn nếu enzym LplA có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.94,

e) enzym GcvL, tốt hơn nếu enzym GcvL có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.96.

Theo phương án đặc biệt ưu tiên, hệ phân cắt glyxin theo sáng chế trong trường hợp này chứa ít nhất hai, ba hoặc bốn, tốt hơn nếu tất cả năm polypeptit nêu trên.

Theo cách khác hoặc ngoài việc sử dụng các enzym thích hợp mà đảm bảo việc tổng hợp axit lipoic và/hoặc lipoamit phù hợp, các hợp chất này còn có thể được bổ sung vào môi trường phản ứng, ví dụ với lượng lên đến 15mM.

Sáng chế cũng đề xuất các polynucleotit mã hoá các enzym theo sáng chế và/hoặc hệ phân cắt glyxin theo sáng chế. Tốt hơn nếu, các polynucleotit này được chọn từ nhóm bao gồm:

a) polynucleotit (gcvP), mã hoá enzym GcvP và có độ tương đồng trình tự ít nhất bằng 70% hoặc 75%, tốt hơn nếu ít nhất bằng 80% hoặc 85%, tốt hơn nữa nếu ít nhất bằng 90% hoặc 95%, tốt nhất nếu ít nhất bằng 98% hoặc 100%, so với trình tự có vị trí từ 301 đến 3162 như nêu trong SEQ ID NO.39 và/hoặc lai hóa trong các điều

kiện nghiêm ngặt với polynucleotit có trình tự bổ sung với trình tự có vị trí từ 301 đến 3162 như nêu trong SEQ ID NO.39;

b) polynucleotit (gcvT), mã hoá enzym GcvT và có độ tương đồng trình tự ít nhất bằng 70% hoặc 75%, tốt hơn nếu ít nhất bằng 80% hoặc 85%, tốt hơn nữa nếu ít nhất bằng 90% hoặc 95%, tốt nhất nếu ít nhất bằng 98% hoặc 100%, so với trình tự có vị trí từ 301 đến 1404 như nêu trong SEQ ID NO.41 và/hoặc lai hóa trong các điều kiện nghiêm ngặt với polynucleotit có trình tự bổ sung với trình tự có vị trí từ 301 đến 1404 như nêu trong SEQ ID NO.41;

c) polynucleotit (gcvH), mã hoá enzym GcvH và có độ tương đồng trình tự ít nhất bằng 70% hoặc 75%, tốt hơn nếu ít nhất bằng 80% hoặc 85%, tốt hơn nữa nếu ít nhất bằng 90% hoặc 95%, tốt nhất nếu ít nhất bằng 98% hoặc 100%, so với trình tự có vị trí từ 301 đến 699 như nêu trong SEQ ID NO.37 và/hoặc lai hóa trong các điều kiện nghiêm ngặt với polynucleotit có trình tự bổ sung với trình tự có vị trí từ 301 đến 699 như nêu trong SEQ ID NO.37.

Theo sáng chế, thuật ngữ "các điều kiện nghiêm ngặt" được hiểu có nghĩa là rửa ở nồng độ muối 1 x SSC và 0,1% khối lượng SDS ở nhiệt độ 80°C.

Sáng chế cũng đề xuất vectơ thích hợp, cụ thể là vectơ tách dòng và biểu hiện, chứa ít nhất một polynucleotit theo sáng chế. Các vectơ này có thể được đưa một cách thích hợp vào các vi sinh vật, cụ thể là vào vi khuẩn Coryneform, đặc biệt là từ chi Corynbebacterium hoặc Enterobacteriaceae, đặc biệt là từ chi Escherichia.

Các vectơ theo sáng chế có thể chứa một hoặc nhiều polynucleotit theo sáng chế. Vectơ được ưu tiên theo sáng chế chứa ít nhất một polynucleotit mã hoá enzym theo sáng chế được chọn từ GcvP, GcvT và GcvH. Vectơ được đặc biệt ưu tiên chứa các polynucleotit mã hoá tất cả ba enzym GcvP, GcvT và GcvH theo sáng chế.

Tốt hơn nếu, các vectơ theo sáng chế có vùng khởi đầu thích hợp và/hoặc các vùng khởi đầu thích hợp và tuỳ ý các đoạn điều hòa bổ sung cho phép biểu hiện các polynucleotit theo sáng chế trong vi khuẩn tái tổ hợp, tốt hơn nếu *Corynebacterium* tái tổ hợp.

Hơn nữa, các polynucleotit theo sáng chế, đối với mục đích biểu hiện các gen được mã hoá, cũng có thể được đưa vào hệ gen của các vi sinh vật, cụ thể là vào hệ

gen của vi khuẩn *Coryneform*, cụ thể là các vi sinh vật thuộc chi *Corynebacterium* hoặc hệ gen của *Enterobacteriaceae*, đặc biệt là thuộc chi *Escherichia*.

Sáng chế cũng đề xuất các vi sinh vật tái tổ hợp tương ứng, tốt hơn nếu vi khuẩn, cụ thể là vi khuẩn *Coryneform*, đặc biệt là các vi khuẩn thuộc chi *Corynebacterium*, đặc biệt tốt hơn nếu thuộc các loài *C. humireducens* hoặc *C. glutamicum* và *Enterobacteriaceae*, đặc biệt là vi khuẩn thuộc chi *Escherichia*, chứa ít nhất một enzym theo sáng chế và/hoặc ít nhất một polynucleotit theo sáng chế và/hoặc ít nhất một vectơ theo sáng chế và/hoặc một hệ phân cắt glyxin theo sáng chế và/hoặc polynucleotit mã hoá hệ phân cắt glyxin theo sáng chế.

Mô tả chi tiết sáng chế

Trong bản mô tả này, đối tượng được ưu tiên là *Corynebacteria* tái tổ hợp, cụ thể là thuộc các loài *C. humireducens* và các loài *C. glutamicum*, chứa ít nhất một enzym theo sáng chế, tốt hơn nếu tất cả enzym theo sáng chế, được chọn từ GcvP, GcvT và GcvH và/hoặc các polynucleotit mã hoá các enzym nêu trên và/hoặc ít nhất một vectơ chứa các polynucleotit nêu trên.

Cụ thể là, sáng chế cũng đề cập đến vi sinh vật tái tổ hợp, tốt hơn nếu vi khuẩn, cụ thể là vi khuẩn *Coryneform*, đặc biệt là các vi khuẩn thuộc chi *Corynebacterium* trừ các loài *C. humireducens*, cụ thể là các vi khuẩn thuộc các loài *C. glutamicum*, chứa ít nhất một enzym theo sáng chế và/hoặc ít nhất một polynucleotit theo sáng chế và/hoặc ít nhất một vectơ theo sáng chế và/hoặc một hệ phân cắt glyxin theo sáng chế và/hoặc polynucleotit mã hoá hệ phân cắt glyxin theo sáng chế.

Trong bản mô tả này, đối tượng được ưu tiên là *Corynebacteria* tái tổ hợp, trừ các loài *C. humireducens*, cụ thể là các loài *C. glutamicum*, chứa ít nhất một enzym theo sáng chế, tốt hơn nếu tất cả enzym theo sáng chế, được chọn từ GcvP, GcvT và GcvH, và/hoặc polynucleotit mã hoá các enzym nêu trên và/hoặc ít nhất một vectơ chứa các polynucleotit nêu trên.

Theo sáng chế, "vi sinh vật tái tổ hợp" hoặc "vi khuẩn tái tổ hợp" được hiểu có nghĩa là vi sinh vật hoặc vi khuẩn mà được áp dụng ít nhất một phương pháp kỹ thuật di truyền. Trong bản mô tả này, phương pháp kỹ thuật di truyền, cụ thể là, có thể là sự đột biến hướng đích hoặc ngẫu nhiên, đưa gen lạ vào và/hoặc sự biểu hiện quá mức

hoặc giảm hoạt lực của gen của vật chủ hoặc gen lạ. Tốt hơn nếu, vi sinh vật tái tổ hợp theo sáng chế hoặc vi khuẩn tái tổ hợp theo sáng chế được đặc trưng bởi sự biểu hiện quá mức hoặc giảm nồng độ hoặc hoạt tính của ít nhất một gen. Theo phương án được đặc biệt ưu tiên, vi sinh vật tái tổ hợp theo sáng chế hoặc vi khuẩn tái tổ hợp theo sáng chế được đặc trưng bởi sự biểu hiện quá mức của ít nhất một enzym theo sáng chế và/hoặc polynucleotit mã hoá enzym nêu trên và/hoặc sự biểu hiện quá mức của hệ phân cắt glyxin theo sáng chế hoặc polynucleotit mã hoá hệ nêu trên.

Thuật ngữ "lượng tương đối thấp", liên quan đến sự tạo ra glyxin, được hiểu có nghĩa lượng lớn nhất là lượng nhiều nhất 0,3g/L, tốt hơn nếu lớn hơn 0,2 hoặc 0,1g/L, đặc biệt tốt hơn nếu lớn nhất là 0,05 hoặc lớn nhất là 0,03g/L, trong mỗi trường hợp tính theo lượng glyxin được tích tụ trong tế bào và/hoặc trong môi trường lên men sau khi hoàn thành quá trình lên men.

Trong chi Corynebacterium, sự ưu tiên được dành cho các chủng theo sáng chế dựa trên các loài sau: Corynebacterium efficiens, chủng điển hình DSM44549, *Corynebacterium glutamicum*, như chủng điển hình ATCC13032 hoặc chủng *R, Corynebacterium ammoniagens*, như chủng điển hình ATCC6871, *Corynebacterium humireducens*, như chủng DSM 45392 và *Corynebacterium pekinese*, như chủng CGMCC số 5361.

Tốt hơn nếu các loài *Corynebacterium glutamicum* và *Corynebacterium humireducens*. Trong bản mô tả này, khi chủng Corynebacterium humireducens được đề cập đến, tốt hơn nếu chủng này là chủng DSM 45392 hoặc chủng thu được từ đó.

Một số đại diện của các loài *Corynebacterium glutamicum* còn được biết trong lĩnh vực này với các tên khác. Các loài này bao gồm, ví dụ *Corynebacterium acetoacidophilum* ATCC13870, *Corynebacterium lilium* DSM20137, Corynebacterium melassecola ATCC17965, *Brevibacterium flavum* ATCC14067, *Brevibacterium lactofermentum* ATCC13869 và *Brevibacterium divaricatum* ATCC14020. Thuật ngữ "Micrococcus glutamicus" đối với *Corynebacterium glutamicum* cũng được sử dụng. Một số đại diện của các loài *Corynebacterium efficiens* còn được dùng trong lĩnh vực kỹ thuật là *Corynebacterium thermoaminogens*, ví dụ chủng FERM BP-1539.

Các thông tin về phân loại các chủng thuộc nhóm vi khuẩn *Coryneform* có thể được tìm thấy, không kể các tài liệu khác, trong bài báo Seiler (Journal of Genral Microbiology 129, 1433-1477 (1983)), Kinoshita (1985, Glutamic Acid Bacteria, 115-142. Trong tạp chí: Demain and Solomon (ed), Biology of Industrial Microorganisms. The Benjamin/Cummins Publishing Co., London, UK), Kämpfer and Kroppenstedt (Canadian Journal of Microbiology 42, 989-1005 (1996)), Liebl et al. (International Journal of Systematic Bacteriology 41, 255-260 (1991)), Fudou et al. (International Journal of Systematic and Evolutionary Microbiology 52, 1127-1131 (2002)) và trong US-A-5,250,434.

Các chủng có ký hiệu "ATCC" có thể nhận được từ American Type Culture Collection (Manassas, VA, USA). Các chủng có ký hiệu "DSM" có thể nhận được từ Deutschen Sammlung von Mikroorganismen und Zellkulturen (Bảo tàng giống chuẩn vi sinh vật và tế bào Đức) (DSMZ, Braunschweig, Germany). Các chủng có ký hiệu "NRRL" có thể nhận được từ Agricultural Research Service Patent Culture Collection (ARS, Peoria, Illinois, US). Các chủng có ký hiệu "FERM" có thể nhận được từ National Institute of Advanced Industrial Science and Technology (AIST Tsukuba Central 6, 1-1-1 Higashi, Tsukuba Ibaraki, Japan). Các chủng có ký hiệu "CGMCC" có thể nhận được từ China Genral Microbiological Culture Collection Center (CGMCC, Beijing, China).

Do đó, sáng chế cũng đề xuất phương pháp sản xuất lượng lớn axit L-amin, khác biệt ở chỗ, ít nhất một enzym theo sáng chế và/hoặc polynucleotit mã hoá enzym nêu trên và/hoặc hệ phân cắt glyxin theo sáng chế và/hoặc các polynucleotit mã hoá hệ nêu trên và/hoặc vi sinh vật tái tổ hợp theo sáng chế, tốt hơn nếu vi khuẩn tái tổ hợp theo sáng chế, cụ thể là vi khuẩn *Coryneform* tái tổ hợp theo sáng chế, đặc biệt tốt hơn nếu *Corynebacterium* tái tổ hợp theo sáng chế, đặc biệt là *Corynebacterium* thuộc các loài *C. humireducens* hoặc *C. glutamicum*, được sử dụng trong phương pháp này. Theo phương án ưu tiên của sáng chế, ít nhất một polynucleotit theo sáng chế được sử dụng trong trường hợp này dưới dạng được biểu hiện quá mức.

Trong trường hợp này, tốt hơn nếu sáng chế đề cập đến phương pháp sản suất với lượng lớn axit L-amin, khác biệt ở chỗ, hệ phân cắt glyxin chứa các enzym GcvP, GcvT và GcvH được sử dụng trong phương pháp này, trong đó hệ phân cắt glyxin

chứa ít nhất một enzym trong số các enzym GcvP, GcvT và GcvH theo sáng chế, và/hoặc các polynucleotit mã hoá các enzym GcvP, GcvT và GcvH của hệ phân cắt glyxin được sử dụng trong phương pháp này, trong đó các polynucleotit này chứa ít nhất một polynucleotit trong số các polynucleotit gcvP, gcvT và gcvH theo sáng chế, và/hoặc *Corynebacterium* tái tổ hợp được sử dụng, tốt hơn nếu thuộc các loài *C. humireducens* hoặc *C. glutamicum*, chứa ít nhất một enzym theo sáng chế, tốt hơn nếu tất cả ba enzym theo sáng chế, được chọn từ GcvP, GcvT và GcvH và/hoặc ít nhất một polynucleotit theo sáng chế, tốt hơn nếu tất cả ba polynucleotit theo sáng chế, được chọn từ gcvP, gcvT và gcvH.

Trong trường hợp này, đặc biệt tốt hơn nếu sáng chế đề xuất phương pháp sản xuất lượng lớn axit L-amin, khác biệt ở chỗ, hệ phân cắt glyxin được sử dụng trong phương pháp này, chứa các enzym GcvP, GcvT và GcvH theo sáng chế và/hoặc các polynucleotit mã hoá các enzym nêu trên và/hoặc *Corynebacterium* tái tổ hợp được sử dụng trong phương pháp này, tốt hơn nếu thuộc các loài *C. humireducens* hoặc *C. glutamicum*, chứa hệ phân cắt glyxin như vậy và/hoặc các polynucleotit mã hoá hệ nêu trên.

Thuật ngữ "axit L-amin" theo sáng chế được hiểu có nghĩa, cụ thể là, axit L-amin sinh protein.

Trong trường hợp này, tốt hơn nếu axit L-amin được chọn từ L-alanin, L-valin, axit L-amin thuộc họ glutamat, cụ thể là L-glutamat, L-glutamin, L-prolin và L-arginin và axit L-amin thuộc họ aspartat, cụ thể là L-aspartat, L-asparagin, L-methionin, L-lysin, L-isoleuxin và L-threonin, đặc biệt tốt hơn nếu được chọn từ L-alanin, L-valin, L-glutamat, L-methionin, L-lysin và L-threonin. Tốt hơn nếu axit L-amin là L-methionin.

Tốt hơn nếu, sự sản sinh lượng lớn các axit L-amin được thực hiện, theo sáng chế, ở C. humireducens hoặc C. glutamicum.

Tốt hơn nếu, các phương pháp theo sáng chế đặc trưng ở chỗ, chỉ lượng nhỏ glyxin có mặt dưới dạng sản phẩm phụ. Trong phương pháp theo sáng chế, tốt hơn nếu glyxin có mặt với lượng nhỏ hơn 0,2g/L, cụ thể là với lượng nhỏ hơn 0,1g/L, đặc biệt tốt hơn nếu với lượng nhỏ hơn 0,05g/L.

Thuật ngữ "sản sinh lượng lớn" hoặc "sự sản sinh lượng lớn" liên quan đến các axit L-amin được hiểu có nghĩa là, theo sáng chế, các vi sinh vật sản sinh các axit L-amin theo yêu cầu của chính chúng, có nhiều trong tế bào hoặc được tiết vào môi trường dinh dưỡng xung quanh mà trong đó chúng tích tụ. Trong trường hợp này, tốt hơn nếu các vi sinh vật có khả năng có nhiều hoặc tích tụ trong tế bào hoặc trong môi trường dinh dưỡng với lượng ≥ (ít nhất) 0,25g/L, ≥ 0,5g/L, ≥ 1,0g/L, ≥ 1,5g/L, ≥ 2,0g/L, ≥ 4g/L hoặc ≥ 10g/L axit L-amin thích hợp trong thời gian ≤ (nhiều nhất) 120 giờ, ≤ 96 giờ, ≤ 48 giờ, ≤ 36 giờ, ≤ 24 giờ hoặc ≤ 12 giờ.

Các vi sinh vật tái tổ hợp theo sáng chế, trong đó các polynucleotit theo sáng chế và/hoặc vectơ theo sáng chế đã được đưa vào, theo phương án ưu tiên, có khả năng sản sinh lượng lớn axit L-amin trước khi đưa các polynucleotit và/hoặc vectơ theo sáng chế vào. Tốt hơn nếu, các chủng ban đầu là các chủng mà được tạo ra bởi sự phát sinh đột biến và chọn lọc, bằng các kỹ thuật ADN tái tổ hợp hoặc bằng cách kết hợp cả hai phương pháp này.

Sẽ là hiển nhiên và không cần phải giải thích thêm nữa, vi sinh vật tái tổ hợp theo sáng chế do đó còn có thể được tạo ra, trong đó chủng thể dại, trong đó polynucleotit theo sáng chế và/hoặc vectơ theo sáng chế có mặt hoặc được đưa vào và các phương pháp kỹ thuật di truyền nữa thích hợp sau đó, khiến cho axit L-amin được sản sinh hoặc lượng sản sinh axit L-amin được gia tăng.

Bằng cách biểu hiện quá mức các polynucleotit hoặc các polypeptit thích hợp, sự sản sinh axit amin của các axit L-amin nhất định có thể được tác động theo cách tích cực.

Do đó, sáng chế cũng đề cập đến:

a) threonin dehydrataza (IlvA, EC 4.3.1.19) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.106 và các polynucleotit mã hoá nó,

b) tiểu đơn vị của axetolactat synthaza (IlvB) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.98 và các polynucleotit mã hoá nó,

c) isomeroreductaza (IlvC, EC 1.1.1.86) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.100 và các polynucleotit mã hoá nó,

d) axit dihydroxy dehydrataza (IlvD, EC 4.2.1.9) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.102 và các polynucleotit mã hoá nó,

e) transaminaza (IlvE, EC 2.6.1.42) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.104 và các polynucleotit mã hoá nó,

f) axetolactat synthaza (IlvH, EC 2.2.1.6) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.122 và các polynucleotit mã hoá nó,

g) 3-metyl-2-oxobutanoat hydroxymetyltransferaza (PanB, EC 2.1.2.11) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.118 và các polynucleotit mã hoá nó,

h) pantothenat synthaza (PanC, EC 6.3.2.1) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.120 và các polynucleotit mã hoá nó,

i) glutamat dehydrogenaza (Gdh) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.124 và các polynucleotit mã hoá nó,

j) glutamin synthetaza (glutamin synthetaza 1) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.126 và các polynucleotit mã hoá nó,

k) glutamin synthetaza (glutamin synthetaza 2) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.128 và các polynucleotit mã hoá nó,

l) glutamat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.130 và các polynucleotit mã hoá nó,

m) isoxitrat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.132 và các polynucleotit mã hoá nó,

n) aconitat hydraza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.134 và các polynucleotit mã hoá nó,

o) xitrat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.136 và các polynucleotit mã hoá nó,

p) aminopeptidaza C (PepC) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.138 và các polynucleotit mã hoá nó,

q) pyruvat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.140 và các polynucleotit mã hoá nó,

r) pyruvat kinaza (pyruvat kinaza 1) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.142 và các polynucleotit mã hoá nó,

s) pyruvat kinaza (pyruvat kinaza 2) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.144 và các polynucleotit mã hoá nó,

t) enolaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.146 và các polynucleotit mã hoá nó,

u) phosphoglyxerat mutaza phụ thuộc 2,3-bisphosphoglyxerat (GpmA) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.148 và các polynucleotit mã hoá nó,

v) phosphoglyxerat kinaza (Pgk) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.150 và các polynucleotit mã hoá nó,

w) glyxeraldehyt-3-phosphat dehydrogenaza (glyxerol-3-phosphat dehydrogenaza 1) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.152 và các polynucleotit mã hoá nó,

x) glyxeraldehyt-3-phosphat dehydrogenaza (glyxerol-3-phosphat dehydrogenaza 2) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.154 và các polynucleotit mã hoá nó,

y) triosephosphat isomeraza (TpiA) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.156 và các polynucleotit mã hoá nó,

z) fructoza bisphosphat aldolaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.158 và các polynucleotit mã hoá nó,

aa) 1-phosphofructokinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.160 và các polynucleotit mã hoá nó,

bb) 6-phosphofructokinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.162 và các polynucleotit mã hoá nó,

cc) homoserin kinaza (ThrB, EC 2.7.1.39) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.4 và các polynucleotit mã hoá nó,

dd) xystein synthaza (CBS, CysK) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.22 và các polynucleotit mã hoá nó,

ee) xystathionin beta-lyaza (AecD) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.26 và các polynucleotit mã hoá nó,

ff) aspartat semialdehyt dehydrogenaza (Asd, EC 1.2.1.11) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.28 và các polynucleotit mã hoá nó,

gg) tiểu đơn vị nhỏ hơn của protein vận chuyển đối với các axit amin mạch nhánh (BrnE) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.30 và các polynucleotit mã hoá nó,

hh) tiểu đơn vị lớn hơn của protein vận chuyển đối với các axit amin mạch nhánh (BrnF) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.32 và các polynucleotit mã hoá nó,

ii) serin axetyltransferaza (CysE) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.34 và các polynucleotit mã hoá nó,

jj) xystein synthaza (CysK) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.36 và các polynucleotit mã hoá nó,

kk) serin hydroxymetyltransferaza (GlyA) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.44 và các polynucleotit mã hoá nó,

ll) homoserin dehydrogenaza chịu tác động ngược tuỳ ý (Hom, EC 1.2.1.11) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.46 và các polynucleotit mã hoá nó,

mm) aspartat kinaza chịu tác động ngược tuỳ ý (LysC, EC 2.7.2.4) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.54 và các polynucleotit mã hoá nó,

nn) xystathionin gama-synthaza (MetB) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.56 và các polynucleotit mã hoá nó,

oo) 5,10-metylentetrahydrofolat reductaza (MetF) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.58 và các polynucleotit mã hoá nó,

pp) homoserin O-axetyltransferaza (MetX) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.60 và các polynucleotit mã hoá nó,

qq) O-axetylhomoserin lyaza (MetY) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.62 và các polynucleotit mã hoá nó,

rr) pyruvat carboxylaza chịu tác động ngược tuỳ ý (Pyc, EC 6.4.1.1) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.64 và các polynucleotit mã hoá nó,

ss) D-3-phosphoglyxerat dehydrogenaza chịu tác động ngược tuỳ ý (SerA) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.66 và các polynucleotit mã hoá nó,

tt) phosphoserin phosphataza (SerB) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.68 và các polynucleotit mã hoá nó,

uu) phosphoserin aminotransferaza (SerC) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.70 và các polynucleotit mã hoá nó,

vv) tiểu đơn vị của sulphat adenylyltransferaza (CysD) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.74 và các polynucleotit mã hoá nó,

ww) adenosin phosphosulphat reductaza (CysH) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.76 và các polynucleotit mã hoá nó,

xx) sulphit reductaza (CysI) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.78 và các polynucleotit mã hoá nó,

yy) chuỗi beta glutamat synthaza phụ thuộc NADPH (CysJ) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.80 và các polynucleotit mã hoá nó,

zz) tiểu đơn vị lớn của sulphat adenylyltransferaza (CysN) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.82 và các polynucleotit mã hoá nó,

aaa) xystathionin beta-synthaza (CysY) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.84 và các polynucleotit mã hoá nó,

bbb) protein vận chuyển sulphat (CysZ) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.86 và các polynucleotit mã hoá nó,

ccc) 5-metyltetrahydropteroyltriglutamat-homoxystein metyltransferaza (MetE) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.88 và các polynucleotit mã hoá nó,

ddd) peptidyl-ARN vận chuyển hydrolaza 1 (PtH1) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.90 và các polynucleotit mã hoá nó,

eee) peptidyl-ARN vận chuyển hydrolaza 2 (PtH2) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.92 và các polynucleotit mã hoá nó,

fff) diaminopimelat dehydrogenaza (Ddh, EC 1.4.1.16) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.202 và các polynucleotit mã hoá nó,

ggg) diaminopimelat decarboxylaza (LysA, EC 4.1.1.20) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.164 và các polynucleotit mã hoá nó,

hhh) aspartat aminotransferaza (AaT, EC 2.6.1.1) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.166 và các polynucleotit mã hoá nó,

iii) đoạn xuất khẩu L-lysin (LysE, permeaza giải phóng lysin) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.168 và các polynucleotit mã hoá nó,

jjj) dihydropicolinat reductaza (DapB, EC 1.3.1.26) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.170 và các polynucleotit mã hoá nó,

kkk) glucoza-6-phosphat dehydrogenaza (EC 1.1.1.49) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.172 và các polynucleotit mã hoá nó,

lll) tiểu đơn vị Zwf của glucoza-6-phosphat dehydrogenaza (Zwf, EC 1.1.1.49) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.186 và các polynucleotit mã hoá nó,

mmm) tiểu đơn vị OpcA của glucoza-6-phosphat dehydrogenaza (OpcA, EC 1.1.1.49) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.188 và các polynucleotit mã hoá nó,

nnn) dehydrogenaza của axit phosphogluconic (Gnd, EC 1.1.1.44) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.174 và các polynucleotit mã hoá nó.

Sáng chế cũng đề xuất các vectơ chứa các polynucleotit nêu trên và các vi sinh vật tái tổ hợp chứa các enzym và/hoặc polynucleotit và/hoặc các vectơ nêu trên. Theo phương án ưu tiên, polypeptit thích hợp và/hoặc polynucleotit có mặt trong trường hợp này trong vi sinh vật dưới dạng được biểu hiện quá mức. Tốt hơn nếu vi sinh vật tái tổ hợp trong trường hợp này là vi khuẩn *Coryneform*, đặc biệt là *Corynebacteria*, cụ thể là các vi khuẩn thuộc các loài *C. humireducens* hoặc *C. glutamicum*.

Do đó, sáng chế cũng đề xuất phương pháp sản xuất lượng lớn axit L-amin, tốt hơn nếu được chọn từ L-alanin, L-valin, các axit L-amin thuộc họ glutamat, cụ thể là L-glutamat, L-glutamin, L-prolin và L-arginin, và axit L-amin thuộc họ aspartat, cụ thể là L-aspartat, L-asparagin, L-methionin, L-lysin, L-isoleuxin và L-threonin, đặc biệt tốt hơn nếu được chọn từ L-alanin, L-valin, L-glutamat, L-methionin, L-lysin và L-threonin, đặc biệt là để sản sinh lượng lớn L-methionin, trong đó ít nhất một, tốt hơn nếu ít nhất bằng hai, ba hoặc bốn polynucleotit này có mặt dưới dạng được biểu hiện quá mức, trong đó tốt hơn nếu phương pháp được thực hiện trong *Corynebacteria*, cụ thể là vi khuẩn thuộc các loài *C. humireducens* hoặc *C. glutamicum*.

Sáng chế cũng đề xuất các polynucleotit khác thu được từ *C. humireducens* và các polypeptit được mã hoá bởi các polynucleotit này. Bằng cách khử hoạt tính hoặc giảm hoạt lực của các polynucleotit thích hợp hoặc các polypeptit, sự sản sinh axit amin của các axit L-amin nhất định có thể được tác động theo cách tích cực.

Do đó, sáng chế cũng đề cập đến các polypeptit được chọn từ danh mục sau:

a) threonin synthaza (ThrC, EC 4.2.3.1) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.108 và các polynucleotit mã hoá nó,

b) isopropylmalat synthaza (LeuA, EC 2.3.3.13) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.110 và các polynucleotit mã hoá nó,

c) isopropylmalat dehydrogenaza (LeuB, EC 1.1.1.85) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.112 và các polynucleotit mã hoá nó,

d) các tiểu đơn vị của isopropylmalat isomeraza (LeuCD, EC 4.2.1.33) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, với các trình tự nêu trong SEQ ID NO.114 hoặc SEQ ID NO.116 và các polynucleotit mã hoá nó,

e) các tiểu đơn vị của sucxinyl-CoA ligaza (SucCD, EC 6.2.1.5), mỗi tiểu đơn vị có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, với các trình tự nêu trong SEQ ID NO.198 hoặc SEQ ID NO.200 và các polynucleotit mã hoá nó,

f) miền gắn kết ADN thuộc loại HTH tetR (McbR) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.2 và các polynucleotit mã hoá nó,

g) homoserin kinaza (ThrB, EC 2.7.1.39) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.4 và các polynucleotit mã hoá nó,

h) glucoza-6-phosphat isomeraza (Pgi, EC 5.3.1.9) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.6 và các polynucleotit mã hoá nó,

i) phosphoenolpyruvat carboxykinaza (Pck, EC 4.1.1.32) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.8 và các polynucleotit mã hoá nó,

j) lipoprotein gắn kết D-methionin (MetQ) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.10 và các polynucleotit mã hoá nó,

k) protein vận chuyển methionin (MetP) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.12 và các polynucleotit mã hoá nó,

l) protein vận chuyển methionin phụ thuộc ATP (MetN) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.14 và các polynucleotit mã hoá nó,

m) S-adenosylmethionin synthaza (MetK) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.16 và các polynucleotit mã hoá nó,

n) permeaza hệ nhập khẩu methionin (MetI) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.18 và các polynucleotit mã hoá nó,

o) 4-hydroxy-tetrahydrodipicolinat synthaza (DapA, EC 4.3.3.7) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.20 và các polynucleotit mã hoá nó,

p) carboxylat-amin ligaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.24 và các polynucleotit mã hoá nó,

q) malat quinon oxidoreductaza (Mqo, EC 1.1.99.16) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.176 và các polynucleotit mã hoá nó,

r) tiểu đơn vị E1p của phức pyruvat dehydrogenaza (AceE, EC 1.2.4.1) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.178 và các polynucleotit mã hoá nó,

s) xitrat synthaza (GltA, EC 4.1.3.7) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.180 và các polynucleotit mã hoá nó,

t) malat dehydrogenaza (Mdh, EC 1.1.1.37) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.182 và các polynucleotit mã hoá nó,

u) UDP-N-axetylmuramoylalanyl-D-glutamat-2,6-diaminopimelat ligaza (MurE, EC 6.3.2.13) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt

hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.184, và các polynucleotit mã hoá nó,

Sáng chế cũng đề xuất các vectơ chứa các polynucleotit nêu trên và các vi sinh vật tái tổ hợp chứa các enzym và/hoặc các polynucleotit và/hoặc vectơ được nêu trên. Theo phương án ưu tiên, polypeptit thích hợp và/hoặc polynucleotit có mặt trong trường hợp này trong vi sinh vật dưới dạng đã được khử hoạt tính hoặc giảm nồng độ hoặc hoạt tính. Tốt hơn nếu, vi sinh vật tái tổ hợp trong trường hợp này là vi khuẩn *Coryneform*, đặc biệt là *Corynebacteria*, cụ thể là các vi khuẩn thuộc các loài *C. humireducens* hoặc *C. glutamicum*, đặc biệt là thuộc các loài *C. humireducens*.

Theo phương án ưu tiên nữa của sáng chế, các vi sinh vật hoặc vi khuẩn theo sáng chế, cụ thể là *Corynebacteria* theo sáng chế, đặc biệt là *Corynebacteria* theo sáng chế thuộc các loài *C. humireducens* hoặc *C. glutamicum*, cụ thể là các chủng sản sinh lượng lớn L-methionin theo sáng chế, ngoài các hệ theo sáng chế, tốt hơn nếu hệ phân cắt glyxin được biểu hiện quá mức hoặc các polynucleotit mã hoá hệ này, có ít nhất một, tốt hơn nếu ít nhất hai hoặc ba, đặc biệt tốt hơn nếu ít nhất bốn hoặc năm polynucleotit trong số các polynucleotit sau:

a) polynucleotit giảm hoạt lực (mcbR), mã hoá miền gắn kết ADN thuộc loại HTH tetR (McbR), tốt hơn nếu miền gắn kết ADN có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.2,

b) polynucleotit giảm hoạt lực (gen thrB), mã hoá homoserin kinaza (ThrB, EC 2.7.1.39), tốt hơn nếu homoserin kinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.4,

c) polynucleotit giảm hoạt lực (pgi), mã hoá glucoza-6-phosphat isomeraza (Pgi, EC 5.3.1.9), tốt hơn nếu glucoza-6-phosphat isomeraza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.6,

d) polynucleotit giảm hoạt lực (pck), mã hoá phosphoenolpyruvat carboxykinaza (Pck, EC 4.1.1.32), tốt hơn nếu phosphoenolpyruvat carboxykinaza có

độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.8,

e) polynucleotit giảm hoạt lực (metQ), mã hoá lipoprotein gắn kết D-methionin (MetQ), tốt hơn nếu lipoprotein gắn kết D-methionin có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.10,

f) polynucleotit giảm hoạt lực (metP), mã hoá protein vận chuyển methionin (MetP), tốt hơn nếu protein vận chuyển methionin có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.12,

g) polynucleotit giảm hoạt lực (metN), mã hoá protein vận chuyển methionin phụ thuộc ATP (MetN), tốt hơn nếu protein vận chuyển methionin phụ thuộc ATP có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.14,

h) polynucleotit giảm hoạt lực (metK), mã hoá S-adenosylmethionin synthaza (MetK), tốt hơn nếu S-adenosylmethionin synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.16,

i) polynucleotit giảm hoạt lực (metI), mã hoá permeaza hệ nhập khẩu methionin (MetI), tốt hơn nếu permeaza hệ nhập khẩu methionin có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.18,

j) polynucleotit giảm hoạt lực (dapA), mã hoá 4-hydroxy-tetrahydrodipicolinat synthaza (DapA), tốt hơn nếu 4-hydroxy-tetrahydrodipicolinat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.20,

k) polynucleotit được biểu hiện quá mức (CBS), mã hoá xystein synthaza (CBS), tốt hơn nếu xystein synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.22,

l) polynucleotit giảm hoạt lực, mã hoá đoạn tương đồng cg3031, tốt hơn nếu đoạn tương đồng cg3031 có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.24,

m) polynucleotit được biểu hiện quá mức (aecD), mã hoá xystathionin beta-lyaza (AecD), tốt hơn nếu xystathionin beta-lyaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.26,

n) polynucleotit được biểu hiện quá mức (asd), mã hoá aspartat semialdehyt dehydrogenaza (Asd), tốt hơn nếu aspartat semialdehyt dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.28,

o) polynucleotit được biểu hiện quá mức (metH), mã hoá 5-metyltetrahydrofolat homoxystein metyltransferaza (MetH, EC 2.1.1.13),

p) polynucleotit được biểu hiện quá mức (brnE), mã hoá tiểu đơn vị nhỏ hơn của protein vận chuyển đối với các axit amin mạch nhánh (BrnE), tốt hơn nếu tiểu đơn vị có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.30,

q) polynucleotit được biểu hiện quá mức (brnF), mã hoá tiểu đơn vị lớn hơn của protein vận chuyển đối với các axit amin mạch nhánh (BrnF), tốt hơn nếu tiểu đơn vị có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.32,

r) polynucleotit được biểu hiện quá mức (cysE), mã hoá serin axetyltransferaza (CysE), tốt hơn nếu serin axetyltransferaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.34,

s) polynucleotit được biểu hiện quá mức (cysK), mã hoá xystein synthaza (CysK), tốt hơn nếu xystein synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.36,

t) polynucleotit được biểu hiện quá mức (glyA), mã hoá serin hydroxymetyltransferaza (GlyA), tốt hơn nếu serin hydroxymetyltransferaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.44,

u) polynucleotit được biểu hiện quá mức (hom), mã hoá homoserin dehydrogenaza chịu tác động ngược tuỳ ý (Hom), tốt hơn nếu homoserin dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.46,

v) polynucleotit được biểu hiện quá mức (lysC), mã hoá aspartat kinaza chịu tác động ngược tuỳ ý (LysC), tốt hơn nếu aspartat kinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.54,

w) polynucleotit được biểu hiện quá mức (metB), mã hoá xystathionin gama-synthaza (MetB), tốt hơn nếu xystathionin gama-synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.56,

x) polynucleotit được biểu hiện quá mức (metF), mã hoá 5,10-metylentetrahydrofolat reductaza (MetF), tốt hơn nếu 5,10-metylentetrahydrofolat reductaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.58,

y) polynucleotit được biểu hiện quá mức (metX), mã hoá homoserin O-axetyltransferaza (MetX), tốt hơn nếu homoserin O-axetyltransferaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.60,

z) polynucleotit được biểu hiện quá mức (metY), mã hoá O-axetylhomoserin lyaza (MetY), tốt hơn nếu O-axetylhomoserin lyaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.62,

aa) polynucleotit được biểu hiện quá mức (pyc), mã hoá pyruvat carboxylaza (Pyc), tốt hơn nếu pyruvat carboxylaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.64,

bb) polynucleotit được biểu hiện quá mức (serA), mã hoá D-3-phosphoglyxerat dehydrogenaza chịu tác động ngược tuỳ ý (SerA), tốt hơn nếu D-3-phosphoglyxerat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.66,

cc) polynucleotit được biểu hiện quá mức (serB), mã hoá phosphoserin phosphataza (SerB), tốt hơn nếu phosphoserin phosphataza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.68,

dd) polynucleotit được biểu hiện quá mức (serC), mã hoá phosphoserin aminotransferaza (SerC), tốt hơn nếu phosphoserin aminotransferaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.70,

ee) polynucleotit được biểu hiện quá mức (ald), mã hoá alanin dehydrogenaza (Ald), tốt hơn nếu alanin dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.72,

ff) polynucleotit được biểu hiện quá mức (cysD), mã hoá tiểu đơn vị của sulphat adenylyltransferaza (CysD), tốt hơn nếu tiểu đơn vị có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.74,

gg) polynucleotit được biểu hiện quá mức (cysH), mã hoá adenosin phosphosulphat reductaza (CysH), tốt hơn nếu adenosin phosphosulphat reductaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.76,

hh) polynucleotit được biểu hiện quá mức (cysI), mã hoá sulphit reductaza (CysI), tốt hơn nếu sulphit reductaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.78,

ii) polynucleotit được biểu hiện quá mức (cysJ), mã hoá (CysJ), tốt hơn nếu (CysJ) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.80,

jj) polynucleotit được biểu hiện quá mức (cysN), mã hoá tiểu đơn vị của sulphat adenylyltransferaza (CysN), tốt hơn nếu tiểu đơn vị có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.82,

kk) polynucleotit được biểu hiện quá mức (cysY), mã hoá xystathionin beta-synthaza (CysY), tốt hơn nếu xystathionin beta-synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.84,

ll) polynucleotit được biểu hiện quá mức (cysZ), mã hoá protein vận chuyển sulphat giả định (CysZ), tốt hơn nếu protein vận chuyển sulphat có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.86,

mm) polynucleotit được biểu hiện quá mức (metE), mã hoá 5-metyltetrahydropteroyltriglutamat-homoxystein metyltransferaza (MetE), tốt hơn nếu protein có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.88,

nn) polynucleotit được biểu hiện quá mức (ptH1), mã hoá peptidyl-ARN vận chuyển hydrolaza 1 (PtH1), tốt hơn nếu peptidyl-ARN vận chuyển hydrolaza 1 có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.90,

oo) polynucleotit được biểu hiện quá mức (ptH2), mã hoá peptidyl-ARN vận chuyển hydrolaza 2 (PtH2), tốt hơn nếu peptidyl-ARN vận chuyển hydrolaza 2 có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.92.

Sáng chế cũng đề xuất phương pháp sản xuất lượng lớn axit L-amin, cụ thể là L-methionin, trong đó vi sinh vật hoặc vi khuẩn nêu trên được sử dụng.

Theo phương án ưu tiên khác, các vi sinh vật hoặc vi khuẩn theo sáng chế, cụ thể là Corynebacteria theo sáng chế, đặc biệt là Corynebacteria theo sáng chế thuộc các loài C. humireducens hoặc C. glutamicum, cụ thể là chủng sản sinh lượng lớn L-valin theo sáng chế, ngoài các hệ theo sáng chế, tốt hơn nếu hệ phân cắt glyxin được biểu hiện quá mức hoặc các polynucleotit mã hoá hệ này, có ít nhất một, tốt hơn nếu ít nhất bằng 2 hoặc 3, đặc biệt tốt hơn nếu ít nhất bằng 4 hoặc 5 polynucleotit trong số các polynucleotit sau đây:

a) polynucleotit được biểu hiện quá mức (gen ilvA), mã hoá threonin dehydrataza (IIvA EC 4.3.1.19), tốt hơn nếu threonin dehydrataza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.106,

b) polynucleotit được biểu hiện quá mức (gen ilvB), mã hoá tiểu đơn vị của axetolactat synthaza (IIvB), tốt hơn nếu tiểu đơn vị của axetolactat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.98,

c) polynucleotit được biểu hiện quá mức (gen ilvN), mã hoá tiểu đơn vị chịu tác động ngược tuỳ ý của axetolactat synthaza (IlvN),

d) polynucleotit được biểu hiện quá mức (gen ilvC), mã hoá isomeroreductaza (IIvC, EC 1.1.1.86), tốt hơn nếu isomeroreductaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.100,

e) polynucleotit được biểu hiện quá mức (gen ilvD), mã hoá axit dihydroxy dehydrataza (IIvD, EC 4.2.1.9), tốt hơn nếu axit dihydroxy dehydrataza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.102,

f) polynucleotit được biểu hiện quá mức (gen ilvE), mã hoá transaminaza (IIvE, EC 2.6.1.42), tốt hơn nếu transaminaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.104,

g) polynucleotit được biểu hiện quá mức (gen ilvH), mã hoá axetolactat synthaza (IIvH, EC 2.2.1.6), tốt hơn nếu axetolactat synthaza có độ tương đồng trình

tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.122,

h) polynucleotit giảm hoạt lực (gen thrB), mã hoá homoserin kinaza (ThrB, EC 2.7.1.39), tốt hơn nếu homoserin kinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.4,

i) polynucleotit giảm hoạt lực (gen thrC), mã hoá threonin synthaza (ThrC, EC 4.2.3.1), tốt hơn nếu threonin synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.108,

j) polynucleotit được biểu hiện quá mức (gen hom), mã hoá homoserin dehydrogenaza chịu tác động ngược tuỳ ý (Hom, EC 1.2.1.11), tốt hơn nếu homoserin dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.46,

k) polynucleotit giảm hoạt lực (gen leuA), mã hoá isopropylmalat synthaza chịu tác động ngược (LeuA, EC 2.3.3.13), tốt hơn nếu isopropylmalat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.110,

l) polynucleotit giảm hoạt lực (gen leuB), mã hoá isopropylmalat dehydrogenaza (LeuB, EC 1.1.1.85), tốt hơn nếu isopropylmalat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.112,

m) polynucleotit giảm hoạt lực (gen leuCD), mã hoá các tiểu đơn vị của isopropylmalat isomeraza (LeuCD, EC 4.2.1.33), tốt hơn nếu các tiểu đơn vị của isopropylmalat isomeraza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, với các trình tự nêu trong SEQ ID NO.114 và SEQ ID NO.116,

n) polynucleotit được biểu hiện quá mức (gen panB), mã hoá 3-metyl-2-oxobutanoat hydroxymetyltransferaza (PanB, EC 2.1.2.11), tốt hơn nếu 3-metyl-2-oxobutanoat hydroxymetyltransferaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.118,

o) polynucleotit được biểu hiện quá mức (gen panC), mã hoá pantothenat synthaza (PanC, EC 6.3.2.1), tốt hơn nếu pantothenat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.120.

Do đó, sáng chế cũng đề xuất phương pháp sản xuất lượng lớn axit L-amin, cụ thể là L-valin, trong đó vi sinh vật hoặc vi khuẩn nêu trên được sử dụng.

Theo phương án ưu tiên khác, các vi sinh vật hoặc vi khuẩn theo sáng chế, cụ thể là *Corynebacteria* theo sáng chế, đặc biệt là *Corynebacteria* theo sáng chế thuộc các loài *C. humireducens* hoặc *C. glutamicum*, cụ thể là các chủng sản sinh lượng lớn L-glutamat theo sáng chế, ngoài các hệ theo sáng chế, tốt hơn nếu hệ phân cắt glyxin được biểu hiện quá mức hoặc các polynucleotit mã hoá hệ này, có ít nhất một, tốt hơn nếu ít nhất hai hoặc ba, đặc biệt tốt hơn nếu ít nhất bốn hoặc năm polynucleotit trong số các polynucleotit sau đây:

a) polynucleotit được biểu hiện quá mức (gdh), mã hoá glutamat dehydrogenaza (Gdh), tốt hơn nếu glutamat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.124,

b) polynucleotit được biểu hiện quá mức, mã hoá glutamin synthetaza (glutamin synthetaza 1), tốt hơn nếu glutamin synthetaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.126,

c) polynucleotit được biểu hiện quá mức, mã hoá glutamin synthetaza (glutamin synthetaza 2), tốt hơn nếu glutamin synthetaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.128,

d) polynucleotit được biểu hiện quá mức, mã hoá glutamat synthaza, tốt hơn nếu glutamat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.130,

e) polynucleotit được biểu hiện quá mức, mã hoá isoxitrat dehydrogenaza, tốt hơn nếu isoxitrat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.132,

f) polynucleotit được biểu hiện quá mức, mã hoá aconitat hydraza, tốt hơn nếu aconitat hydraza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.134,

g) polynucleotit được biểu hiện quá mức, mã hoá xitrat synthaza, tốt hơn nếu xitrat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.136,

h) polynucleotit được biểu hiện quá mức (pepC), mã hoá aminopeptidaza C (PepC), tốt hơn nếu aminopeptidaza C có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.138,

i) polynucleotit được biểu hiện quá mức, mã hoá pyruvat dehydrogenaza, tốt hơn nếu pyruvat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.140,

j) polynucleotit được biểu hiện quá mức, mã hoá pyruvat kinaza (pyruvat kinaza 1), tốt hơn nếu pyruvat kinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.142,

k) polynucleotit được biểu hiện quá mức, mã hoá pyruvat kinaza (pyruvat kinaza 2), tốt hơn nếu pyruvat kinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.144,

l) polynucleotit được biểu hiện quá mức, mã hoá enolaza, tốt hơn nếu enolaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.146,

m) polynucleotit được biểu hiện quá mức (gpmA), mã hoá phosphoglyxerat mutaza phụ thuộc 2,3-bisphosphoglyxerat (GpmA), tốt hơn nếu phosphoglyxerat mutaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.148,

n) polynucleotit được biểu hiện quá mức (pgk), mã hoá phosphoglyxerat kinaza (Pgk), tốt hơn nếu phosphoglyxerat kinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.150,

o) polynucleotit được biểu hiện quá mức, mã hoá glyxeraldehyt-3-phosphat dehydrogenaza (glyxerol-3-phosphat dehydrogenaza 1), tốt hơn nếu glyxeraldehyt-3-phosphat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.152,

p) polynucleotit được biểu hiện quá mức, mã hoá glyxeraldehyt-3-phosphat dehydrogenaza (glyxerol-3-phosphat dehydrogenaza 2), tốt hơn nếu glyxeraldehyt-3-phosphat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.154,

q) polynucleotit được biểu hiện quá mức (tpiA), mã hoá triosephosphat isomeraza (TpiA), tốt hơn nếu triosephosphat isomeraza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.156,

r) polynucleotit được biểu hiện quá mức, mã hoá fructoza bisphosphat aldolaza, tốt hơn nếu fructoza bisphosphat aldolaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.158,

s) polynucleotit được biểu hiện quá mức, mã hoá 1-phosphofructokinaza, tốt hơn nếu 1-phosphofructokinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.160,

t) polynucleotit được biểu hiện quá mức, mã hoá 6-phosphofructokinaza, tốt hơn nếu 6-phosphofructokinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.162,

u) polynucleotit được biểu hiện quá mức (pgi), mã hoá glucoza-6-phosphat isomeraza, tốt hơn nếu glucoza-6-phosphat isomeraza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.6,

v) polynucleotit giảm hoạt lực (sucCD), mã hoá các tiểu đơn vị của sucxinyl-CoA ligaza (SucCD, EC 6.2.1.5), tốt hơn nếu các tiểu đơn vị của sucxinyl-CoA ligaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, với các trình tự nêu trong SEQ ID NO.198 hoặc SEQ ID NO.200.

Do đó, sáng chế cũng đề xuất phương pháp sản xuất lượng lớn axit L-amin, cụ thể là L-glutamat, trong đó vi sinh vật hoặc vi khuẩn nêu trên được sử dụng.

Theo phương án ưu tiên khác, các vi sinh vật hoặc vi khuẩn theo sáng chế, cụ thể là *Corynebacteria* theo sáng chế, đặc biệt là *Corynebacteria* theo sáng chế thuộc các loài *C. humireducens* hoặc *C. glutamicum*, cụ thể là các chủng sản sinh lượng lớn L-alanin theo sáng chế, ngoài các hệ theo sáng chế, tốt hơn nếu hệ phân cắt glyxin được biểu hiện quá mức hoặc các polynucleotit mã hoá hệ này, có ít nhất một, tốt hơn nếu ít nhất hai hoặc ba, đặc biệt tốt hơn nếu ít nhất bốn hoặc năm polynucleotit trong số các polynucleotit sau đây:

a) polynucleotit được biểu hiện quá mức (alaD), mã hoá alanin dehydrogenaza (AlaD), tốt hơn nếu alanin dehydrogenaza từ *Corynebacteria*,

b) polynucleotit được biểu hiện quá mức (gapA), mã hoá glyxeraldehyt-3-phosphat dehydrogenaza (GapA), tốt hơn nếu glyxeraldehyt-3-phosphat dehydrogenaza từ *Corynebacteria*,

c) polynucleotit được khử hoạt tính hoặc giảm nồng độ hoặc hoạt tính (IdhA), mã hoá L-lactat dehydrogenaza (LdhA), tốt hơn nếu L-lactat dehydrogenaza từ *Corynebacteria*,

d) polynucleotit được khử hoạt tính hoặc giảm nồng độ hoặc hoạt tính (ppc), mã hoá phosphoenolpyruvat carboxylaza (Ppc), tốt hơn nếu phosphoenolpyruvat carboxylaza từ *Corynebacteria*,

e) polynucleotit được khử hoạt tính hoặc giảm nồng độ hoặc hoạt tính (alr), mã hoá alanin racemaza (Alr), tốt hơn nếu alanin racemaza từ *Corynebacteria*.

Do đó, sáng chế cũng đề xuất phương pháp sản xuất lượng lớn axit L-amin, cụ thể là L-alanin, trong đó vi sinh vật hoặc vi khuẩn nêu trên được sử dụng.

Theo phương án ưu tiên khác, các vi sinh vật hoặc vi khuẩn theo sáng chế, cụ thể là *Corynebacteria* theo sáng chế, đặc biệt là *Corynebacteria* theo sáng chế thuộc các loài *C. humireducens* hoặc *C. glutamicum*, cụ thể là chủng sản sinh lượng lớn L-lysin theo sáng chế, ngoài các hệ theo sáng chế, tốt hơn nếu hệ phân cắt glyxin được biểu hiện quá mức hoặc các polynucleotit mã hoá hệ này, có ít nhất một, tốt hơn nếu ít nhất hai hoặc ba, đặc biệt tốt hơn nếu ít nhất bốn hoặc năm polynucleotit trong số các polynucleotit sau đây:

a) polynucleotit được biểu hiện quá mức (gen dapA), mã hoá dihydrodipicolinat synthaza (DapA, EC 4.2.1.52), tốt hơn nếu dihydrodipicolinat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.20,

b) polynucleotit được biểu hiện quá mức (lysC), tốt hơn nếu mã hoá aspartat kinaza chịu tác động ngược (LysC, EC 2.7.2.4), tốt hơn nếu aspartat kinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.54,

c) polynucleotit được biểu hiện quá mức (ddh), mã hoá diaminopimelat dehydrogenaza (Ddh, EC 1.4.1.16), tốt hơn nếu diaminopimelat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.202,

d) polynucleotit được biểu hiện quá mức (gen asd), mã hoá aspartat semialdehyt dehydrogenaza (Asd, EC 1.2.1.11), tốt hơn nếu aspartat semialdehyt dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.28,

e) polynucleotit được biểu hiện quá mức (gen lysA), mã hoá diaminopimelat decarboxylaza (LysA, EC 4.1.1.20), tốt hơn nếu diaminopimelat decarboxylaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.164,

f) polynucleotit được biểu hiện quá mức (gen aat), mã hoá aspartat aminotransferaza (AaT, EC 2.6.1.1), tốt hơn nếu aspartat aminotransferaza có độ

tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.166,

g) polynucleotit được biểu hiện quá mức (gen lysE), mã hoá đoạn xuất khẩn L-lysin (LysE, permeaza bơm thoát lysin), tốt hơn nếu đoạn xuất khẩu L-lysin có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.168,

h) polynucleotit được biểu hiện quá mức (gen pyc), mã hoá pyruvat carboxylaza (Pyc, EC 6.4.1.1), tốt hơn nếu pyruvat carboxylaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.64,

i) polynucleotit được biểu hiện quá mức (gen dapF), mã hoá diaminopimelat epimeraza (DapF, EC 5.1.1.7),

j) polynucleotit được biểu hiện quá mức (gen dapB), mã hoá dihydropicolinat reductaza (DapB, EC 1.3.1.26), tốt hơn nếu dihydropicolinat reductaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.172,

k) polynucleotit được biểu hiện quá mức, mã hoá glucoza-6-phosphat dehydrogenaza (EC 1.1.1.49), tốt hơn nếu glucoza-6-phosphat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.174,

l) polynucleotit được biểu hiện quá mức (gen zwf), mã hoá tiểu đơn vị Zwf của glucoza-6-phosphat dehydrogenaza (Zwf, EC 1.1.1.49), tốt hơn nếu tiểu đơn vị Zwf có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.188,

m) polynucleotit được biểu hiện quá mức (gen opcA), mã hoá tiểu đơn vị OpcA của glucoza-6-phosphat dehydrogenaza (OpcA, EC 1.1.1.49), tốt hơn nếu tiểu đơn vị OpcA có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.190,

n) polynucleotit được biểu hiện quá mức (gen gnd), mã hoá dehydrogenaza của axit phosphogluconic (Gnd, EC 1.1.1.44), tốt hơn nếu dehydrogenaza của axit phosphogluconic có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.176,

o) polynucleotit được khử hoạt tính hoặc giảm nồng độ hoặc hoạt tính (mqo), mã hoá malat quinon oxidoreductaza (Mqo, EC 1.1.99.16), tốt hơn nếu malat quinon oxidoreductaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.178,

p) polynucleotit được khử hoạt tính hoặc giảm nồng độ hoặc hoạt tính (aceE), mã hoá tiểu đơn vị E1p của phức pyruvat dehydrogenaza (AceE, EC 1.2.4.1), tốt hơn nếu tiểu đơn vị E1p có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.180,

q) polynucleotit được khử hoạt tính hoặc giảm nồng độ hoặc hoạt tính (gltA), mã hoá xitrat synthaza (GltA, EC 4.1.3.7), tốt hơn nếu xitrat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.182,

r) polynucleotit được khử hoạt tính hoặc giảm nồng độ hoặc hoạt tính (mdh), mã hoá malat dehydrogenaza (Mdh, EC 1.1.1.37), tốt hơn nếu malat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.184,

s) polynucleotit được khử hoạt tính hoặc giảm nồng độ hoặc hoạt tính (murE), mã hoá UDP-N-axetylmuramoylalanyl-D-glutamat-2,6-diaminopimelat ligaza (MurE, EC 6.3.2.13), tốt hơn nếu enzym có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.186.

Do đó, sáng chế cũng đề xuất phương pháp sản xuất lượng lớn axit L-amin, cụ thể là L-lysin, trong đó vi sinh vật hoặc vi khuẩn nêu trên được sử dụng.

Tốt hơn nếu, các polynucleotit và polypeptit được sử dụng hoặc để được sử dụng trong phương pháp theo sáng chế nêu trên có nguồn gốc từ *Corynebacteria*, đặc biệt là từ *C. glutamicum* hoặc *C. humireducens*, đặc biệt tốt hơn nếu từ *C. humireducens*.

Thuật ngữ "sự biểu hiện quá mức" theo sáng chế thường được hiểu có nghĩa là sự gia tăng nồng độ nội bào hoặc hoạt tính của axit ribonucleic, protein (polypeptit) hoặc enzym, được mã hoá bởi ADN tương ứng, ở vi sinh vật, so với chủng ban đầu (chủng gốc) hoặc chủng thể dại. Chủng ban đầu (chủng gốc) có nghĩa là chủng mà trong đó phương pháp tạo ra sự biểu hiện quá mức được thực hiện.

Sự gia tăng về nồng độ hoặc hoạt tính có thể đạt được, ví dụ bằng cách gia tăng số lượng bản sao của các polynucleotit mã hoá tương ứng, theo nhiễm sắc thể hoặc ngoài nhiễm sắc thể, ít nhất một bản sao.

Phương pháp phổ biến để gia tăng số lượng bản sao bao gồm việc đưa polynucleotit mã hoá tương ứng vào vectơ, tốt hơn nếu plasmit, được tái bản từ vi sinh vật, cụ thể là vi khuẩn Coryneform. Hơn nữa, gen nhảy, gen cài nhập (gen IS) hoặc các thể thực khuẩn có thể được sử dụng làm các vectơ. Nhiều vectơ thích hợp được mô tả trong lĩnh vực này.

Phương pháp phổ biến khác để đạt được sự biểu hiện quá mức là phương pháp khuếch đại gen nhiễm sắc thể. Trong phương pháp này, ít nhất một bản sao bổ sung của polynucleotit quan tâm được cài vào nhiễm sắc thể của vi khuẩn Coryneform. Các phương pháp khuếch đại như vậy được mô tả, ví dụ trong WO03/014330 hoặc WO03/040373.

Phương pháp khác để đạt được sự biểu hiện quá mức bao gồm việc liên kết gen tương ứng hoặc alen theo chức năng (liên kết điều khiển) với vùng khởi đầu hoặc cat-xet biểu hiện. Các vùng khởi đầu thích hợp dùng cho Corynebacterium glutamicum được mô tả, ví dụ trên Fig.1 của bài báo đánh giá của Patek et al. (Journal of Biotechnology 104(1-3), 311-323 (2003)) và trong các bài báo đánh giá toàn diện như "*Handbook of Corynebacterium glutamicum*" (Eds.: Lothar Eggeling and Michael Bott, CRC Press, Boca Raton, US (2005)) hoặc cuốn sách "Corynebacteria, Genomics and Molecular Biology" (Ed.: Andreas Burkovski, Caister Academic Press, Norfolk, UK (2008)). Theo cùng cách này, các biến thể của vùng khởi đầu dapA, vùng khởi đầu A25 ví dụ, được mô tả trong bài báo Vasicova et al. (Journal of Bacteriology 181, 6188-6191 (1999)), có thể được sử dụng. Hơn nữa, vùng khởi đầu có khoảng trống của *Corynebacterium* glutamicum (EP 06007373) có thể được sử dụng. Cuối cùng,

các vùng khởi đầu T3, T7, SP6, M13, lac, tac và trc đã biết, được mô tả bởi Amann et al. (Gen 69(2), 301-315 (1988)) và Amann và Brosius (Gen 40(2-3), 183-190 (1985)), có thể được sử dụng. Vùng khởi đầu như vậy có thể được xen vào, ví dụ vị trí nằm trước gen thích hợp, thường là ở khoảng cách khoảng tính từ 1 đến 500 nucleobazơ từ codon khởi đầu.

Các phương pháp biểu hiện quá mức làm gia tăng hoạt tính hoặc nồng độ của polypeptit tương ứng tốt hơn nếu ít nhất bằng 10%, 25%, 50%, 75%, 100%, 150%, 200%, 300%, 400% hoặc 500%, tốt hơn nếu nhiều nhất là 1000% hoặc 2000%, tính theo hoạt tính hoặc nồng độ polypeptit nêu trên trong chủng trước khi thực hiện phương pháp tạo ra sự biểu hiện quá mức.

Nồng độ protein có thể được xác định thông qua sự phân đoạn gel protein 1 chiều và 2 chiều và xác định quang học sau đó về nồng độ protein bằng phần mềm đánh giá thích hợp trong gel. Phương pháp thông thường để tạo ra gel protein dùng cho vi khuẩn Coryneform và xác định các protein là quy trình đã được mô tả bởi Hermann et al. (Electrophoresis, 22:1712-23 (2001)). Nồng độ protein cũng có thể được xác định bằng phương pháp thấm tách Western bằng cách sử dụng kháng thể đặc hiệu với protein để được phát hiện (Sambrook et al., Molecular Cloning: a laboratory manual 2nd Ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989) và sự đánh giá quang học sau đó bằng cách sử dụng phần mềm tương ứng để xác định nồng độ (Lohaus and Meyer (1998) Biospektrum 5:32-39; Lottspeich, Angewandte Chemie 38: 2630-2647 (1999)). Hoạt tính có thể được xác định bằng thử nghiệm enzym thích hợp.

Thuật ngữ "giảm hoạt lực" theo sáng chế được dùng để chỉ việc làm giảm nồng độ nội bào hoặc hoạt tính của axit ribonucleic, protein (polypeptit) hoặc enzym, được mã hoá bởi ADN tương ứng, ở vi sinh vật, so với chủng ban đầu (chủng gốc) hoặc chủng thể dại. Chủng ban đầu (chủng gốc) được dùng để chỉ chủng mà trong đó phương pháp làm giảm nồng độ hoặc hoạt tính được thực hiện.

Việc giảm hoạt lực có thể đạt được bằng cách làm giảm mức biểu hiện của polypeptit, ví dụ bằng cách sử dụng vùng khởi đầu yếu hoặc sử dụng alen mã hoá polypeptit có hoạt tính thấp hơn và tuỳ ý các phương pháp này có thể được kết hợp.

Cũng có thể đạt được việc giảm hoạt lực bằng cách ngăn đến một cách hoàn toàn sự biểu hiện của polypeptit, ví dụ bằng cách khử hoạt tính gen mã hoá.

Phương pháp làm giảm nồng độ hoặc hoạt tính làm giảm hoạt tính hoặc nồng độ polypeptit tương ứng tốt hơn nếu ít nhất bằng 10%, 25%, 50% hoặc 75%, nhiều nhất 100%, tính theo hoạt tính hoặc nồng độ polypeptit nêu trên trong chủng trước phương pháp giảm hoạt lực. Theo phương án ưu tiên, việc giảm hoạt lực là việc khử hoạt tính một cách hoàn toàn sự biểu hiện của polypeptit thích hợp.

Enzym chịu tác động ngược liên quan đến sự sản sinh axit amin thường được hiểu có nghĩa là các enzym mà, so với dạng thể dại, có độ nhạy với sự ức chế thấp hơn bởi các axit L-amin và/hoặc chất tương tự của chúng được tạo ra.

Cụ thể là, aspartat kinaza chịu tác động ngược ($LysC^{FBR}$) có nghĩa là aspartat kinaza mà, so với dạng thể dại, thể hiện độ nhạy với sự ức chế ít hơn bởi hỗn hợp gồm lysin và threonin hoặc hỗn hợp gồm AEC (aminoetylxystein) và threonin hoặc lysin đơn lẻ hoặc AEC đơn lẻ. Để sản sinh lysin, tốt hơn nếu các chủng tương ứng được sử dụng mà chứa các aspartat kinaza chịu tác động ngược như vậy hoặc đã được khử độ nhạy.

Ví dụ, các aspartat kinaza chịu tác động ngược sau thu được từ C. Glutamicum đã biết từ tài liệu chuyên ngành: A279T, A279V, S301F, S301Y, T308I, T311I, R320G, G345D, S381F. Đối với các aspartat kinaza chịu tác động ngược thu được từ C. glutamicum, cũng hãy xem các tài liệu công bố sau: JP1993184366-A, JP1994062866-A, JP1994261766-A, JP1997070291-A, JP1997322774-A, JP1998165180-A, JP1998215883-A, US5688671-A, EP0387527, WO00/63388, US3732144, JP6261766, các bài báo Jetten et al. (1995; Applied Microbiology Biotechnology 43: 76-82). Các aspartat kinaza chịu tác động ngược thu được từ C. Glutamicum được lưu trữ ở Ngân hàng gen NCBI dưới các số hiệu lưu trữ sau: E05108, E06825, E06826, E06827, E08177, E08178, E08179, E08180, E08181, E08182, E12770, E14514, E16352, E16745, E16746, I74588, I74589, I74590, I74591, I74592, I74593, I74594, I74595, I74596, I74597, X57226, L16848, L27125.

Tốt hơn nếu, các aspartat kinaza chịu tác động ngược sau thu được từ C. humireducens theo sáng chế được sử dụng: D274Y, A279E, S301Y, T308I, T311I, G359D.

Để sản sinh threonin, tốt hơn nếu sử dụng các chủng chứa homoserin dehydrogenaza chịu tác động ngược tương ứng (Hom^{FBR}).

Để sản sinh isoleuxin và sản sinh valin, tốt hơn nếu sử dụng các chủng chứa axetolactat synthaza chịu tác động ngược tương ứng.

Để sản sinh leuxin, tốt hơn nếu sử dụng các chủng chứa isopropylmalat synthaza chịu tác động ngược tương ứng ($LeuA^{FBR}$).

Để sản sinh prolin, tốt hơn nếu sử dụng các chủng chứa glutamat-5-kinaza chịu tác động ngược tương ứng ($ProB^{FBR}$).

Để sản sinh arginin, tốt hơn nếu sử dụng các chủng chứa ornithin carbamoyltransferaza chịu tác động ngược tương ứng ($ArgF^{FBR}$).

Để sản sinh serin, tốt hơn nếu sử dụng các chủng chứa D-3-phosphoglyxerat dehydrogenaza chịu tác động ngược tương ứng ($SerA^{FBR}$).

Để sản xinh methionin, tốt hơn nếu sử dụng các chủng chứa D-3-phosphoglyxerat dehydrogenaza chịu tác động ngược tương ứng ($SerA^{FBR}$) và/hoặc pyruvat carboxylaza chịu tác động ngược (Pyc^{FBR}).

Để sản sinh tryptophan, tốt hơn nếu sử dụng các chủng chứa phospho-2-dehydro-3-deoxyheptonat aldolaza chịu tác động ngược tương ứng ($AroG^{FBR}$ hoặc $AroH^{FBR}$).

Đối với các đặc tính được ưu tiên hơn của chủng *C. humireducens* sản sinh lượng lớn axit L-amin để được sử dụng theo sáng chế, hãy xem tài liệu công bố của Wu et al. (2011) được trích dẫn trên đây và các tài liệu công bố khác nêu trên.

Các vi sinh vật theo sáng chế, cụ thể là vi khuẩn thuộc chi *Corynebacterium*, có thể được nuôi cấy theo cách liên tục - như được mô tả ví dụ trong WO05/021772 - hoặc theo cách gián đoạn trong quy trình theo mẻ (nuôi cấy theo mẻ hoặc phương pháp theo mẻ) hoặc trong quy trình mẻ nạp hoặc quy trình mẻ nạp lặp lại nhằm mục đích sản sinh axit L-amin. Đánh giá chung về các phương pháp nuôi cấy đã biết có

trong sách giáo khoa của Chmiel (Bioprozesstechnik 1. Einführung in die Bioverfahrenstechnik [Bioprocess Technology 1. Introduction to Bioprocess Technology] (Gustav Fischer Verlag, Stuttgart, 1991)) hoặc trong sách giáo khoa của Storhas (Bioreaktoren und periphere Einrichtungen [Bioreactors and Peripheral Devices] (Vieweg Verlag, Braunschweig/ Wiesbaden, 1994)).

Môi trường nuôi cấy hoặc môi trường lên men để được sử dụng phải đáp ứng các yêu cầu về các chủng cụ thể theo cách thích hợp. Phần mô tả về các môi trường nuôi cấy của các vi sinh vật khác nhau có mặt trong sổ tay hướng dẫn "Manual of Methods for Genral Bacteriology" của the American Society for Bacteriology (Hiệp hội vi khuẩn học Hoa kỳ) (Washington D.C., USA, 1981). Các thuật ngữ môi trường nuôi cấy và môi trường lên men hoặc môi trường có thể được sử dụng thay thế cho nhau.

Các nguồn cacbon được sử dụng có thể là các đường và hydratcacbon như các dung dịch chứa glucoza, sucroza, lactoza, fructoza, maltoza, molaza, sucroza từ quy trình sản xuất củ cải đường hoặc mía, tinh bột, hydrolysat dạng tinh bột và xenluloza, các dầu và các chất béo như dầu đậu nành, dầu hướng dương, dầu lạc và chất béo từ dừa, các axit béo như axit palmitic, axit stearic và axit linoleic, các rượu như glyxerol, metanol và etanol và các axit hữu cơ như axit axetic hoặc axit lactic.

Có thể sử dụng các hợp chất chứa nitơ hữu cơ làm nguồn nitơ như pepton, chiết xuất nấm men, chiết phẩm từ thịt, chiết phẩm từ mạch nha, dung dịch ngâm ngô, bột đậu nành và ure hoặc các hợp chất vô cơ như amoni sulphat, amoni clorua, amoni phosphat, amoni cacbonat và amoni nitrat. Các nguồn nitơ có thể được sử dụng theo cách riêng biệt hoặc dưới dạng hỗn hợp.

Các nguồn photpho được sử dụng có thể là axit phosphoric, kali dihydro phosphat hoặc dikali hydro phosphat hoặc các muối chứa natri tương ứng.

Ngoài ra, môi trường nuôi cấy phải chứa các muối, ví dụ dưới dạng clorua hoặc sulphat của các kim loại như natri, kali, magie, canxi và sắt, ví dụ magie sulphat hoặc sắt sulphat, là cần thiết đối với sự sinh trưởng. Cuối cùng, các yếu tố sinh trưởng thiết yếu như các axit amin, ví dụ homoserin và các vitamin, ví dụ thiamin, biotin hoặc axit pantothenic, có thể được sử dụng ngoài các chất nêu trên.

Các nguyên liệu gốc này có thể được bổ sung vào môi trường nuôi cấy dưới dạng một hỗn hợp duy nhất hoặc có thể được nạp vào trong quá trình nuôi cấy theo cách thích hợp.

Độ pH của môi trường nuôi cấy có thể được kiểm soát bằng cách dùng các hợp chất có tính bazơ như natri hydroxit, kali hydroxit, amoniac hoặc dung dịch nước amoniac hoặc các hợp chất có tính axit như axit phosphoric hoặc axit sulphuric theo cách thích hợp. Độ pH thường được điều chỉnh đến trị số nằm trong khoảng từ 6,0 đến 9,0, tốt hơn nếu nằm trong khoảng từ 6,5 đến 8. Để kiểm soát sự thoát bọt, có thể sử dụng các chất chống tạo bọt, ví dụ các polyglycol este của axit béo. Để duy trì độ ổn định của plasmit, có thể bổ sung các chất chọn lọc thích hợp vào môi trường này, ví dụ các chất kháng sinh. Để duy trì các điều kiện hiếu khí, oxy hoặc hỗn hợp khí oxy, ví dụ không khí, được đưa vào môi trường nuôi cấy. Cũng có thể sử dụng các chất lỏng giàu hydro peroxit. Nếu thích hợp, việc lên men được thực hiện ở áp suất cao, ví dụ ở áp suất nằm trong khoảng từ 0,03 đến 0,2MPa. Nhiệt độ của môi trường nuôi cấy thường nằm trong khoảng từ 20°C đến 45°C và tốt hơn nếu từ 25°C đến 40°C. Trong các quy trình theo mẻ, việc nuôi cấy được tiếp tục cho đến khi tạo ra lượng tối đa axit L-amin mong muốn. Thông thường, mục đích này đạt được trong khoảng thời gian từ 10 giờ đến 160 giờ. Trong các quy trình liên tục, có thể cần thời gian nuôi cấy dài hơn. Hoạt tính của vi khuẩn tạo ra nồng độ (sự tích tụ) axit L-amin trong môi trường lên men và/hoặc trong tế bào vi khuẩn.

Các ví dụ về các môi trường lên men thích hợp được tìm thấy, không kể các tài liệu khác, trong các bản mô tả sáng chế của patent Mỹ số US5,770,409, US 5,840,551 và US 5,990,350 hoặc US 5,275,940.

Phương pháp phân tích axit L-amin để xác định nồng độ tại một hoặc nhiều thời điểm trong quá trình lên men có thể thực hiện bằng cách chia tách các axit L-amin bằng phương pháp sắc ký trao đổi ion, tốt hơn nếu bằng phương pháp sắc ký trao đổi cation, với quá trình tạo dẫn xuất sau cột sau đó bằng cách sử dụng ninhydrin, như được mô tả trong bài báo Spackman et al. (Analytical Chemistry 30: 1190-1206 (1958)). Cũng có thể dùng ortho-phtalaldehyt không phải là ninhydrin cho quá trình dẫn xuất sau cột. Nội dung tổng quan về phương pháp sắc ký trao đổi ion có thể được

tìm thấy trong tạp chí: Pickering (LC·GC (Magazine of Chromatographic Science) 7(6), 484-487 (1989)).

Cũng có thể thực hiện quá trình dẫn xuất sau cột, ví dụ sử dụng ortho-phtalaldehyt hoặc phenyl isothioxyanat và phân đoạn các dẫn xuất axit amin thu được bằng phương pháp sắc ký đảo pha đảo (reversed-phase-RP), tốt hơn nếu dưới dạng phương pháp sắc ký lỏng hiệu năng cao (high-performance liquid chromatography-HPLC). Phương pháp thuộc loại này được mô tả, ví dụ trong Lindroth et al. (Analytical Chemistry 51: 1167 - 1174 (1979)).

Việc phát hiện được thực hiện bằng phương pháp quang phổ (hấp thụ, huỳnh quang).

Việc đánh giá liên quan đến phương pháp phân tích axit amin có thể được tìm thấy, không kể các tài liệu khác, trong sách giáo khoa "Bioanalytik" của Lottspeich và Zorbas (Spektrum Akademischer Verlag, Heidelberg, Đức 1998).

Do đó, sáng chế cũng đề cập đến phương pháp sản xuất axit L-amin, khác biệt ở chỗ, phương pháp này bao gồm các bước sau:

a) lên men các vi sinh vật theo sáng chế, cụ thể là vi khuẩn *Coryneform*, tốt hơn nếu thuộc chi *Corynebacterium*, đặc biệt tốt hơn nếu thuộc các loài *Corynebacterium glutamicum* hoặc *Corynebacterium humireducens*, trong môi trường dinh dưỡng thích hợp, và

b) tích tụ các axit L-amin trong môi trường dinh dưỡng và/hoặc trong tế bào vi khuẩn nêu trên.

Sau đó, sản phẩm chứa axit L-amin được tạo ra hoặc được sản sinh hoặc được thu gom dưới dạng lỏng hoặc dạng rắn.

Các phương pháp lên men tạo ra môi trường lên men chứa axit L-amin thích hợp.

Môi trường lên men có nghĩa là môi trường lên men hoặc môi trường dinh dưỡng, trong đó vi sinh vật được nuôi cấy trong thời gian nhất định và ở nhiệt độ nhất định. Môi trường hoặc các môi trường lên men dùng trong quá trình lên men chứa tất

cả chất hoặc thành phần mà đảm bảo sự nhân giống của vi sinh vật và sự tạo ra axit L-amin mong muốn.

Khi quá trình lên men hoàn thành, thì môi trường lên men thu được chứa:

a) sinh khối (khối tế bào) của vi sinh vật, sinh khối này đã được tạo ra do sự nhân giống tế bào của vi sinh vật này,

b) axit L-amin đã được tạo ra trong quá trình lên men,

c) các sản phẩm phụ hữu cơ đã được tạo ra trong quá trình lên men, và

d) các thành phần của môi trường lên men được dùng hoặc của các chất ban đầu, ví dụ các vitamin như biotin hoặc các muối như magie sulphat, không được tiêu thụ trong quá trình lên men.

Các sản phẩm phụ hữu cơ bao gồm các chất mà được tạo ra bởi các vi sinh vật được dùng trong quá trình lên men ngoài axit L-amin mong muốn và tuỳ ý được tiết. Các sản phẩm này cũng bao gồm các đường như, ví dụ trehaloza.

Môi trường lên men được lấy ra khỏi bình nuôi cấy hoặc bể lên men, được gom nếu thích hợp và được sử dụng để tạo ra sản phẩm chứa axit L-amin, dưới dạng lỏng hoặc dạng rắn. Thuật ngữ "thu gom sản phẩm chứa axit L-amin" cũng được sử dụng trong trường hợp này. Trong trường hợp đơn giản nhất, môi trường lên men chứa axit L-amin tự cấu thành sản phẩm đã được thu gom.

Một hoặc nhiều phương pháp được chọn từ nhóm bao gồm các biện pháp sau:

a) loại bỏ nước từ một phần (> 0% đến < 80%) đến hoàn toàn (100%) hoặc gần như hoàn toàn (≥ 80%, ≥ 90%, ≥ 95%, ≥ 96%, ≥ 97%, ≥ 98%, ≥ 99%),

b) loại bỏ sinh khối từ một phần (> 0% đến < 80%) đến hoàn toàn (100%) hoặc gần như hoàn toàn (≥ 80%, ≥ 90%, ≥ 95%, ≥ 96%, ≥ 97%, ≥ 98%, ≥ 99%), sinh khối tuỳ ý được làm bất hoạt trước khi loại bỏ,

c) loại bỏ các sản phẩm phụ hữu cơ đã được tạo ra trong quá trình lên men từ một phần (> 0% đến < 80%) đến hoàn toàn (100%) hoặc gần như hoàn toàn (≥ 80%, ≥ 90%, ≥ 95%, ≥ 96%, ≥ 97%, ≥ 98%, ≥ 99%, ≥ 99,3%, ≥ 99,7%), và

d) loại bỏ các thành phần của môi trường lên men được dùng hoặc của các chất ban đầu, không được tiêu thụ trong quá trình lên men từ một phần (> 0%) đến hoàn toàn (100%) hoặc gần như hoàn toàn (≥ 80%, ≥ 90%, ≥ 95%, ≥ 96%, ≥ 97%, ≥ 98%, ≥ 99%, ≥ 99,3%, ≥ 99,7%), ra khỏi môi trường lên men đạt được nồng độ hoặc độ tinh khiết của axit L-amin. Các sản phẩm có hàm lượng axit L-amin mong muốn được phân lập theo cách này.

Việc loại bỏ nước (phương pháp a)) từ một phần (> 0% đến < 80%) đến hoàn toàn (100%) hoặc gần như hoàn toàn (≥ 80% đến < 100%) cũng được dùng để chỉ việc làm khô.

Việc loại bỏ hoàn toàn hoặc gần như hoàn toàn nước, sinh khối, các sản phẩm phụ hữu cơ và các thành phần không được tiêu thụ của môi trường lên men được dùng tạo ra các dạng sản phẩm axit L-amin có độ tinh khiết (≥ 80% khối lượng, ≥ 90% khối lượng) hoặc độ tinh khiết ở mức cao (≥ 95% khối lượng, ≥ 97% khối lượng, ≥ 99% khối lượng). Nhiều hướng dẫn kỹ thuật đối với các phương pháp a), b), c) và d) là sẵn có trong lĩnh vực này.

Ví dụ thực hiện sáng chế

Ví dụ 1: Thử nghiệm đánh giá khả năng sản sinh alanin và valin bởi *C. humireducens*

Để thực hiện thử nghiệm đánh giá khả năng sản sinh alanin và valin, nuôi cấy chủng *C. humireducens* (DSM 45392) theo mẻ trong bình lắc. Đối với mục đích này, ủ chủng *C. humireducens* trong 10mL môi trường BHI dạng lỏng (Brain Heart Infusion; Merck) (37g/L H_2O) ở nhiệt độ 37°C và tốc độ lắc bằng 200 vòng/phút trong 24 giờ làm chủng nuôi cấy sơ bộ. Sau đó, cấy 10mL môi trường trong bình lắc đến mật độ quang ở bước sóng 660nm bằng 0,2 và nuôi cấy ở nhiệt độ 37°C và tốc độ lắc bằng 200 vòng/phút trong 48 giờ. Để điều chế môi trường này, hoà tan 20g amoni sulphat, 0,4g $MgSO_4*7H_2O$, 0,6g KH_2PO_4 và 10g chiết xuất nấm men trong 750mL H_2O. Điều chỉnh độ pH của dung dịch này đến 7,8 bằng dung dịch NH_4OH 20%, sau đó hấp dung dịch này. Sau đó, bổ sung 4mL dung dịch vitamin (độ pH=7 bằng NH_4OH), chứa 0,25g/L thiamin, 50mg/L xyanocobalamin, 25mg/L biotin và 1,25g/L pyridoxin. Ngoài

ra, bổ sung 140mL dung dịch glucoza 50% lọc vô trùng vào và 50g $CaCO_3$ được hấp khô vào, sau đó môi trường này được điều chỉnh đến thể tích bằng 1L.

Sau khi nuôi cấy, phân tích dịch nổi của bốn môi trường nuôi cấy song song trong mỗi trường hợp bằng phương pháp HPLC để xác định hàm lượng alanin và valin với giới hạn phát hiện ≥0,01g/L.

Chủng điển hình *C. humireducens* sau khi nuôi cấy trong 48 giờ trong môi trường bình lắc ở nhiệt độ 37°C và tốc độ lắc bằng trên quy mô bình lắc tạo ra khoảng 0,81g/L alanin (hiệu suất thực tế: $0,011g_{alanin}/g_{glucoza}$) và 1,6g/L valin (hiệu suất thực tế: $0,022g_{valin}/g_{glucoza}$) (Bảng 1). Glyxin chỉ được tạo ra với lượng nhỏ dưới dạng sản phẩm phụ.

Bảng 1: Dữ liệu phân tích từ thử nghiệm bình lắc với chủng *C. humireducens*. Các trị số được đo sau khi nuôi cấy với tế bào và môi trường trống rỗng được thể hiện.

	Alanin (g/L)	**Valin (g/L)**
C. humireducens	1,27	1,9
Môi trường trống rỗng không có tế bào	0,46	0,3

Ví dụ 2: Thử nghiệm đánh giá khả năng sản sinh glutamat

Để thực hiện thử nghiệm đánh giá khả năng sản sinh L-glutamat, nuôi cấy chủng *C. humireducens* (DSM 45392) theo mẻ trong bình lắc. Đối với mục đích này, ủ chủng *C. humireducens* trong 10mL môi trường BHI dạng lỏng (Brain Heart Infusion; Merck) (37g/L H_2O) ở nhiệt độ 37°C và tốc độ lắc bằng 200 vòng/phút trong 24 giờ làm chủng nuôi cấy sơ bộ. Sau đó, cấy 10mL môi trường trong bình lắc đến mật độ quang ở bước sóng 660nm bằng 0,2 và nuôi cấy ở nhiệt độ 37°C và tốc độ lắc bằng 200 vòng/phút trong 48 giờ. Để điều chế môi trường này, hoà tan 20g amoni sulphat, 0,4g $MgSO_4*7H_2O$, 0,6g KH_2PO_4 và 10g chiết xuất nấm men trong 750mL H_2O. Điều chỉnh độ pH của dung dịch này đến 7,8 bằng dung dịch NH_4OH 20%, sau đó hấp dung dịch này. Sau đó, bổ sung 4mL dung dịch vitamin (độ pH=7 bằng NH_4OH), chứa 0,25g/L thiamin, 50mg/L xyanocobalamin, 25mg/L biotin và 1,25g/L pyridoxin vào. Ngoài ra, bổ sung 140mL dung dịch glucoza 50% lọc vô trùng và 50g $CaCO_3$ được

hấp khô vào. Sau đó, bổ sung 5ml dung dịch gốc threonin 400mM lọc vô trùng vào, sau đó môi trường này được điều chỉnh đến thể tích bằng 1L.

Sau khi nuôi cấy, phân tích dịch nổi của bốn môi trường nuôi cấy song song trong mỗi trường hợp bằng phương pháp HPLC để xác định hàm lượng glutamat với giới hạn phát hiện ≥0,01g/L.

Chủng *C. humireducens* sau khi nuôi cấy trong 48 giờ trong môi trường bình lắc ở nhiệt độ 37°C và tốc độ lắc bằng trên quy mô bình lắc tạo ra 1,8 (+/-0,6)g/L L-glutamat. Nồng độ ban đầu của L-glutamat trong môi trường bằng 0,78 (+/-0,1)g/L. Glyxin chỉ được tạo ra với lượng nhỏ dưới dạng sản phẩm phụ.

DANH MỤC TRÌNH TỰ

<110> EVONIK DEGUSSA GMBH
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Asp Leu Ala Ile Ala Glu Glu Pro Gly Lys Glu Phe Arg Gly Ser His
            100                 105                 110
Phe Gln Asn Ala Ala Asn Glu Tyr Pro Arg Pro Glu Thr Glu Ser Glu
        115                 120                 125
His Gly Ile Val Ala Ala Cys Arg Glu His Arg Arg Trp Met His Gln
    130                 135                 140
Thr Met Thr Asp Leu Leu Thr Ala Lys Asn Gly Tyr Pro Ser Ala Thr
145                 150                 155                 160
Gln Ala Asn Gln Leu Leu Ile Phe Leu Asp Gly Gly Leu Ala Gly Ala
                165                 170                 175
Arg Phe Ala Arg Glu Val Thr Pro Leu Gln Thr Ala Arg Asp Leu Ala
            180                 185                 190
Arg Gln Met Leu Ser Ala Pro Pro Ala Asp Tyr Ser Ile
        195                 200                 205
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cccacgacat ctccctcaag accgtccgcc aggaggaggc cggcgaccac gcccgcctca      180
tcgtcgtcac gcattccgca cgtgaggccg acctggccgc caccgtcgag gacctgaaga      240
aggccccggc ggtcaagtcc gtcgacagcg tcctgcgact catctaggga gcgttgagct      300
gtg agc atc cag ctt gag gtg ggc acc cgg gcc acc gtc acc gtc ccc        348
Val Ser Ile Gln Leu Glu Val Gly Thr Arg Ala Thr Val Thr Val Pro
1               5                   10                  15
ggc tcc tcc gcg aac ctg ggc ccc gga ttc gac acc ctc ggc ctg gcc        396
Gly Ser Ser Ala Asn Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala
            20                  25                  30
gtg ggc atc tac gac acc gtc gag gtc gag gtc atc gag tcg ggc ctc        444
Val Gly Ile Tyr Asp Thr Val Glu Val Glu Val Ile Glu Ser Gly Leu
        35                  40                  45
gag gtc gag gtc ttc ggc gag ggc gag gac gac ctg ccc cgc gac ggt        492
Glu Val Glu Val Phe Gly Glu Gly Glu Asp Asp Leu Pro Arg Asp Gly
    50                  55                  60
tcc cac ctg gtg gtc aag gcc atc cgg tcg ggc ctc aac gcc gcc cac        540
Ser His Leu Val Val Lys Ala Ile Arg Ser Gly Leu Asn Ala Ala His
65                  70                  75                  80
gcc gag gcc ccg ggc ctg cgc gtg gtg tgc acc aac gcc atc ccg cag        588
Ala Glu Ala Pro Gly Leu Arg Val Val Cys Thr Asn Ala Ile Pro Gln
                85                  90                  95
tcc cgt ggc ctg ggc tcc tcc gcc gcc gca gcc gtc gcg gga gtt ctg        636
Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Ala Val Ala Gly Val Leu
            100                 105                 110
gcc gcc aac ggt ctg gcg ggc aac ccg ctg acc acc gac cag gtg gtc        684
Ala Ala Asn Gly Leu Ala Gly Asn Pro Leu Thr Thr Asp Gln Val Val
        115                 120                 125
cag ctg tcc tcc gcc ttc gag ggg cac ccc gac aac gcc gcg gcc tcc        732
Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser
    130                 135                 140
gtc ctc ggt tcc gcc gtg gtc tcc tgg acc acg acc ccg gtc gac ggc        780
Val Leu Gly Ser Ala Val Val Ser Trp Thr Thr Thr Pro Val Asp Gly
145                 150                 155                 160
tcg cag ccg ggg tac cgg gcg gtg gcg gtg gac gtc gac aag cgc atc        828
Ser Gln Pro Gly Tyr Arg Ala Val Ala Val Asp Val Asp Lys Arg Ile
                165                 170                 175
cgg gcg acg gct ctc gtg ccg gac ttc cac gcc tcc acc cag gcg gtg        876
Arg Ala Thr Ala Leu Val Pro Asp Phe His Ala Ser Thr Gln Ala Val
            180                 185                 190
cgt cgc gtg ctg ccg agc cac gtc acc cac acg gac gcg cgt ttc aac        924
Arg Arg Val Leu Pro Ser His Val Thr His Thr Asp Ala Arg Phe Asn
        195                 200                 205
gtc tcg cgc acc gcg gtg atg acc gtg gcg ctg cag aac cac ccg gag        972
Val Ser Arg Thr Ala Val Met Thr Val Ala Leu Gln Asn His Pro Glu
    210                 215                 220
ctg ctg tgg gag ggc acc cgt gac cgc ctg cac cag ccc tac cgc gcc       1020
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Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg Ala
225                 230                 235                 240
gac gtg ctg ccg gtg acc gcc gag tgg gtc aac cgt ctg cgc aac cgc      1068
Asp Val Leu Pro Val Thr Ala Glu Trp Val Asn Arg Leu Arg Asn Arg
                245                 250                 255
ggt tac gcc gcg tac ctc tcc ggc gcc ggc ccg acc tgc atg gtc ctg      1116
Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Cys Met Val Leu
            260                 265                 270
tcg gtc gac ccg atc gag gag gcc atc ctc gag gag gcc cgc gcc gcc      1164
Ser Val Asp Pro Ile Glu Glu Ala Ile Leu Glu Glu Ala Arg Ala Ala
        275                 280                 285
ggt ctg cgc gtc ctc gag ctg gag gtc gcc ggt ccg gcg acc gtc gag      1212
Gly Leu Arg Val Leu Glu Leu Glu Val Ala Gly Pro Ala Thr Val Glu
    290                 295                 300
gtc agc cgg gtc tga cctaccggtc gtcggcgggg gtccccctgt cggcgaccac      1267
Val Ser Arg Val
305
cgagcacgcg cccgagggct ggaaggggcg caggctcagc cggacggggg cggagccgac     1327
ggactcctgc aggaaaccct cgtggatggc gcagatcatg agcgagggtc ggtgccctc      1387
ggcgacgaag gggcacgcct gcagctcgat gtcgaccgac tccgcgtcgg tgcccccgtc     1447
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gtcgagcgcc gtgtccatgg                                                1527
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<212>  PRT
<213>  Corynebacterium humireducens
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Val Ser Ile Gln Leu Glu Val Gly Thr Arg Ala Thr Val Thr Val Pro
1               5                  10                  15
Gly Ser Ser Ala Asn Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala
            20                  25                  30
Val Gly Ile Tyr Asp Thr Val Glu Val Glu Val Ile Glu Ser Gly Leu
        35                  40                  45
Glu Val Glu Val Phe Gly Glu Gly Glu Asp Asp Leu Pro Arg Asp Gly
    50                  55                  60
Ser His Leu Val Val Lys Ala Ile Arg Ser Gly Leu Asn Ala Ala His
65                  70                  75                  80
Ala Glu Ala Pro Gly Leu Arg Val Val Cys Thr Asn Ala Ile Pro Gln
                85                  90                  95
Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Ala Val Ala Gly Val Leu
            100                 105                 110
Ala Ala Asn Gly Leu Ala Gly Asn Pro Leu Thr Thr Asp Gln Val Val
        115                 120                 125
Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser
    130                 135                 140
Val Leu Gly Ser Ala Val Val Ser Trp Thr Thr Thr Pro Val Asp Gly
145                 150                 155                 160
Ser Gln Pro Gly Tyr Arg Ala Val Ala Val Asp Val Asp Lys Arg Ile
                165                 170                 175
Arg Ala Thr Ala Leu Val Pro Asp Phe His Ala Ser Thr Gln Ala Val
            180                 185                 190
Arg Arg Val Leu Pro Ser His Val Thr His Thr Asp Ala Arg Phe Asn
        195                 200                 205
Val Ser Arg Thr Ala Val Met Thr Val Ala Leu Gln Asn His Pro Glu
    210                 215                 220
Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg Ala
225                 230                 235                 240
Asp Val Leu Pro Val Thr Ala Glu Trp Val Asn Arg Leu Arg Asn Arg
                245                 250                 255
Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Cys Met Val Leu
            260                 265                 270
Ser Val Asp Pro Ile Glu Glu Ala Ile Leu Glu Glu Ala Arg Ala Ala
        275                 280                 285
Gly Leu Arg Val Leu Glu Leu Glu Val Ala Gly Pro Ala Thr Val Glu
    290                 295                 300
Val Ser Arg Val
305
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<212>  ADN
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<222>  (301)..(1938)
<223>  gen pgi
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gccacggggc ggagaagctg gaaaccctcg aagccgggtg cctggtcgac ggcgttcttc      120
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cgggcggcga agcgctcctc cagctgcggg ccggcgccct cggggacggt gatggcgttg      180
attttcacga tgctcatgcc ccccattgtg cccaaccggc cgcttccccg gcggacaccc      240

gggaaagtca ctagattcgt gagtgtcccg aacatatccc cgcattgagg agcccgaccc      300
atg gcc gac atc acc acc tcc gct gaa tgg aag aac ctg gag tcc gag         348
Met Ala Asp Ile Thr Thr Ser Ala Glu Trp Lys Asn Leu Glu Ser Glu
1               5                  10                  15
ttc gag cgc acc cag ggt cag acc ctg cgg gag ctg ttc gcc gcg gat         396
Phe Glu Arg Thr Gln Gly Gln Thr Leu Arg Glu Leu Phe Ala Ala Asp
            20                  25                  30
ccg cag cgt gcg gag aag ctg acc ttc gat gcg gcc ggt ctc cac gtc         444
Pro Gln Arg Ala Glu Lys Leu Thr Phe Asp Ala Ala Gly Leu His Val
        35                  40                  45
gac ctc tcc aag aac ctg ctt gac gac gcc acc gtg gcc tcc ctc gtc         492
Asp Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Val Ala Ser Leu Val
    50                  55                  60
gcc ctc gcc aag gag gcg cag ctc acc gag gcc atc gag gcg atg ttc         540
Ala Leu Ala Lys Glu Ala Gln Leu Thr Glu Ala Ile Glu Ala Met Phe
65                  70                  75                  80
agc ggc gtg cac atc aac aac acc gag gac cgc gcc gtg ctg cac acc         588
Ser Gly Val His Ile Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr
                85                  90                  95
gcc ctg cgt ctg ccg gtc gag gag gac ctc gag gtc gac ggc cag gac         636
Ala Leu Arg Leu Pro Val Glu Glu Asp Leu Glu Val Asp Gly Gln Asp
            100                 105                 110
gtc gcc gcc gac gtc cac gag gtg ctc ggc cgc atg cgc gac ttc gcc         684
Val Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala
        115                 120                 125
tcc tcc ctg cgt gcg ggc acc tgg ctc ggc cac acc ggc cgc acc atc         732
Ser Ser Leu Arg Ala Gly Thr Trp Leu Gly His Thr Gly Arg Thr Ile
    130                 135                 140
aag aag gtc gtc aac atc ggc atc ggc ggc tcc gac ctg ggc ccg gcc         780
Lys Lys Val Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala
145                 150                 155                 160
atg gcc gcc cgg gcg ctg cgc tcc tac gcc acc gcc ggc atc acc gcc         828
Met Ala Ala Arg Ala Leu Arg Ser Tyr Ala Thr Ala Gly Ile Thr Ala
                165                 170                 175
gag ttc gtc tcc aac gtc gac ccg gcc gac atg tcc gcc acc ctc gac         876
Glu Phe Val Ser Asn Val Asp Pro Ala Asp Met Ser Ala Thr Leu Asp
            180                 185                 190
gag ctc gac ccc gag tcg acc ctg ttc atc atc gcc tcc aag acc ttc         924
Glu Leu Asp Pro Glu Ser Thr Leu Phe Ile Ile Ala Ser Lys Thr Phe
        195                 200                 205
acc acc cag gag acc ctc gcc aac gcg cac gcc gcg aag cgc tgg ctg         972
Thr Thr Gln Glu Thr Leu Ala Asn Ala His Ala Ala Lys Arg Trp Leu
    210                 215                 220
ctg cag gcc ttc gac ggg gac gag tcg gcc gtc gcg aag cac ttc gtg        1020
Leu Gln Ala Phe Asp Gly Asp Glu Ser Ala Val Ala Lys His Phe Val
225                 230                 235                 240
gcg gtg tcc acc aac gcc cag aag gtc gcc gag ttc ggc atc gac acc        1068
Ala Val Ser Thr Asn Ala Gln Lys Val Ala Glu Phe Gly Ile Asp Thr
                245                 250                 255
gac aac atg ttc ggc ttc tgg gac tgg gta ggc ggc cgc tac tcc gtc        1116
Asp Asn Met Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val
            260                 265                 270
gac tcc gcc atc ggc ctg tcc ctc atg gcc gtc atc ggc ccg ctg gac        1164
Asp Ser Ala Ile Gly Leu Ser Leu Met Ala Val Ile Gly Pro Leu Asp
        275                 280                 285
ttc atg cgc ttc ctc gag ggc ttc cgc gcc atg gac gag cac ttc cgc        1212
Phe Met Arg Phe Leu Glu Gly Phe Arg Ala Met Asp Glu His Phe Arg
    290                 295                 300
gcg acc ccc ttc gag aag aac gtg ccc gtc ctc atg gcg ctg ctg ggc        1260
Ala Thr Pro Phe Glu Lys Asn Val Pro Val Leu Met Ala Leu Leu Gly
305                 310                 315                 320
atc tgg tac gtc aac ttc cac ggc ttc gag acc cac gcg gtc ctc ccc        1308
Ile Trp Tyr Val Asn Phe His Gly Phe Glu Thr His Ala Val Leu Pro
                325                 330                 335
tac tct cag gac ctc tcc cgt ttc gcc gcc tac ctg cag cag ctg acc        1356
Tyr Ser Gln Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr
            340                 345                 350
atg gag tcc aac ggc aag tcc gtc cga cac gac ggc acc gcc gtc gac        1404
Met Glu Ser Asn Gly Lys Ser Val Arg His Asp Gly Thr Ala Val Asp
        355                 360                 365
tac gcc acc ggt gag atc tac tgg ggc gag ccg ggc acc aac ggc cag        1452
Tyr Ala Thr Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln
    370                 375                 380
cac gcc ttc tac cag ctc atg cac cag ggc acc cgc gtc gtc ccg gcc        1500
His Ala Phe Tyr Gln Leu Met His Gln Gly Thr Arg Val Val Pro Ala
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385                 390                 395                 400
gac ttc atc ggc ttc gcc cgc ccg aag aac gac ctg ccg acc gcc acc      1548
Asp Phe Ile Gly Phe Ala Arg Pro Lys Asn Asp Leu Pro Thr Ala Thr
                405                 410                 415
ggc gag ggc tcc atg cac gac ctg ctc atg ggc aac ctc ttc gcc cag      1596
Gly Glu Gly Ser Met His Asp Leu Leu Met Gly Asn Leu Phe Ala Gln
            420                 425                 430
agc aag gtg ctg gcc ttc ggc aag acc gcc gag gag atc gcc gcc gag      1644
Ser Lys Val Leu Ala Phe Gly Lys Thr Ala Glu Glu Ile Ala Ala Glu
        435                 440                 445
gga gtg tcc gcg gac ctc gtc gcc cac aag gtc atg ccg ggc aac cgc      1692
Gly Val Ser Ala Asp Leu Val Ala His Lys Val Met Pro Gly Asn Arg
    450                 455                 460
ccg tcc acg acc atc ctc gcg gag gag ctc acc ccg gcg gtg ctc ggc      1740
Pro Ser Thr Thr Ile Leu Ala Glu Glu Leu Thr Pro Ala Val Leu Gly
465                 470                 475                 480
gcg ctc atc gcc ctc tac gag cac atc acc ttc gtc cag ggc gtc atc      1788
Ala Leu Ile Ala Leu Tyr Glu His Ile Thr Phe Val Gln Gly Val Ile
                485                 490                 495
tgg gac atc aac tcc ttc gac cag tgg ggc gtg gag ctg ggc aag cag      1836
Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln
            500                 505                 510
cag gcc aac cag ctg gcc gcc gcc gtc tcc ggc gcc gag gag gtc gac      1884
Gln Ala Asn Gln Leu Ala Ala Ala Val Ser Gly Ala Glu Glu Val Asp
        515                 520                 525
tcc ggc gac tcc tcc acc gac gcg ctc gtg cgc tgg tac cgc gcg aac      1932
Ser Gly Asp Ser Ser Thr Asp Ala Leu Val Arg Trp Tyr Arg Ala Asn
    530                 535                 540
cgc tag ttcggcaggg ccggcatccc gaggggggtg ccggccctct gcttctcgac      1988
Arg
545
gtcgccccgt tccccgtaac tgaaccggaa ctcgtggaac ggcaggttca cggtctccag     2048
gtggtagaag gcgttccggg cgtgcttgga gtagtggtac tcgcgggccc ggagggtggt     2108
caccgacagc aggttgccgt agccgggcag cagcaggtgc gcgtactgcc ggaggaaggg     2168
caccaggtcg aggctccatc cctcccccgt gcgggtcagt tccgccgggt acaggtcgac     2228
ggtggccacg                                                           2238
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1               5                   10                  15
Phe Glu Arg Thr Gln Gly Gln Thr Leu Arg Glu Leu Phe Ala Ala Asp
            20                  25                  30
Pro Gln Arg Ala Glu Lys Leu Thr Phe Asp Ala Ala Gly Leu His Val
        35                  40                  45
Asp Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Val Ala Ser Leu Val
    50                  55                  60
Ala Leu Ala Lys Glu Ala Gln Leu Thr Glu Ala Ile Glu Ala Met Phe
65                  70                  75                  80
Ser Gly Val His Ile Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr
                85                  90                  95
Ala Leu Arg Leu Pro Val Glu Glu Asp Leu Glu Val Asp Gly Gln Asp
            100                 105                 110
Val Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala
        115                 120                 125
Ser Ser Leu Arg Ala Gly Thr Trp Leu Gly His Thr Gly Arg Thr Ile
    130                 135                 140
Lys Lys Val Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala
145                 150                 155                 160
Met Ala Ala Arg Ala Leu Arg Ser Tyr Ala Thr Ala Gly Ile Thr Ala
                165                 170                 175
Glu Phe Val Ser Asn Val Asp Pro Ala Asp Met Ser Ala Thr Leu Asp
            180                 185                 190
Glu Leu Asp Pro Glu Ser Thr Leu Phe Ile Ile Ala Ser Lys Thr Phe
        195                 200                 205
Thr Thr Gln Glu Thr Leu Ala Asn Ala His Ala Ala Lys Arg Trp Leu
    210                 215                 220
Leu Gln Ala Phe Asp Gly Asp Glu Ser Ala Val Ala Lys His Phe Val
225                 230                 235                 240
Ala Val Ser Thr Asn Ala Gln Lys Val Ala Glu Phe Gly Ile Asp Thr
                245                 250                 255
Asp Asn Met Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val
            260                 265                 270
Asp Ser Ala Ile Gly Leu Ser Leu Met Ala Val Ile Gly Pro Leu Asp
        275                 280                 285
Phe Met Arg Phe Leu Glu Gly Phe Arg Ala Met Asp Glu His Phe Arg
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    290                 295                 300
Ala Thr Pro Phe Glu Lys Asn Val Pro Val Leu Met Ala Leu Leu Gly
305                 310                 315                 320
Ile Trp Tyr Val Asn Phe His Gly Phe Glu Thr His Ala Val Leu Pro
                325                 330                 335
Tyr Ser Gln Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr
            340                 345                 350
Met Glu Ser Asn Gly Lys Ser Val Arg His Asp Gly Thr Ala Val Asp
        355                 360                 365
Tyr Ala Thr Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln
    370                 375                 380
His Ala Phe Tyr Gln Leu Met His Gln Gly Thr Arg Val Val Pro Ala
385                 390                 395                 400
Asp Phe Ile Gly Phe Ala Arg Pro Lys Asn Asp Leu Pro Thr Ala Thr
                405                 410                 415
Gly Glu Gly Ser Met His Asp Leu Leu Met Gly Asn Leu Phe Ala Gln
            420                 425                 430
Ser Lys Val Leu Ala Phe Gly Lys Thr Ala Glu Glu Ile Ala Ala Glu
        435                 440                 445
Gly Val Ser Ala Asp Leu Val Ala His Lys Val Met Pro Gly Asn Arg
    450                 455                 460
Pro Ser Thr Thr Ile Leu Ala Glu Glu Leu Thr Pro Ala Val Leu Gly
465                 470                 475                 480
Ala Leu Ile Ala Leu Tyr Glu His Ile Thr Phe Val Gln Gly Val Ile
                485                 490                 495
Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln
            500                 505                 510
Gln Ala Asn Gln Leu Ala Ala Ala Val Ser Gly Ala Glu Glu Val Asp
        515                 520                 525
Ser Gly Asp Ser Ser Thr Asp Ala Leu Val Arg Trp Tyr Arg Ala Asn
    530                 535                 540
Arg
545
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gaaagtgtgg cctccaacca gggcatttcc ggggaaaagg cacggtggcg gcggatcgac      180
ggcggataaa cccgctggat atgacctgtg acccgtacct catgtcctgt gagaccgtca      240
caaccgcgat ttaatggata ccctgtatag agagaactgc cgcaaacgtc aggagaacac      300
atg acc act gcc atc aag ggc ctc gtc ggc ccc gca ccg acc gat aac        348
Met Thr Thr Ala Ile Lys Gly Leu Val Gly Pro Ala Pro Thr Asp Asn
1               5                   10                  15
gag aag ctc ctc acc tgg atc gcc gag gca gtg gag ctg atg cag ccg        396
Glu Lys Leu Leu Thr Trp Ile Ala Glu Ala Val Glu Leu Met Gln Pro
            20                  25                  30
gag aag gtc gtc ttc gcc gac ggc tcc cag gag gag tgg gac cgc ctc        444
Glu Lys Val Val Phe Ala Asp Gly Ser Gln Glu Glu Trp Asp Arg Leu
        35                  40                  45
tcc gcc gag ctc gtg gag gca ggc acc ttc atc cgc ctc aac gag gag        492
Ser Ala Glu Leu Val Glu Ala Gly Thr Phe Ile Arg Leu Asn Glu Glu
    50                  55                  60
aag cgc ccg aac agc ttc ctg gcc cgc tcc aac ccg gac gat gtc gcc        540
Lys Arg Pro Asn Ser Phe Leu Ala Arg Ser Asn Pro Asp Asp Val Ala
65                  70                  75                  80
cgc gtc gag tcc cgc acc ttc atc tgc tcc gag aag gag gag gac gcc        588
Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala
                85                  90                  95
ggc ccg acc aac aac tgg gcg gac ccg gtc gag atg aag aag gag atg        636
Gly Pro Thr Asn Asn Trp Ala Asp Pro Val Glu Met Lys Lys Glu Met
            100                 105                 110
acc gag gta tac cgc ggc tcc atg aag ggc cgc acc atg tac gtc gtg        684
Thr Glu Val Tyr Arg Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val
        115                 120                 125
ccg ttc tgc atg ggc ccg atc acc gac ccg gag ccg aag ctc ggt gtc        732
Pro Phe Cys Met Gly Pro Ile Thr Asp Pro Glu Pro Lys Leu Gly Val
    130                 135                 140
cag ctc acc gac tcc gcc tac gtc gtc ctc tcc atg cgc atc atg acc        780
Gln Leu Thr Asp Ser Ala Tyr Val Val Leu Ser Met Arg Ile Met Thr
145                 150                 155                 160
cgt atg ggc tcc gag gcg ctc gag aag atc ggc acc gac ggc gat ttc        828
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Arg Met Gly Ser Glu Ala Leu Glu Lys Ile Gly Thr Asp Gly Asp Phe
                165                 170                 175
gtc cgc gca ctc cac tcc gtc ggc gcc ccg ctg gag ccg ggc cag gag        876
Val Arg Ala Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu
            180                 185                 190

gac gtc atc tgg ccg tgc aac gac acc aag tac atc acc cag ttc ccg        924
Asp Val Ile Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro
        195                 200                 205
gag acc aag gag atc tgg tcc tac ggc tcc ggt tac ggc ggc aac gcc        972
Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala
    210                 215                 220

atc ctg gcc aag aag tgc tac gcc ctg cgc atc gcc tcc gtc atg gcc       1020
Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala
225                 230                 235                 240

aag gag gag ggc tgg atg gct gag cac atg ctc atc ctg aag ctc aac       1068
Lys Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Asn
                245                 250                 255

tcc ccg gag ggc aag agc tac cac atc gcg gca gct ttc ccg tcc gcc       1116
Ser Pro Glu Gly Lys Ser Tyr His Ile Ala Ala Ala Phe Pro Ser Ala
            260                 265                 270
tgc ggc aag acc aac ctc gcc atg atc acc ccg acc atc gag ggc tgg       1164
Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Glu Gly Trp
        275                 280                 285
acc gcc gag gtc gtc ggc gac gac atc gcc tgg ctc aag ctg cgc gag       1212
Thr Ala Glu Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu
    290                 295                 300
gac ggc ctc tac gcc gtc aac ccg gag aac ggc ttc ttc ggc gtc gca       1260
Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala
305                 310                 315                 320
ccg ggc acc aac tac gcc tcc aac ccg atc gcc atg gag acc atg gag       1308
Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Glu Thr Met Glu
                325                 330                 335
ccg ggc aac acc ctg ttc acc aac gtc gca ctg acc gac gac ggt gac       1356
Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp
            340                 345                 350
gtc tgg tgg gag ggc atg gac ggc gag aag ccg gag cac ctc atc gac       1404
Val Trp Trp Glu Gly Met Asp Gly Glu Lys Pro Glu His Leu Ile Asp
        355                 360                 365
tgg ctg ggc aac gac tgg acc ccg gag tcc ggc acc aac gcc gca cac       1452
Trp Leu Gly Asn Asp Trp Thr Pro Glu Ser Gly Thr Asn Ala Ala His
    370                 375                 380
ccg aac tcc cgc tac tgc gtg gcc atc gag cag tgc ccg gtc gcc gca       1500
Pro Asn Ser Arg Tyr Cys Val Ala Ile Glu Gln Cys Pro Val Ala Ala
385                 390                 395                 400
ccg gag ttc aac gac ccg aag ggc gtc aag atc gac gcc atc ctc ttc       1548
Pro Glu Phe Asn Asp Pro Lys Gly Val Lys Ile Asp Ala Ile Leu Phe
                405                 410                 415
ggt ggc cgt cgt gcc gac acc gtc ccg ctg gtc acc cag tcc tac gac       1596
Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Ser Tyr Asp
            420                 425                 430
tgg gag cac ggc acc ttc atc ggt gcg acc ctg gcc tcc ggc cag acc       1644
Trp Glu His Gly Thr Phe Ile Gly Ala Thr Leu Ala Ser Gly Gln Thr
        435                 440                 445
gcc gca tcc gct gag gcg aag gtc ggc tcc ctg cgc cac gac ccg atg       1692
Ala Ala Ser Ala Glu Ala Lys Val Gly Ser Leu Arg His Asp Pro Met
    450                 455                 460
gcc atg ctg ccg ttc atg ggc tac aac gcc ggt gac tac ctg cag cac       1740
Ala Met Leu Pro Phe Met Gly Tyr Asn Ala Gly Asp Tyr Leu Gln His
465                 470                 475                 480
tgg atc gac atg ggc aag aag ggc ggc gac cgt atg ccg gcc atc ttc       1788
Trp Ile Asp Met Gly Lys Lys Gly Gly Asp Arg Met Pro Ala Ile Phe
                485                 490                 495
ctg gtc aac tgg ttc cgc cgt ggc gag gac ggc cgc ttc ctg tgg ccg       1836
Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro
            500                 505                 510
ggc ttc ggt gac aac tcc cgt gtc ctg aag tgg atc att gac cgc atc       1884
Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Ile Ile Asp Arg Ile
        515                 520                 525
gag ggc aag gtc gac gcc gag gag acc gtc gtg ggc cac acc gcc cgc       1932
Glu Gly Lys Val Asp Ala Glu Glu Thr Val Val Gly His Thr Ala Arg
    530                 535                 540
gcc gag gac ctc gac ctg acc ggc ctg gac acc ccg ctc gag gac gtc       1980
Ala Glu Asp Leu Asp Leu Thr Gly Leu Asp Thr Pro Leu Glu Asp Val
545                 550                 555                 560
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aag gag gcc ctg act gcg ccg gcc gca gac tgg gag cgc gac gtc gcc       2028
Lys Glu Ala Leu Thr Ala Pro Ala Ala Asp Trp Glu Arg Asp Val Ala
                565                 570                 575
gac aac gag gag tac ctg gca ttc ctc ggc ccg cgt gtc ccg aac gag       2076
Asp Asn Glu Glu Tyr Leu Ala Phe Leu Gly Pro Arg Val Pro Asn Glu
            580                 585                 590

gtc cac gag cag ctg ggc aag ctc aag gag cgc atc gag gcg aac aag       2124
Val His Glu Gln Leu Gly Lys Leu Lys Glu Arg Ile Glu Ala Asn Lys
        595                 600                 605
aac tag ttcgtctccc ctcagaactt ccaccctcca ggttgactca gtccctgggg        2180
Asn

ggtgggattt tttctgcccc ggtcgcaccg taagtccgag agaggatgtt cgagaggaga     2240
gtcctctcga acgtgcggga cccccgcggg actcctctcg acgatgtgat ctcgacgtca     2300
gggaagaggg gggaagggga acgccgtcag tgcttccgca gcacgaccac caggttcgac     2360
acgaggaact cccgcagcag cggcacccgc accatccacc acgcccacga ggggtggtag     2420
cgggggaagg                                                           2430
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Glu Lys Leu Leu Thr Trp Ile Ala Glu Ala Val Glu Leu Met Gln Pro
            20                  25                  30
Glu Lys Val Val Phe Ala Asp Gly Ser Gln Glu Glu Trp Asp Arg Leu
        35                  40                  45
Ser Ala Glu Leu Val Glu Ala Gly Thr Phe Ile Arg Leu Asn Glu Glu
    50                  55                  60
Lys Arg Pro Asn Ser Phe Leu Ala Arg Ser Asn Pro Asp Asp Val Ala
65                  70                  75                  80
Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala
                85                  90                  95
Gly Pro Thr Asn Asn Trp Ala Asp Pro Val Glu Met Lys Lys Glu Met
            100                 105                 110
Thr Glu Val Tyr Arg Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val
        115                 120                 125
Pro Phe Cys Met Gly Pro Ile Thr Asp Pro Glu Pro Lys Leu Gly Val
    130                 135                 140
Gln Leu Thr Asp Ser Ala Tyr Val Val Leu Ser Met Arg Ile Met Thr
145                 150                 155                 160
Arg Met Gly Ser Glu Ala Leu Glu Lys Ile Gly Thr Asp Gly Asp Phe
                165                 170                 175
Val Arg Ala Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu
            180                 185                 190
Asp Val Ile Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro
        195                 200                 205
Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala
    210                 215                 220
Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala
225                 230                 235                 240
Lys Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Asn
                245                 250                 255
Ser Pro Glu Gly Lys Ser Tyr His Ile Ala Ala Ala Phe Pro Ser Ala
            260                 265                 270
Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Glu Gly Trp
        275                 280                 285
Thr Ala Glu Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu
    290                 295                 300
Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala
305                 310                 315                 320
Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Glu Thr Met Glu
                325                 330                 335
Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp
            340                 345                 350
Val Trp Trp Glu Gly Met Asp Gly Glu Lys Pro Glu His Leu Ile Asp
        355                 360                 365
Trp Leu Gly Asn Asp Trp Thr Pro Glu Ser Gly Thr Asn Ala Ala His
    370                 375                 380
Pro Asn Ser Arg Tyr Cys Val Ala Ile Glu Gln Cys Pro Val Ala Ala
385                 390                 395                 400
Pro Glu Phe Asn Asp Pro Lys Gly Val Lys Ile Asp Ala Ile Leu Phe
                405                 410                 415
Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Ser Tyr Asp
            420                 425                 430
Trp Glu His Gly Thr Phe Ile Gly Ala Thr Leu Ala Ser Gly Gln Thr
```

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        435                 440                 445
Ala Ala Ser Ala Glu Ala Lys Val Gly Ser Leu Arg His Asp Pro Met
    450                 455                 460
Ala Met Leu Pro Phe Met Gly Tyr Asn Ala Gly Asp Tyr Leu Gln His
465                 470                 475                 480
Trp Ile Asp Met Gly Lys Lys Gly Gly Asp Arg Met Pro Ala Ile Phe
                485                 490                 495


Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro
            500                 505                 510
Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Ile Ile Asp Arg Ile
        515                 520                 525
Glu Gly Lys Val Asp Ala Glu Glu Thr Val Val Gly His Thr Ala Arg
    530                 535                 540
Ala Glu Asp Leu Asp Leu Thr Gly Leu Asp Thr Pro Leu Glu Asp Val
545                 550                 555                 560
Lys Glu Ala Leu Thr Ala Pro Ala Ala Asp Trp Glu Arg Asp Val Ala
                565                 570                 575
Asp Asn Glu Glu Tyr Leu Ala Phe Leu Gly Pro Arg Val Pro Asn Glu
            580                 585                 590
Val His Glu Gln Leu Gly Lys Leu Lys Glu Arg Ile Glu Ala Asn Lys
        595                 600                 605
Asn
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ccggagagga tgcgctccag ccgcgaccag ccgaggtgtg ccccaccgtg gaatcccatg       180
ccccgcaatc taccctgat cgaacagatg tgccacactg cccgcggcaa ggactagaca       240
gagcggtacg cccggtgcta ggtttcagaa ccaacgaacc gaacacgtaa ggacaccacc       300
atg act ttc cgt cgc ctc ctg gcc ggc acc gcc gcc gcc gtc atc gcc         348
Met Thr Phe Arg Arg Leu Leu Ala Gly Thr Ala Ala Ala Val Ile Ala
1               5                   10                  15
tcc gtg ggc ctc gtc gcc tgc ggc tcc ggc tcc tcc ggg gag acc gtc         396
Ser Val Gly Leu Val Ala Cys Gly Ser Gly Ser Ser Gly Glu Thr Val
            20                  25                  30
cgc atc ggc acc acc gac gcc cag ctc aag gag tgg gac gtc ttc gcc         444
Arg Ile Gly Thr Thr Asp Ala Gln Leu Lys Glu Trp Asp Val Phe Ala
        35                  40                  45
gac atc gtc gag gcg gag ggc atc gac atc gag atc gtg ccg ttc tcc         492
Asp Ile Val Glu Ala Glu Gly Ile Asp Ile Glu Ile Val Pro Phe Ser
    50                  55                  60
gac tac aac acc ccg aac gac gcg ctc gtg cag ggt gag atc gac gtc         540
Asp Tyr Asn Thr Pro Asn Asp Ala Leu Val Gln Gly Glu Ile Asp Val
65                  70                  75                  80
aac aag ttc cag cac ctg gac ttc ctc gcc tcc tac aac aaa ggc gcc         588
Asn Lys Phe Gln His Leu Asp Phe Leu Ala Ser Tyr Asn Lys Gly Ala
                85                  90                  95
aac gcc gac ctc gtg ccg tac gcc gcc acc gag atc aac ccg ctg tcc         636
Asn Ala Asp Leu Val Pro Tyr Ala Ala Thr Glu Ile Asn Pro Leu Ser
            100                 105                 110
ctg ttc tgg aag gac cac gac tcc ctc gac ggc atc gag ggc gag ggc         684
Leu Phe Trp Lys Asp His Asp Ser Leu Asp Gly Ile Glu Gly Glu Gly
        115                 120                 125
gtc gtc atc ccc aac gac gac acc aac cag ggc cgc gcc atc aac gtc         732
Val Val Ile Pro Asn Asp Asp Thr Asn Gln Gly Arg Ala Ile Asn Val
    130                 135                 140
ctc gcc cag gcc ggt ctg gtg acc ctg cgc gac gac agc gtc tac aac         780
Leu Ala Gln Ala Gly Leu Val Thr Leu Arg Asp Asp Ser Val Tyr Asn
145                 150                 155                 160
ccg acc ccg gcc gac gtc gac acc gag aag tcc aag gtc tcc atc gtc         828
Pro Thr Pro Ala Asp Val Asp Thr Glu Lys Ser Lys Val Ser Ile Val
                165                 170                 175
acc gtc gac gcc gcc cag acc acc acc gcc tac cac gag ggt cgc ccg         876
Thr Val Asp Ala Ala Gln Thr Thr Thr Ala Tyr His Glu Gly Arg Pro
            180                 185                 190
gcc atc atc aac aac tcc ttc ctg gag cgc gcc agc atc gac ccg tcc         924
Ala Ile Ile Asn Asn Ser Phe Leu Glu Arg Ala Ser Ile Asp Pro Ser
        195                 200                 205
ctc gcc atc ttc cag gat gac ccg agc acc gag cag gcc gag ccg tac         972
```

```
Leu Ala Ile Phe Gln Asp Asp Pro Ser Thr Glu Gln Ala Glu Pro Tyr
    210                 215                 220
atc aac gcc tgg gtg acc acc cgc gac aag gcc gac gac gag acc ctc      1020
Ile Asn Ala Trp Val Thr Thr Arg Asp Lys Ala Asp Asp Glu Thr Leu
225                 230                 235                 240
atc cgt ctc gcc gag ctg tgg aag gac ccg gcc gtc acc gcc gcc gtc      1068
Ile Arg Leu Ala Glu Leu Trp Lys Asp Pro Ala Val Thr Ala Ala Val
                245                 250                 255

ctg gag acc tcc ggc aac acc gcc gtc acc gtc gag cgc tcg ccc gag      1116
Leu Glu Thr Ser Gly Asn Thr Ala Val Thr Val Glu Arg Ser Pro Glu
            260                 265                 270
gag ctc gcc gcg atc atg gag cgc ctc gcg gcc cgc gag cag tag          1161
Glu Leu Ala Ala Ile Met Glu Arg Leu Ala Ala Arg Glu Gln
        275                 280                 285
gccgcactcc gcccacctgc cccgtcgcgt tcccgcggcg gggtttagca tttacctgac    1221
cagtccccct cccagaacgg cccccagaac accgtgaccg aacctgtgac cgcaccaccc    1281
acccggccgc gtaccggtac ccgcatcgag ttccgcgatg tgaccaaggt cttcaccaac    1341
cagcggaaga ccgagacccg cgccgtcgac ggcgtcaccc tgaccgtcga acccggcgag    1401
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1               5                   10                  15
Ser Val Gly Leu Val Ala Cys Gly Ser Gly Ser Ser Gly Glu Thr Val
            20                  25                  30
Arg Ile Gly Thr Thr Asp Ala Gln Leu Lys Glu Trp Asp Val Phe Ala
        35                  40                  45
Asp Ile Val Glu Ala Glu Gly Ile Asp Ile Glu Ile Val Pro Phe Ser
    50                  55                  60
Asp Tyr Asn Thr Pro Asn Asp Ala Leu Val Gln Gly Glu Ile Asp Val
65                  70                  75                  80
Asn Lys Phe Gln His Leu Asp Phe Leu Ala Ser Tyr Asn Lys Gly Ala
                85                  90                  95
Asn Ala Asp Leu Val Pro Tyr Ala Ala Thr Glu Ile Asn Pro Leu Ser
            100                 105                 110
Leu Phe Trp Lys Asp His Asp Ser Leu Asp Gly Ile Glu Gly Glu Gly
        115                 120                 125
Val Val Ile Pro Asn Asp Asp Thr Asn Gln Gly Arg Ala Ile Asn Val
    130                 135                 140
Leu Ala Gln Ala Gly Leu Val Thr Leu Arg Asp Asp Ser Val Tyr Asn
145                 150                 155                 160
Pro Thr Pro Ala Asp Val Asp Thr Glu Lys Ser Lys Val Ser Ile Val
                165                 170                 175
Thr Val Asp Ala Ala Gln Thr Thr Thr Ala Tyr His Glu Gly Arg Pro
            180                 185                 190
Ala Ile Ile Asn Asn Ser Phe Leu Glu Arg Ala Ser Ile Asp Pro Ser
        195                 200                 205
Leu Ala Ile Phe Gln Asp Asp Pro Ser Thr Glu Gln Ala Glu Pro Tyr
    210                 215                 220
Ile Asn Ala Trp Val Thr Thr Arg Asp Lys Ala Asp Asp Glu Thr Leu
225                 230                 235                 240
Ile Arg Leu Ala Glu Leu Trp Lys Asp Pro Ala Val Thr Ala Ala Val
                245                 250                 255
Leu Glu Thr Ser Gly Asn Thr Ala Val Thr Val Glu Arg Ser Pro Glu
            260                 265                 270
Glu Leu Ala Ala Ile Met Glu Arg Leu Ala Ala Arg Glu Gln
        275                 280                 285
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<223>  gen metP
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agggtggact tgccgacgtt gggcagaccg acgattccaa gagtaaggct cacgggcgta     120
gatcctagca gccagcggtt ttgcctctcc ggtcagcgcc cgtacctgtg ttgcgggatg     180
atacggacgt cattatatga tcaggccact tcaacgataa atacgtcgca ccctggacgt     240
tttcctctcc ctaaccatcg ggagccaact acacatcctc cacctcagac aggtatacac     300
atg tct tcg acc acc ccg cag ccc gcg ccg tcg ggc cag gag cag ggc       348
Met Ser Ser Thr Thr Pro Gln Pro Ala Pro Ser Gly Gln Glu Gln Gly
1               5                   10                  15
```

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gag cgg cgc gag atc ttc tcg tcc cgt tgg gcg ttc ctg ctg gcc gcc      396
Glu Arg Arg Glu Ile Phe Ser Ser Arg Trp Ala Phe Leu Leu Ala Ala
            20                  25                  30
atc ggc tcc gcc gtc ggc ctg ggc aac atc tgg cgc ttc ccc tac gtc      444
Ile Gly Ser Ala Val Gly Leu Gly Asn Ile Trp Arg Phe Pro Tyr Val
        35                  40                  45
gct tac gac aac ggc ggc ggc gcc ttc ctc atc ccc tac ctc gtg gca      492
Ala Tyr Asp Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr Leu Val Ala
    50                  55                  60

ctg ctg tcc gct ggt atc ccg ctg ctc ttc ctc gac tac gcc ctg ggc      540
Leu Leu Ser Ala Gly Ile Pro Leu Leu Phe Leu Asp Tyr Ala Leu Gly
65                  70                  75                  80
cac cgc tac cgt ggt tcc gcc ccg ctg gtg ttc cgt cgc atc aag tcc      588
His Arg Tyr Arg Gly Ser Ala Pro Leu Val Phe Arg Arg Ile Lys Ser
                85                  90                  95
tgg gct gag ccg gtc ggc tgg gtc cag gtc ggt gtg tcc ttt ttc atc      636
Trp Ala Glu Pro Val Gly Trp Val Gln Val Gly Val Ser Phe Phe Ile
            100                 105                 110
act atc tac tac gcc gcg atc atc ggc tgg gcc gcg ctc tac gcg gtc      684
Thr Ile Tyr Tyr Ala Ala Ile Ile Gly Trp Ala Ala Leu Tyr Ala Val
        115                 120                 125
aag tcc ttc aac aag gcg tgg ggc acc gac ccg aac agc tac ttc ttc      732
Lys Ser Phe Asn Lys Ala Trp Gly Thr Asp Pro Asn Ser Tyr Phe Phe
    130                 135                 140
ggc gat ttc ctc cag ttc gac gag acc gcc acc ttc tcc acc gac ttc      780
Gly Asp Phe Leu Gln Phe Asp Glu Thr Ala Thr Phe Ser Thr Asp Phe
145                 150                 155                 160
gtc ccg cag atc gcc ctg gcc ctg gcc ggc gtg tgg atc gcc gcg atc      828
Val Pro Gln Ile Ala Leu Ala Leu Ala Gly Val Trp Ile Ala Ala Ile
                165                 170                 175
atc gtg ctg gcg atc ggc gtg gac aag ggc atc ggc aag gtc tcc aag      876
Ile Val Leu Ala Ile Gly Val Asp Lys Gly Ile Gly Lys Val Ser Lys
            180                 185                 190
atc ttc atc ccc ctg ctg gcg gtc ctc ttc ctc atc gtc gta gtc cag      924
Ile Phe Ile Pro Leu Leu Ala Val Leu Phe Leu Ile Val Val Val Gln
        195                 200                 205
gcg ctc atg ctg ccg ggt gcc gcc acg ggt ctc gac gcc ctg ttc acc      972
Ala Leu Met Leu Pro Gly Ala Ala Thr Gly Leu Asp Ala Leu Phe Thr
    210                 215                 220
ccg gac tgg aac gcc ctg acc aac ggc act gtg tgg atc gcc gcc tac     1020
Pro Asp Trp Asn Ala Leu Thr Asn Gly Thr Val Trp Ile Ala Ala Tyr
225                 230                 235                 240
ggc cag atc ttc ttc tcc ctg tcc gtg agc ttc ggc atc atg ctc acc     1068
Gly Gln Ile Phe Phe Ser Leu Ser Val Ser Phe Gly Ile Met Leu Thr
                245                 250                 255
tac tcc tcc tac ctg cgt ccg cgc acc aac ctg acg ggc acc ggc ctg     1116
Tyr Ser Ser Tyr Leu Arg Pro Arg Thr Asn Leu Thr Gly Thr Gly Leu
            260                 265                 270
acc acc gcc ttc gcg aac tcc tcc ttc gag gtc ctc gcc ggc gtc ggt     1164
Thr Thr Ala Phe Ala Asn Ser Ser Phe Glu Val Leu Ala Gly Val Gly
        275                 280                 285
gtc ttc gcc gcc ctg ggc ttc atg gcc gtg cag cag tcg gtc gcc gtc     1212
Val Phe Ala Ala Leu Gly Phe Met Ala Val Gln Gln Ser Val Ala Val
    290                 295                 300
gac gag gtc gcg acc tcg ggc atc ggt ctg gcc ttc gtg gcc ttc ccg     1260
Asp Glu Val Ala Thr Ser Gly Ile Gly Leu Ala Phe Val Ala Phe Pro
305                 310                 315                 320
gcg atc atc aac gag atg gcc ttc ggc ccg atc ttc ggc gtc ctg ttc     1308
Ala Ile Ile Asn Glu Met Ala Phe Gly Pro Ile Phe Gly Val Leu Phe
                325                 330                 335
ttc ggc tcc ctc acc atc gcc ggc ttc acc tcg ctg ttc tcc ctg ctc     1356
Phe Gly Ser Leu Thr Ile Ala Gly Phe Thr Ser Leu Phe Ser Leu Leu
            340                 345                 350
gag gtc gtc gtc tcc gcc gtc aag gac aag ctg aac ctg ccg cgc aag     1404
Glu Val Val Val Ser Ala Val Lys Asp Lys Leu Asn Leu Pro Arg Lys
        355                 360                 365
acc gtc gcc atc ggc atc ggc acc ttc atg gcg ctg atc tcc ctg gcg     1452
Thr Val Ala Ile Gly Ile Gly Thr Phe Met Ala Leu Ile Ser Leu Ala
    370                 375                 380
ctg ttc tcc acg acg tcc ggc ctc atg gcc ctg gac atc atg gac aag     1500
Leu Phe Ser Thr Thr Ser Gly Leu Met Ala Leu Asp Ile Met Asp Lys
385                 390                 395                 400
ttc acc aac aac atc ggc atc gtc gcc atc gcc ctg atc gcg gtc atc     1548
Phe Thr Asn Asn Ile Gly Ile Val Ala Ile Ala Leu Ile Ala Val Ile
                405                 410                 415
atc ctc gat tgg gtc ctg cgc cgg atc gac gag ttc tcg ctc cac atc     1596
Ile Leu Asp Trp Val Leu Arg Arg Ile Asp Glu Phe Ser Leu His Ile
```

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            420                 425                 430
aac gcc gtg tcc tcc ttc aag gtg ggc acg ctg tgg cgc atc ttc gtg      1644
Asn Ala Val Ser Ser Phe Lys Val Gly Thr Leu Trp Arg Ile Phe Val
        435                 440                 445
gtc aac gtc acc acc ctg gtg ctg gga ttc acc ctg gcg cag gag ctc      1692
Val Asn Val Thr Thr Leu Val Leu Gly Phe Thr Leu Ala Gln Glu Leu
    450                 455                 460
atc tcc ctg atc cag gag ccc tac ggc ggc tac acg acg acg cag atc      1740
Ile Ser Leu Ile Gln Glu Pro Tyr Gly Gly Tyr Thr Thr Thr Gln Ile
465                 470                 475                 480

gcc atc tac ggc tgg gcc gtc ctg gcg ctc atc ggt atc aac gcc ctc      1788
Ala Ile Tyr Gly Trp Ala Val Leu Ala Leu Ile Gly Ile Asn Ala Leu
                485                 490                 495
gtc ttc tcc ctg gtg ccg tgg cgc ggc aac ctg ccg ctc aac ggt ccg      1836
Val Phe Ser Leu Val Pro Trp Arg Gly Asn Leu Pro Leu Asn Gly Pro
            500                 505                 510
ccg ggc tcc gac ttc ggt gtt gac ccg gag gtc cac cgc gag ctc cac      1884
Pro Gly Ser Asp Phe Gly Val Asp Pro Glu Val His Arg Glu Leu His
        515                 520                 525
gcg ccg cgc aag tac aac ggt gac cac cgg gtg ggc gtc gac aag cac      1932
Ala Pro Arg Lys Tyr Asn Gly Asp His Arg Val Gly Val Asp Lys His
    530                 535                 540
acc acc gag gaa gga acg atc cga tga gcggtctcgc aatcatgatg            1979
Thr Thr Glu Glu Gly Thr Ile Arg
545                 550
atggtcctgt tcatggtcgt catctggggt ggtttcatcg ccagcgccct gcacctgcgg     2039
gcgaaccccg atgacacctc cggcgccctg ggcgtcgcgg accatgcgcg cgacgagcac     2099
ctcgccgcgc aggaactcca ctagtcacac cacaccggga tgtcaggcaa tatggagtct     2159
gtgactgacc agccgacctc ccgcatcccc ggggacgaga ctcccccgac cggctcctcc     2219
ggcgacgccg ggtccaccgc cttcggcagc atggacctgg                           2259
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1               5                   10                  15
Glu Arg Arg Glu Ile Phe Ser Ser Arg Trp Ala Phe Leu Leu Ala Ala
            20                  25                  30
Ile Gly Ser Ala Val Gly Leu Gly Asn Ile Trp Arg Phe Pro Tyr Val
        35                  40                  45
Ala Tyr Asp Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr Leu Val Ala
    50                  55                  60
Leu Leu Ser Ala Gly Ile Pro Leu Leu Phe Leu Asp Tyr Ala Leu Gly
65                  70                  75                  80
His Arg Tyr Arg Gly Ser Ala Pro Leu Val Phe Arg Arg Ile Lys Ser
                85                  90                  95
Trp Ala Glu Pro Val Gly Trp Val Gln Val Gly Val Ser Phe Phe Ile
            100                 105                 110
Thr Ile Tyr Tyr Ala Ala Ile Ile Gly Trp Ala Ala Leu Tyr Ala Val
        115                 120                 125
Lys Ser Phe Asn Lys Ala Trp Gly Thr Asp Pro Asn Ser Tyr Phe Phe
    130                 135                 140
Gly Asp Phe Leu Gln Phe Asp Glu Thr Ala Thr Phe Ser Thr Asp Phe
145                 150                 155                 160
Val Pro Gln Ile Ala Leu Ala Leu Ala Gly Val Trp Ile Ala Ala Ile
                165                 170                 175
Ile Val Leu Ala Ile Gly Val Asp Lys Gly Ile Gly Lys Val Ser Lys
            180                 185                 190
Ile Phe Ile Pro Leu Leu Ala Val Leu Phe Leu Ile Val Val Val Gln
        195                 200                 205
Ala Leu Met Leu Pro Gly Ala Ala Thr Gly Leu Asp Ala Leu Phe Thr
    210                 215                 220
Pro Asp Trp Asn Ala Leu Thr Asn Gly Thr Val Trp Ile Ala Ala Tyr
225                 230                 235                 240
Gly Gln Ile Phe Phe Ser Leu Ser Val Ser Phe Gly Ile Met Leu Thr
                245                 250                 255
Tyr Ser Ser Tyr Leu Arg Pro Arg Thr Asn Leu Thr Gly Thr Gly Leu
            260                 265                 270
Thr Thr Ala Phe Ala Asn Ser Ser Phe Glu Val Leu Ala Gly Val Gly
        275                 280                 285
Val Phe Ala Ala Leu Gly Phe Met Ala Val Gln Gln Ser Val Ala Val
    290                 295                 300
Asp Glu Val Ala Thr Ser Gly Ile Gly Leu Ala Phe Val Ala Phe Pro
305                 310                 315                 320
Ala Ile Ile Asn Glu Met Ala Phe Gly Pro Ile Phe Gly Val Leu Phe
                325                 330                 335
```

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Phe Gly Ser Leu Thr Ile Ala Gly Phe Thr Ser Leu Phe Ser Leu Leu
            340                 345                 350
Glu Val Val Val Ser Ala Val Lys Asp Lys Leu Asn Leu Pro Arg Lys
        355                 360                 365
Thr Val Ala Ile Gly Ile Gly Thr Phe Met Ala Leu Ile Ser Leu Ala
    370                 375                 380
Leu Phe Ser Thr Thr Ser Gly Leu Met Ala Leu Asp Ile Met Asp Lys
385                 390                 395                 400
Phe Thr Asn Asn Ile Gly Ile Val Ala Ile Ala Leu Ile Ala Val Ile
                405                 410                 415
Ile Leu Asp Trp Val Leu Arg Arg Ile Asp Glu Phe Ser Leu His Ile
            420                 425                 430
Asn Ala Val Ser Ser Phe Lys Val Gly Thr Leu Trp Arg Ile Phe Val
        435                 440                 445
Val Asn Val Thr Thr Leu Val Leu Gly Phe Thr Leu Ala Gln Glu Leu
    450                 455                 460
Ile Ser Leu Ile Gln Glu Pro Tyr Gly Gly Tyr Thr Thr Thr Gln Ile
465                 470                 475                 480
Ala Ile Tyr Gly Trp Ala Val Leu Ala Leu Ile Gly Ile Asn Ala Leu
                485                 490                 495
Val Phe Ser Leu Val Pro Trp Arg Gly Asn Leu Pro Leu Asn Gly Pro
            500                 505                 510
Pro Gly Ser Asp Phe Gly Val Asp Pro Glu Val His Arg Glu Leu His
        515                 520                 525
Ala Pro Arg Lys Tyr Asn Gly Asp His Arg Val Gly Val Asp Lys His
    530                 535                 540
Thr Thr Glu Glu Gly Thr Ile Arg
545                 550
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ccgtacatca acgcctgggt gaccacccgc gacaaggccg acgacgagac cctcatccgt      60
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accgccgtca ccgtcgagcg ctcgcccgag gagctcgccg cgatcatgga gcgcctcgcg     180
gcccgcgagc agtaggccgc actccgccca cctgccccgt cgcgttcccg cggcggggtt     240
tagcatttac ctgaccagtc cccctcccag aacggccccc agaacaccgt gaccgaacct     300
gtg acc gca cca ccc acc cgg ccg cgt acc ggt acc cgc atc gag ttc       348
Val Thr Ala Pro Pro Thr Arg Pro Arg Thr Gly Thr Arg Ile Glu Phe
1               5                  10                  15
cgc gat gtg acc aag gtc ttc acc aac cag cgg aag acc gag acc cgc       396
Arg Asp Val Thr Lys Val Phe Thr Asn Gln Arg Lys Thr Glu Thr Arg
            20                  25                  30
gcc gtc gac ggc gtc acc ctg acc gtc gaa ccc ggc gag atc ctc ggc       444
Ala Val Asp Gly Val Thr Leu Thr Val Glu Pro Gly Glu Ile Leu Gly
        35                  40                  45
gtc atc ggc tac tcc ggc gcc ggc aag tcg acg ctc gtc cgc ctc atc       492
Val Ile Gly Tyr Ser Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile
    50                  55                  60
aac ggg ctg gac tcc aca acc tcc ggc cag ctg ctt ctc gac ggc acc       540
Asn Gly Leu Asp Ser Thr Thr Ser Gly Gln Leu Leu Leu Asp Gly Thr
65                  70                  75                  80
gac atc gtc gga ctc ccc gag tcc aag ctg cgc tcg atc cgc cgg ggc       588
Asp Ile Val Gly Leu Pro Glu Ser Lys Leu Arg Ser Ile Arg Arg Gly
                85                  90                  95
atc ggc atg atc ttc cag cag ttc aac ctc ttc cag tcc cgc acg gcc       636
Ile Gly Met Ile Phe Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala
            100                 105                 110
gcc ggc aac atc gcc tac ccg ctg gag ctg gcc ggc atg ccg cgc gcg       684
Ala Gly Asn Ile Ala Tyr Pro Leu Glu Leu Ala Gly Met Pro Arg Ala
        115                 120                 125
gag cgg cgg cgg cgc gtc gcc gag ctc ctc gac ttc gtc ggc ctg ggc       732
Glu Arg Arg Arg Arg Val Ala Glu Leu Leu Asp Phe Val Gly Leu Gly
    130                 135                 140
gac aag ggc gac aac tac ccg gag cag ctg tcg ggc ggc cag aag cag       780
Asp Lys Gly Asp Asn Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln
145                 150                 155                 160
cgc gtc ggc atc gcc cgc gcc ctg gcc acc aac ccg cgg ctc ctg ctc       828
Arg Val Gly Ile Ala Arg Ala Leu Ala Thr Asn Pro Arg Leu Leu Leu
                165                 170                 175
gcc gac gag gcc acc tcg gcc ctc gac ccg gag acc acc cag gac gtg       876
Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro Glu Thr Thr Gln Asp Val
            180                 185                 190
```

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ctc gac ctg ctc cgg gag atc aac cgc gag ctg ggc atc acc atc gtc        924
Leu Asp Leu Leu Arg Glu Ile Asn Arg Glu Leu Gly Ile Thr Ile Val
        195                 200                 205
gta atc acc cat gag atg gac gtc gtg cgt tcc atc gcc gac aag gtc        972
Val Ile Thr His Glu Met Asp Val Val Arg Ser Ile Ala Asp Lys Val
    210                 215                 220
gcc gtc atg gag gcc ggc cgg gtg gtc gag cac ggc agc gtc tac gag       1020
Ala Val Met Glu Ala Gly Arg Val Val Glu His Gly Ser Val Tyr Glu
225                 230                 235                 240
gtg ttc tcc cgc ccg cag act gcg gtg gcg cgg cgc ttc gtg tcc acc       1068
Val Phe Ser Arg Pro Gln Thr Ala Val Ala Arg Arg Phe Val Ser Thr
                245                 250                 255
tcg ctg cgc aac acc ccc gac cag gtc gag gcg gag gac ctg ctg gcc       1116
Ser Leu Arg Asn Thr Pro Asp Gln Val Glu Ala Glu Asp Leu Leu Ala
            260                 265                 270
cac gag ggc cgc ctg ttc acc atc acc ctc acg gag gac tcc ggg ttc       1164
His Glu Gly Arg Leu Phe Thr Ile Thr Leu Thr Glu Asp Ser Gly Phe
        275                 280                 285
ttc gcc gcg gcc gcc gcc ggc cgt gag gag ggg atg ctc atc aac atc       1212
Phe Ala Ala Ala Ala Ala Gly Arg Glu Glu Gly Met Leu Ile Asn Ile
    290                 295                 300
gtc cac ggc ggc gtc acc acg ctg cag cgg cag tcc ttc ggc aag atg       1260
Val His Gly Gly Val Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met
305                 310                 315                 320
acc gtc cgg gtg acg ggg ccg gac gcg gcc gtc gag aag ttc cgt gac       1308
Thr Val Arg Val Thr Gly Pro Asp Ala Ala Val Glu Lys Phe Arg Asp
                325                 330                 335
acg ctg tcc cgc acc acc gac atc cag gag atc acg cga tga               1350
Thr Leu Ser Arg Thr Thr Asp Ile Gln Glu Ile Thr Arg
            340                 345
acgagaccct cctcgccgca gactggaacc gtctcggccc gaccttcatc gacgccatcg     1410
gcgacaccct cgtcatggtg tccctcacga tggtgctcgg cggcctcggc ggcctgctca     1470
tcggcctgct gctgtacacg tcccgcgcgg gcggcatcct gcagtcgaag ccgctgtact     1530
ggacgctcaa catcctggtg aacttcgtcc gcccgatccc cttcatcgtg ctcatcgcca     1590
tgctggcgcc ggtgacggtc caggtcgtgg gcaccaccat cggccggtcc gcggcgatct     1650
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<213>  Corynebacterium humireducens
<400>  14
Val Thr Ala Pro Pro Thr Arg Pro Arg Thr Gly Thr Arg Ile Glu Phe
1               5                  10                  15
Arg Asp Val Thr Lys Val Phe Thr Asn Gln Arg Lys Thr Glu Thr Arg
            20                  25                  30
Ala Val Asp Gly Val Thr Leu Thr Val Glu Pro Gly Glu Ile Leu Gly
        35                  40                  45
Val Ile Gly Tyr Ser Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile
    50                  55                  60
Asn Gly Leu Asp Ser Thr Thr Ser Gly Gln Leu Leu Leu Asp Gly Thr
65                  70                  75                  80
Asp Ile Val Gly Leu Pro Glu Ser Lys Leu Arg Ser Ile Arg Arg Gly
                85                  90                  95
Ile Gly Met Ile Phe Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala
            100                 105                 110
Ala Gly Asn Ile Ala Tyr Pro Leu Glu Leu Ala Gly Met Pro Arg Ala
        115                 120                 125
Glu Arg Arg Arg Arg Val Ala Glu Leu Leu Asp Phe Val Gly Leu Gly
    130                 135                 140
Asp Lys Gly Asp Asn Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln
145                 150                 155                 160
Arg Val Gly Ile Ala Arg Ala Leu Ala Thr Asn Pro Arg Leu Leu Leu
                165                 170                 175
Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro Glu Thr Thr Gln Asp Val
            180                 185                 190
Leu Asp Leu Leu Arg Glu Ile Asn Arg Glu Leu Gly Ile Thr Ile Val
        195                 200                 205
Val Ile Thr His Glu Met Asp Val Val Arg Ser Ile Ala Asp Lys Val
    210                 215                 220
Ala Val Met Glu Ala Gly Arg Val Val Glu His Gly Ser Val Tyr Glu
225                 230                 235                 240
Val Phe Ser Arg Pro Gln Thr Ala Val Ala Arg Arg Phe Val Ser Thr
                245                 250                 255
Ser Leu Arg Asn Thr Pro Asp Gln Val Glu Ala Glu Asp Leu Leu Ala
            260                 265                 270
His Glu Gly Arg Leu Phe Thr Ile Thr Leu Thr Glu Asp Ser Gly Phe
        275                 280                 285
Phe Ala Ala Ala Ala Ala Gly Arg Glu Glu Gly Met Leu Ile Asn Ile
    290                 295                 300
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Val His Gly Gly Val Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met
305                 310                 315                 320
Thr Val Arg Val Thr Gly Pro Asp Ala Ala Val Glu Lys Phe Arg Asp
                325                 330                 335
Thr Leu Ser Arg Thr Thr Asp Ile Gln Glu Ile Thr Arg
            340                 345
<210>  15
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<213>  Corynebacterium humireducens
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<222>  (301)..(1554)
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ctgctcatgg ccaacgaggt gggggagggc cgggtcttcg gccagacccg caacagcggc      120
tggctgctca ccgccgacgg cgctgtcacg gaggttccgg acggttccaa gcacgtggtg      180
gcggcggcga tcctcagcgc cgtcgacgac ctgcgcaatt gacgctttta gaccgcttgg      240
tctatattgg gcgggacgct cagtcatatc attaatttga cccccgaaaa ggacccgccc      300
gtg tca gag aac ccc gcc acc acc acg gtg gcc ttc gac aag ccc gcc         348
Val Ser Glu Asn Pro Ala Thr Thr Thr Val Ala Phe Asp Lys Pro Ala
1               5                   10                  15
acg atc cgc ctg ttc acc agc gag tcc gtc acc gag ggc cac ccg gac        396
Thr Ile Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
            20                  25                  30
aag atc tgc gac gcc atc tcg gac acc atc ctc gac gcc atg ctc gag        444
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Met Leu Glu
        35                  40                  45
cag gac ccg acc gcg cgc gtg gcc gtc gag acg ctc gtg acc acc ggc        492
Gln Asp Pro Thr Ala Arg Val Ala Val Glu Thr Leu Val Thr Thr Gly
    50                  55                  60
cag gtc cac gtc gtc ggt gag gtc cgc acc acc ggc tac gtc gag atc        540
Gln Val His Val Val Gly Glu Val Arg Thr Thr Gly Tyr Val Glu Ile
65                  70                  75                  80
ccg cag ctc gtg cgc aag acc ctc gtg gac atc ggc ttc atc tcc tcc        588
Pro Gln Leu Val Arg Lys Thr Leu Val Asp Ile Gly Phe Ile Ser Ser
                85                  90                  95
gag gtc ggc ttc gac ggc acc acc tgc ggc gtc aac atc gcc atc ggc        636
Glu Val Gly Phe Asp Gly Thr Thr Cys Gly Val Asn Ile Ala Ile Gly
            100                 105                 110
gag cag tcc cag gag atc gcc gac ggc gtc gac tcc tcc cac gag gag        684
Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Ser Ser His Glu Glu
        115                 120                 125
cgt tcc ggc gtc gag atc gac gag gac gac cgc gcc ggc gcc ggc gac        732
Arg Ser Gly Val Glu Ile Asp Glu Asp Asp Arg Ala Gly Ala Gly Asp
    130                 135                 140
cag ggc ctc atg ttc ggc tac gcc agc aac gag acc ccc gag tac atg        780
Gln Gly Leu Met Phe Gly Tyr Ala Ser Asn Glu Thr Pro Glu Tyr Met
145                 150                 155                 160
ccg ctg ccc atc gcc ctg gcc cac cgc ctg gcc cgc cgc ctc acc gag        828
Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ala Arg Arg Leu Thr Glu
                165                 170                 175
gtg cgc aac cag ggc atc gtc ccg cac ctg cgt ccc gac ggc aag acc        876
Val Arg Asn Gln Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr
            180                 185                 190
cag gtc acc ttc gcc tac gac gag cag gac cgc ccg gtc cgc ctc gac        924
Gln Val Thr Phe Ala Tyr Asp Glu Gln Asp Arg Pro Val Arg Leu Asp
        195                 200                 205
acc gtg gtc atc tcc acg cag cac gac ccg gag gtc acc cag gac tgg        972
Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Thr Gln Asp Trp
    210                 215                 220
ctg cac gag cag ctg cgc gag cac gtc ctc gac tgg gtc atc gcc gac       1020
Leu His Glu Gln Leu Arg Glu His Val Leu Asp Trp Val Ile Ala Asp
225                 230                 235                 240
gcc ggc ctg atc ggc atg gtc gac gag gag ctc acc ctc ctg gtc aac       1068
Ala Gly Leu Ile Gly Met Val Asp Glu Glu Leu Thr Leu Leu Val Asn
                245                 250                 255
ccg tcc ggc tcc ttc atc ctc ggc ggc ccg atg ggc gac gct ggc ctg       1116
Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu
            260                 265                 270
acg ggc cgc aag atc atc gtc gac acc tac ggc ggc atg gcc cgc cac       1164
Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His
        275                 280                 285
ggc ggc ggc gcc ttc tcc ggc aag gac ccg tcc aag gtg gac cgt tcc       1212
Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser
    290                 295                 300
gcc gcg tac gcc atg cgc tgg gtg gcc aag aac atc gtc gcc gcc ggc       1260
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Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
305                 310                 315                 320
ctg gcc gag cgc gtc gag gtc cag gtg gcc tac gcc atc ggc cgc gcg      1308
Leu Ala Glu Arg Val Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
                325                 330                 335
aag ccg gtc ggc ctc tac gtg gag tcc ttc ggc acc gcc gcc gcg ggc      1356
Lys Pro Val Gly Leu Tyr Val Glu Ser Phe Gly Thr Ala Ala Ala Gly
            340                 345                 350
ctc agt gac gcg gac atc cag ggc gcc gtc gag aag gtc ttc gac ctg      1404
Leu Ser Asp Ala Asp Ile Gln Gly Ala Val Glu Lys Val Phe Asp Leu
        355                 360                 365
cgg ccc gcc gcc atc atc cgc gag ctc gac ctg ctg cgc ccg atc tac      1452
Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
    370                 375                 380

gcg cag acc tcc gcc tac ggc cac ttc ggc cgc ctc gac ctg gat ctg      1500
Ala Gln Thr Ser Ala Tyr Gly His Phe Gly Arg Leu Asp Leu Asp Leu
385                 390                 395                 400
ccc tgg gag cgg ctc aac cgg gtg gac gag ctc aag gcg gct ctg ggc      1548
Pro Trp Glu Arg Leu Asn Arg Val Asp Glu Leu Lys Ala Ala Leu Gly
                405                 410                 415
cgc tag agtattcggc atggcctccc cccgcgtccc cgcagaacac ctgccggtgg      1604
Arg

cgcgggttct gcctctcctg ggcctggccc acctcgaccg gcccttcgac taccaggtgc     1664
cgtcgacgct ggatgacgac gcccagcccg gcgtccgcgt ccgcatccgc ttcgccgggc     1724
ggcttgtcga cgccgtcctc ctcgaacgcc gcgccgacac cgagcacgag ggcgggctga     1784
gctggatcga gcgggtgatc tccccgcacg tcgtgtaccc gccgcgcacc gcccggctca     1844
tcgaggcgct                                                           1854
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<211>  417
<212>  PRT
<213>  Corynebacterium humireducens
<400>  16
Val Ser Glu Asn Pro Ala Thr Thr Thr Val Ala Phe Asp Lys Pro Ala
1               5                   10                  15
Thr Ile Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
            20                  25                  30
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Met Leu Glu
        35                  40                  45
Gln Asp Pro Thr Ala Arg Val Ala Val Glu Thr Leu Val Thr Thr Gly
    50                  55                  60
Gln Val His Val Val Gly Glu Val Arg Thr Thr Gly Tyr Val Glu Ile
65                  70                  75                  80
Pro Gln Leu Val Arg Lys Thr Leu Val Asp Ile Gly Phe Ile Ser Ser
                85                  90                  95
Glu Val Gly Phe Asp Gly Thr Thr Cys Gly Val Asn Ile Ala Ile Gly
            100                 105                 110
Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Ser Ser His Glu Glu
        115                 120                 125
Arg Ser Gly Val Glu Ile Asp Glu Asp Asp Arg Ala Gly Ala Gly Asp
    130                 135                 140
Gln Gly Leu Met Phe Gly Tyr Ala Ser Asn Glu Thr Pro Glu Tyr Met
145                 150                 155                 160
Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ala Arg Arg Leu Thr Glu
                165                 170                 175
Val Arg Asn Gln Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr
            180                 185                 190
Gln Val Thr Phe Ala Tyr Asp Glu Gln Asp Arg Pro Val Arg Leu Asp
        195                 200                 205
Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Thr Gln Asp Trp
    210                 215                 220
Leu His Glu Gln Leu Arg Glu His Val Leu Asp Trp Val Ile Ala Asp
225                 230                 235                 240
Ala Gly Leu Ile Gly Met Val Asp Glu Glu Leu Thr Leu Leu Val Asn
                245                 250                 255
Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu
            260                 265                 270
Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His
        275                 280                 285
Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser
    290                 295                 300
Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
305                 310                 315                 320
Leu Ala Glu Arg Val Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
                325                 330                 335
Lys Pro Val Gly Leu Tyr Val Glu Ser Phe Gly Thr Ala Ala Ala Gly
            340                 345                 350
```

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Leu Ser Asp Ala Asp Ile Gln Gly Ala Val Glu Lys Val Phe Asp Leu
        355                 360                 365
Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
    370                 375                 380
Ala Gln Thr Ser Ala Tyr Gly His Phe Gly Arg Leu Asp Leu Asp Leu
385                 390                 395                 400
Pro Trp Glu Arg Leu Asn Arg Val Asp Glu Leu Lys Ala Ala Leu Gly
                405                 410                 415
Arg
<210>  17
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<222>  (301)..(978)
<223>  gen metI
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cctgctggcc cacgagggcc gcctgttcac catcaccctc acggaggact ccgggttctt      120
cgccgcggcc gccgccggcc gtgaggaggg gatgctcatc aacatcgtcc acggcggcgt      180
caccacgctg cagcggcagt ccttcggcaa gatgaccgtc cgggtgacgg ggccggacgc      240
ggccgtcgag aagttccgtg acacgctgtc ccgcaccacc gacatccagg agatcacgcg      300
atg aac gag acc ctc ctc gcc gca gac tgg aac cgt ctc ggc ccg acc         348
Met Asn Glu Thr Leu Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr
1               5                   10                  15
ttc atc gac gcc atc ggc gac acc ctc gtc atg gtg tcc ctc acg atg        396
Phe Ile Asp Ala Ile Gly Asp Thr Leu Val Met Val Ser Leu Thr Met
            20                  25                  30
gtg ctc ggc ggc ctc ggc ggc ctg ctc atc ggc ctg ctg ctg tac acg        444
Val Leu Gly Gly Leu Gly Gly Leu Leu Ile Gly Leu Leu Leu Tyr Thr
        35                  40                  45
tcc cgc gcg ggc ggc atc ctg cag tcg aag ccg ctg tac tgg acg ctc        492
Ser Arg Ala Gly Gly Ile Leu Gln Ser Lys Pro Leu Tyr Trp Thr Leu
    50                  55                  60
aac atc ctg gtg aac ttc gtc cgc ccg atc ccc ttc atc gtg ctc atc        540
Asn Ile Leu Val Asn Phe Val Arg Pro Ile Pro Phe Ile Val Leu Ile
65                  70                  75                  80
gcc atg ctg gcg ccg gtg acg gtc cag gtc gtg ggc acc acc atc ggc        588
Ala Met Leu Ala Pro Val Thr Val Gln Val Val Gly Thr Thr Ile Gly
                85                  90                  95
cgg tcc gcg gcg atc ttc gtc atg tgc atc gcc gcc gcc ttc gcc gtg        636
Arg Ser Ala Ala Ile Phe Val Met Cys Ile Ala Ala Ala Phe Ala Val
            100                 105                 110
gcc cgc atc gtc gag cag aac ctc gtg gcc atc gac ccc ggc gtc atc        684
Ala Arg Ile Val Glu Gln Asn Leu Val Ala Ile Asp Pro Gly Val Ile
        115                 120                 125
gag gcc gcc cgc gcc atg ggg gcg ggg ccg tgg cgg atc atc cgc acg        732
Glu Ala Ala Arg Ala Met Gly Ala Gly Pro Trp Arg Ile Ile Arg Thr
    130                 135                 140
gtg atc atc ccg gag gcc ctc ggc ccg ctg gtc ctc ggc tac acg ttc        780
Val Ile Ile Pro Glu Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe
145                 150                 155                 160
atc ttc atc gcg gtg gtc gac atg tcc gcg atg gcc ggc tac atc ggc        828
Ile Phe Ile Ala Val Val Asp Met Ser Ala Met Ala Gly Tyr Ile Gly
                165                 170                 175
ggt ggt ggc ctg ggt gac ttc gcc atc gtc tac ggc tac cgc gcc tac        876
Gly Gly Gly Leu Gly Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Tyr
            180                 185                 190
gac ctg gag gtc acg tac gcg gcg gtc atc gtc atc gtc atc atc gtg        924
Asp Leu Glu Val Thr Tyr Ala Ala Val Ile Val Ile Val Ile Ile Val
        195                 200                 205
cag atc gcg cag ctg ctg ggc aac tgg ctc tcg cga aag ctc atg cgg        972
Gln Ile Ala Gln Leu Leu Gly Asn Trp Leu Ser Arg Lys Leu Met Arg
    210                 215                 220
cgt tag cgtcgcccgc cgttcacacc cccgaccccg tgtcgggggt tttgcgtacc       1028
Arg
225
cggagccgaa acgggggctc ccgatcgaga acacgtcggg gcgacgacct gccgtgcgga     1088
agtacccttc tgcccgctcg accgcactgt ttccccagga cacaacctgg cctgcagaca     1148
cagacgggta cctcagaacg cagctagcct ggatgtcatg aagatcgccg ccttcgacat     1208
cgacgacacc ctgctgttcc cccacggcat cgccgaggag gacatccgcg ccatccgcgc     1268
ctggcaggag                                                           1278
<210>  18
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<212>  PRT
<213>  Corynebacterium humireducens
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Met Asn Glu Thr Leu Leu Ala Ala Asp Trp Asn Arg Leu Gly Pro Thr
1               5                  10                  15
Phe Ile Asp Ala Ile Gly Asp Thr Leu Val Met Val Ser Leu Thr Met
            20                  25                  30
Val Leu Gly Gly Leu Gly Gly Leu Leu Ile Gly Leu Leu Leu Tyr Thr
        35                  40                  45
Ser Arg Ala Gly Gly Ile Leu Gln Ser Lys Pro Leu Tyr Trp Thr Leu
    50                  55                  60
Asn Ile Leu Val Asn Phe Val Arg Pro Ile Pro Phe Ile Val Leu Ile
65                  70                  75                  80
Ala Met Leu Ala Pro Val Thr Val Gln Val Val Gly Thr Thr Ile Gly
                85                  90                  95
Arg Ser Ala Ala Ile Phe Val Met Cys Ile Ala Ala Ala Phe Ala Val
            100                 105                 110
Ala Arg Ile Val Glu Gln Asn Leu Val Ala Ile Asp Pro Gly Val Ile
        115                 120                 125
Glu Ala Ala Arg Ala Met Gly Ala Gly Pro Trp Arg Ile Ile Arg Thr
    130                 135                 140
Val Ile Ile Pro Glu Ala Leu Gly Pro Leu Val Leu Gly Tyr Thr Phe
145                 150                 155                 160
Ile Phe Ile Ala Val Val Asp Met Ser Ala Met Ala Gly Tyr Ile Gly
                165                 170                 175
Gly Gly Gly Leu Gly Asp Phe Ala Ile Val Tyr Gly Tyr Arg Ala Tyr
            180                 185                 190
Asp Leu Glu Val Thr Tyr Ala Ala Val Ile Val Ile Val Ile Ile Val
        195                 200                 205
Gln Ile Ala Gln Leu Leu Gly Asn Trp Leu Ser Arg Lys Leu Met Arg
    210                 215                 220
Arg
225
<210>  19
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<220>
<221>  CDS
<222>  (301)..(1209)
<223>  gen dapA
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actaccgggc gtggcgccac ttcatcggcg cccgggccac cgagcacgcg gacgtcgaga      120
tccgggcact ggcggtggcg tgcctccgcc tcctcgcgca gcagtccccg gtgctcttcg      180
ccgatttcca gatctccact ctctccgacg gcacagagat ggccgtcagt ccctacgcca      240
ccgacttctg accagcgagg gattccccag cggaaaggta aacaggtaac cttgaacacc      300
atg agt aca ggt atg act tcg aag acc gga gtc gag gac ttc ggt acc         348
Met Ser Thr Gly Met Thr Ser Lys Thr Gly Val Glu Asp Phe Gly Thr
1               5                  10                  15
gtc tgc gtc gcc atg gtc acg ccc ttc gac cgg gac ggc gcc ctg gac         396
Val Cys Val Ala Met Val Thr Pro Phe Asp Arg Asp Gly Ala Leu Asp
            20                  25                  30
ctc gag gcc ggt cgc cgc atc gcg gcc cac ctc gtc gac aac ggt ctg         444
Leu Glu Ala Gly Arg Arg Ile Ala Ala His Leu Val Asp Asn Gly Leu
        35                  40                  45
gac gcc ctc gtg ctc gca ggc acg acc ggt gag tcc ccg acc acc acg         492
Asp Ala Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
    50                  55                  60
ctc gac gag aag atc agc ctg ctc aag gcg gtg aag gag gag gtc ggc         540
Leu Asp Glu Lys Ile Ser Leu Leu Lys Ala Val Lys Glu Glu Val Gly
65                  70                  75                  80
gac cgc tgc aag ctc atc gcg ggt gcc ggc acc aac gac acc gcc tcc         588
Asp Arg Cys Lys Leu Ile Ala Gly Ala Gly Thr Asn Asp Thr Ala Ser
                85                  90                  95
tcc atc gag ctc gcc cgc gcc tcc gcc gag gcc ggc gcc gac gcc ctg         636
Ser Ile Glu Leu Ala Arg Ala Ser Ala Glu Ala Gly Ala Asp Ala Leu
            100                 105                 110
ctc gtg gtc acc ccc tac tac tcg aag ccg agc cag gag ggt gtc tac         684
Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Val Tyr
        115                 120                 125
cag cac ttc aag gcc gtc gcc ggg gcc acc gac ctg ccc atc atg ctc         732
Gln His Phe Lys Ala Val Ala Gly Ala Thr Asp Leu Pro Ile Met Leu
    130                 135                 140
tac gac atc ccg ccg cgc tcc tcg atc ccg atc gag ggg gac acc atc         780
Tyr Asp Ile Pro Pro Arg Ser Ser Ile Pro Ile Glu Gly Asp Thr Ile
145                 150                 155                 160
cgc cga ctc gcg gag ctg ccc acc att cgt gcg gtg aag gat gca aag         828
Arg Arg Leu Ala Glu Leu Pro Thr Ile Arg Ala Val Lys Asp Ala Lys
                165                 170                 175
ggt aac atg gct gag tct gca ccg ctc atg cat gag acc ggt ctc gcc         876
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Gly Asn Met Ala Glu Ser Ala Pro Leu Met His Glu Thr Gly Leu Ala
            180                 185                 190
tgg tac tcg ggc gat gat ccg ctc aac gtc ccg tgg ctg tcg ctc ggc        924
Trp Tyr Ser Gly Asp Asp Pro Leu Asn Val Pro Trp Leu Ser Leu Gly
        195                 200                 205
gcc tcg gga ttc gtt tcc gtg gtc ggc cat gcc gca ccc cag gca ctg        972
Ala Ser Gly Phe Val Ser Val Val Gly His Ala Ala Pro Gln Ala Leu
    210                 215                 220
cgt gag ctg tac aca agt ttc gag gaa ggc gac ctc gcc cgt gcg cgg       1020
Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Ala Arg Ala Arg
225                 230                 235                 240
gaa atc aac gcc act gtt ctt tca ccg ctg atc gcc gct cag ggt cgc       1068
Glu Ile Asn Ala Thr Val Leu Ser Pro Leu Ile Ala Ala Gln Gly Arg
                245                 250                 255
ctg ggt ggt gtc agc atg gcc aag gct gcc ctg cgt ctg cag ggc att       1116
Leu Gly Gly Val Ser Met Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile
            260                 265                 270

gag gtg ggg gac ccg cgt ctg cct gtc gtc gct ccc gac gag cag gag       1164
Glu Val Gly Asp Pro Arg Leu Pro Val Val Ala Pro Asp Glu Gln Glu
        275                 280                 285
atc gag gcc ctc cgc cgt gac atg gaa aag gct gga gtc ctt taa           1209
Ile Glu Ala Leu Arg Arg Asp Met Glu Lys Ala Gly Val Leu
    290                 295                 300
atatgactga atcccgtagt cgtgcccgga aggtcacccg caaggcgggc ccgccggaga     1269
ccgagagcac tggtgcatcc ccggttttcc aggcaccgac cccggaaacg aacggaaacg     1329
gcgcatccgc cgagaagaag accaccgaaa ggaagtccgc ggacaccgac aacgccccgc     1389
ggggcggcgg caaccgctcc cggaacggtg gcggccgcgc ccgcggcggc cgtggtggcc     1449
gcggcggtca gggtggccag ggccagggcg gtcagggtgg tcagcagggg ggacggggac     1509
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<213>  Corynebacterium humireducens
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1               5                   10                  15
Val Cys Val Ala Met Val Thr Pro Phe Asp Arg Asp Gly Ala Leu Asp
            20                  25                  30
Leu Glu Ala Gly Arg Arg Ile Ala Ala His Leu Val Asp Asn Gly Leu
        35                  40                  45
Asp Ala Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
    50                  55                  60
Leu Asp Glu Lys Ile Ser Leu Leu Lys Ala Val Lys Glu Glu Val Gly
65                  70                  75                  80
Asp Arg Cys Lys Leu Ile Ala Gly Ala Gly Thr Asn Asp Thr Ala Ser
                85                  90                  95
Ser Ile Glu Leu Ala Arg Ala Ser Ala Glu Ala Gly Ala Asp Ala Leu
            100                 105                 110
Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Val Tyr
        115                 120                 125
Gln His Phe Lys Ala Val Ala Gly Ala Thr Asp Leu Pro Ile Met Leu
    130                 135                 140
Tyr Asp Ile Pro Pro Arg Ser Ser Ile Pro Ile Glu Gly Asp Thr Ile
145                 150                 155                 160
Arg Arg Leu Ala Glu Leu Pro Thr Ile Arg Ala Val Lys Asp Ala Lys
                165                 170                 175
Gly Asn Met Ala Glu Ser Ala Pro Leu Met His Glu Thr Gly Leu Ala
            180                 185                 190
Trp Tyr Ser Gly Asp Asp Pro Leu Asn Val Pro Trp Leu Ser Leu Gly
        195                 200                 205
Ala Ser Gly Phe Val Ser Val Val Gly His Ala Ala Pro Gln Ala Leu
    210                 215                 220
Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Ala Arg Ala Arg
225                 230                 235                 240
Glu Ile Asn Ala Thr Val Leu Ser Pro Leu Ile Ala Ala Gln Gly Arg
                245                 250                 255
Leu Gly Gly Val Ser Met Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile
            260                 265                 270
Glu Val Gly Asp Pro Arg Leu Pro Val Val Ala Pro Asp Glu Gln Glu
        275                 280                 285
Ile Glu Ala Leu Arg Arg Asp Met Glu Lys Ala Gly Val Leu
    290                 295                 300
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<213>  Corynebacterium humireducens
<220>
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<222> (301)..(1215)
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gagtggcgga cagggtgagg gcgacggcca gggcggccgc gctgatctga cggtgtcggc 120
gggtgaaagc catgttcatc atctcctatg agctctattg gcgtaagggt ggatgatagg 180
gcagaaaatg caggttagat accctgccgg gtatgggata tctcacgggc tgcgacggga 240
acttcgcggt ccggaaaaag ttcccgcctt cccttgactt tgcggcgtaa gatgtcattt 300
atg agt ctc gag ccc ggg aac acc ccg ctc gta cgt ctg gac cgg ctc 348
Met Ser Leu Glu Pro Gly Asn Thr Pro Leu Val Arg Leu Asp Arg Leu
1 5 10 15
ccc ggc cgg ccc ggt gtc acc ctg tgg gcg aag ctg gag ggc cac aac 396
Pro Gly Arg Pro Gly Val Thr Leu Trp Ala Lys Leu Glu Gly His Asn
20 25 30
ccc agc ggc agt gcc aag gac cgg acc gcg cac gcc atc ctc gcg gcg 444
Pro Ser Gly Ser Ala Lys Asp Arg Thr Ala His Ala Ile Leu Ala Ala
35 40 45
gcg gat ctg cgg ccc ggc gcg gtc atc gtc gag tcg agc tcg ggc aac 492
Ala Asp Leu Arg Pro Gly Ala Val Ile Val Glu Ser Ser Ser Gly Asn
50 55 60
ctc ggc gtc gcc ctg gcc cgg gag gcg gtc ctc ggc ggc tgg acc ttc 540
Leu Gly Val Ala Leu Ala Arg Glu Ala Val Leu Gly Gly Trp Thr Phe
65 70 75 80
cac tgt gtc gtc gat ccg aag gcg aat cgc tcg acc atc gcc acc atg 588
His Cys Val Val Asp Pro Lys Ala Asn Arg Ser Thr Ile Ala Thr Met
85 90 95
cgc gcg ttc ggg gcg gtc gtc cac gag gtc acc gca ccc gat ccg gcc 636
Arg Ala Phe Gly Ala Val Val His Glu Val Thr Ala Pro Asp Pro Ala
100 105 110
acc ggt gac tgg ctc gcc gcc cgg cgc gcg cgg gtc gcg gaa ctg ctc 684
Thr Gly Asp Trp Leu Ala Ala Arg Arg Ala Arg Val Ala Glu Leu Leu
115 120 125
acc gag atc ccc ggg gcc gtc tgc ctc gac cag tac tcc aac cgg gcg 732
Thr Glu Ile Pro Gly Ala Val Cys Leu Asp Gln Tyr Ser Asn Arg Ala
130 135 140
gcc ttc acg gcc cac gac gag ggc acg atg gcc gag atc gtc gcg cag 780
Ala Phe Thr Ala His Asp Glu Gly Thr Met Ala Glu Ile Val Ala Gln
145 150 155 160
ctc ggc cac acc ccc gcg cac ctg ttc gtg gcg gtg agc acc acc ggc 828
Leu Gly His Thr Pro Ala His Leu Phe Val Ala Val Ser Thr Thr Gly
165 170 175
acg atc ggc ggc tgc ctg cgc cgc atc gcc cgg gag ggg tgg gac acg 876
Thr Ile Gly Gly Cys Leu Arg Arg Ile Ala Arg Glu Gly Trp Asp Thr
180 185 190
gag gtc acc gcc gtc gac gcc gag ggt tcc gtg ctt ttc gac ggc gcc 924
Glu Val Thr Ala Val Asp Ala Glu Gly Ser Val Leu Phe Asp Gly Ala
195 200 205
cgt ggc cgc cgc cac ctt ccc ggc ttc ggc gcc ggc atc gtc ccg gac 972
Arg Gly Arg Arg His Leu Pro Gly Phe Gly Ala Gly Ile Val Pro Asp
210 215 220
ctg gcc gcc gag gtg acc ccg gac cgc atc gtc cgg gtc ggc gac cgt 1020
Leu Ala Ala Glu Val Thr Pro Asp Arg Ile Val Arg Val Gly Asp Arg
225 230 235 240
gac tcc gtc gcc gcc gcg cgg cag ctg gcc cgc acg gaa ggg gtg ttg 1068
Asp Ser Val Ala Ala Ala Arg Gln Leu Ala Arg Thr Glu Gly Val Leu
245 250 255
tgc ggt gcc tcg ggt ggg gcg gtg gtg gcg gcc gtc ggg aag ctc ctg 1116
Cys Gly Ala Ser Gly Gly Ala Val Val Ala Ala Val Gly Lys Leu Leu
260 265 270
ccg gag ctg cac ggg gac gtc gtc ctc gtg ctc cac gac ggt ggc acc 1164
Pro Glu Leu His Gly Asp Val Val Leu Val Leu His Asp Gly Gly Thr
275 280 285
cac tac ctg gac acc gtg tac aac gac gac tgg gtg gag gag aac ctg 1212
His Tyr Leu Asp Thr Val Tyr Asn Asp Asp Trp Val Glu Glu Asn Leu
290 295 300
tga caaccgtggt gatcatcggc ggcggcccgc gcggactgtg ggcggcggag 1265
gaactgctgg gcctggcacg cgagaggggc gcggccctcg acgtccacgt catcgacgac 1325
ggcggaccgc aggcctacga cccggggcag ccggaggagt ggctcatcaa cgtgcgggcc 1385
tccgtgatcc gcacgggggct gggctccttc gacgagtggc gcggggccgc cgacccctcc 1445
ccgccgcgac gcgaggtggc ccgtttcctc gccgcctcct gggaggagct cgcacagcac 1505
gtgtcgccgc 1515
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<212> PRT
<213> Corynebacterium humireducens
<400> 22
Met Ser Leu Glu Pro Gly Asn Thr Pro Leu Val Arg Leu Asp Arg Leu
1 5 10 15

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Pro Gly Arg Pro Gly Val Thr Leu Trp Ala Lys Leu Glu Gly His Asn
            20                  25                  30
Pro Ser Gly Ser Ala Lys Asp Arg Thr Ala His Ala Ile Leu Ala Ala
        35                  40                  45
Ala Asp Leu Arg Pro Gly Ala Val Ile Val Glu Ser Ser Ser Gly Asn
    50                  55                  60
Leu Gly Val Ala Leu Ala Arg Glu Ala Val Leu Gly Gly Trp Thr Phe
65                  70                  75                  80
His Cys Val Val Asp Pro Lys Ala Asn Arg Ser Thr Ile Ala Thr Met
                85                  90                  95
Arg Ala Phe Gly Ala Val Val His Glu Val Thr Ala Pro Asp Pro Ala
            100                 105                 110
Thr Gly Asp Trp Leu Ala Ala Arg Arg Ala Arg Val Ala Glu Leu Leu
        115                 120                 125
Thr Glu Ile Pro Gly Ala Val Cys Leu Asp Gln Tyr Ser Asn Arg Ala
    130                 135                 140
Ala Phe Thr Ala His Asp Glu Gly Thr Met Ala Glu Ile Val Ala Gln
145                 150                 155                 160
Leu Gly His Thr Pro Ala His Leu Phe Val Ala Val Ser Thr Thr Gly
                165                 170                 175
Thr Ile Gly Gly Cys Leu Arg Arg Ile Ala Arg Glu Gly Trp Asp Thr
            180                 185                 190
Glu Val Thr Ala Val Asp Ala Glu Gly Ser Val Leu Phe Asp Gly Ala
        195                 200                 205
Arg Gly Arg Arg His Leu Pro Gly Phe Gly Ala Gly Ile Val Pro Asp
    210                 215                 220
Leu Ala Ala Glu Val Thr Pro Asp Arg Ile Val Arg Val Gly Asp Arg
225                 230                 235                 240
Asp Ser Val Ala Ala Ala Arg Gln Leu Ala Arg Thr Glu Gly Val Leu
                245                 250                 255
Cys Gly Ala Ser Gly Gly Ala Val Val Ala Ala Val Gly Lys Leu Leu
            260                 265                 270
Pro Glu Leu His Gly Asp Val Val Leu Val Leu His Asp Gly Gly Thr
        275                 280                 285
His Tyr Leu Asp Thr Val Tyr Asn Asp Asp Trp Val Glu Glu Asn Leu
    290                 295                 300
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ggtcgcggac cgcctgcggg aggacggttt cgaggtcggg gaggtcggca acctggcgga      120
ccacatcctc ccggagacca ccgtcttctt ccagcccggc aacgccgccg cggagcagcg      180
ggcgcgggag ctcgccgacc gcctcggcgg cgtcgcccgc gagtacgagg gcttcctccc      240
ggagaacacc gccggtcgca acgacctgac tctggtgctg gtgaaccagg tggcgctctg      300
atg ggc ccg ggg acc ggc atc gag ccg atc ccg ttc cgc cgc tcc ccg        348
Met Gly Pro Gly Thr Gly Ile Glu Pro Ile Pro Phe Arg Arg Ser Pro
1               5                   10                  15
cgg ccg acg ctc ggc gtc gag tgg gag atc gcg ctc atc gac ccc gag        396
Arg Pro Thr Leu Gly Val Glu Trp Glu Ile Ala Leu Ile Asp Pro Glu
            20                  25                  30
acc cgc gac ctg gcg ccc aag gcc gtc gag gtc atc gac ctc gtc cgg        444
Thr Arg Asp Leu Ala Pro Lys Ala Val Glu Val Ile Asp Leu Val Arg
        35                  40                  45
tcc cgc cac ccg gag gtg cac ctg gag aag gag ttc ctg cag aac acc        492
Ser Arg His Pro Glu Val His Leu Glu Lys Glu Phe Leu Gln Asn Thr
    50                  55                  60
gtc gaa ctg gtc acc ggc atc cac gaa acc gtg ccg gag gcg gtc gcg        540
Val Glu Leu Val Thr Gly Ile His Glu Thr Val Pro Glu Ala Val Ala
65                  70                  75                  80
gaa ctc gcc cgc gac ctg gcc gcc gtg aag gag gcc gcc gcc gac ctc        588
Glu Leu Ala Arg Asp Leu Ala Ala Val Lys Glu Ala Ala Ala Asp Leu
                85                  90                  95
gga ctg tgc ctg tgg tcc tcc ggc tcg cac ccc ttc tcg gac tgg cgg        636
Gly Leu Cys Leu Trp Ser Ser Gly Ser His Pro Phe Ser Asp Trp Arg
            100                 105                 110
aag aac ccg gtc agc gcg aag atg gcc tac gcc gag atc atc gag cgc        684
Lys Asn Pro Val Ser Ala Lys Met Ala Tyr Ala Glu Ile Ile Glu Arg
        115                 120                 125
acc cgc tac tgg ggt tcg cag atg ctc atc tgg ggc atc cac gtg cac        732
Thr Arg Tyr Trp Gly Ser Gln Met Leu Ile Trp Gly Ile His Val His
    130                 135                 140
gtc ggg atc agc cac gag gac cgg gtg tgg ccg atc atc aac gcc ctg        780
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Val Gly Ile Ser His Glu Asp Arg Val Trp Pro Ile Ile Asn Ala Leu
145                 150                 155                 160
atg acc cgc tac ccg cac ctg ctg gcg ctg acg gcg tcg tcg ccg ggc  828
Met Thr Arg Tyr Pro His Leu Leu Ala Leu Thr Ala Ser Ser Pro Gly
                165                 170                 175
tgg gac ggc atc gac acg ggc tac gcc tcc aac cgc acg atg ctc tac  876
Trp Asp Gly Ile Asp Thr Gly Tyr Ala Ser Asn Arg Thr Met Leu Tyr
            180                 185                 190
cag cag ctg ccc acc gcc ggc ctg ccc ttc cag ttc cgg aac tgg gcc  924
Gln Gln Leu Pro Thr Ala Gly Leu Pro Phe Gln Phe Arg Asn Trp Ala
        195                 200                 205
gag tgg gag tcc tac atg cac gac cag ggc atc tcg ggc gtg atc aac  972
Glu Trp Glu Ser Tyr Met His Asp Gln Gly Ile Ser Gly Val Ile Asn
    210                 215                 220
cac acc ggg tcg atg cac ttc gac atc cgt ccc gcc ccg aag tgg ggc 1020
His Thr Gly Ser Met His Phe Asp Ile Arg Pro Ala Pro Lys Trp Gly
225                 230                 235                 240
acg gtc gag gtg cgg gtc tcc gac gcc acc tcc aac ctg cgg gaa ctc 1068
Thr Val Glu Val Arg Val Ser Asp Ala Thr Ser Asn Leu Arg Glu Leu
                245                 250                 255

gcc gcc gtc gtg gcg ctc acg cac tgc ctg gtc gtc cac tac gac cgc 1116
Ala Ala Val Val Ala Leu Thr His Cys Leu Val Val His Tyr Asp Arg
            260                 265                 270
atg atc gac cgc ggt gag gaa ctg ccc gtc ctg cag ccc tgg cac gtc 1164
Met Ile Asp Arg Gly Glu Glu Leu Pro Val Leu Gln Pro Trp His Val
        275                 280                 285
gcc gag aac aag tgg cgg gcc gcc cgc tac ggg ctg gag gca ctc gtg 1212
Ala Glu Asn Lys Trp Arg Ala Ala Arg Tyr Gly Leu Glu Ala Leu Val
    290                 295                 300
atc acc agc cgt gac acc gac gag cgc tgg gtc acc cag gag ctc gcg 1260
Ile Thr Ser Arg Asp Thr Asp Glu Arg Trp Val Thr Gln Glu Leu Ala
305                 310                 315                 320
gag ctt gtc gac gaa ctc gcg ccc ctc gcc acc gaa ctc ggc tgc ctc 1308
Glu Leu Val Asp Glu Leu Ala Pro Leu Ala Thr Glu Leu Gly Cys Leu
                325                 330                 335
gcc gaa ctc cag ctg gtc tcc gag atc ctc gaa cgt ggc gcc ggc tac 1356
Ala Glu Leu Gln Leu Val Ser Glu Ile Leu Glu Arg Gly Ala Gly Tyr
            340                 345                 350
cag cgt cag cgt cgc atc cac gac gtc acc ggc agc tgg atc ccc gtc 1404
Gln Arg Gln Arg Arg Ile His Asp Val Thr Gly Ser Trp Ile Pro Val
        355                 360                 365
atc gac gcc gcc tgc cgg gag atg gag gag atg gtc ccg tga          1446
Ile Asp Ala Ala Cys Arg Glu Met Glu Glu Met Val Pro
    370                 375                 380
gcgacgtcgt cctcgtccac tccaccgggc acctgccgga cgtgtggacg gaggtggtgc 1506
gcgccttccc ggccgactgg aagccgtggc tgcccaatct gggcgtgcag tccctcgagc 1566
agtacctgga ccggcaggag ctgcgccggg tggtgctcgt cggtcacggc accggcgccc 1626
tggccgtggc acgcctggcc cgggagcagc cgcagcgggt cacccacgcg gtgctgtccg 1686
tgccggaggc gccccgcctc gtgccacgtt tcctgcggcg ccggcaggag gaggccctgg 1746
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<213>  Corynebacterium humireducens
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1               5                   10                  15
Arg Pro Thr Leu Gly Val Glu Trp Glu Ile Ala Leu Ile Asp Pro Glu
            20                  25                  30
Thr Arg Asp Leu Ala Pro Lys Ala Val Glu Val Ile Asp Leu Val Arg
        35                  40                  45
Ser Arg His Pro Glu Val His Leu Glu Lys Glu Phe Leu Gln Asn Thr
    50                  55                  60
Val Glu Leu Val Thr Gly Ile His Glu Thr Val Pro Glu Ala Val Ala
65                  70                  75                  80
Glu Leu Ala Arg Asp Leu Ala Ala Val Lys Glu Ala Ala Ala Asp Leu
                85                  90                  95
Gly Leu Cys Leu Trp Ser Ser Gly Ser His Pro Phe Ser Asp Trp Arg
            100                 105                 110
Lys Asn Pro Val Ser Ala Lys Met Ala Tyr Ala Glu Ile Ile Glu Arg
        115                 120                 125
Thr Arg Tyr Trp Gly Ser Gln Met Leu Ile Trp Gly Ile His Val His
    130                 135                 140
Val Gly Ile Ser His Glu Asp Arg Val Trp Pro Ile Ile Asn Ala Leu
145                 150                 155                 160
Met Thr Arg Tyr Pro His Leu Leu Ala Leu Thr Ala Ser Ser Pro Gly
                165                 170                 175
Trp Asp Gly Ile Asp Thr Gly Tyr Ala Ser Asn Arg Thr Met Leu Tyr
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            180                 185                 190
Gln Gln Leu Pro Thr Ala Gly Leu Pro Phe Gln Phe Arg Asn Trp Ala
        195                 200                 205
Glu Trp Glu Ser Tyr Met His Asp Gln Gly Ile Ser Gly Val Ile Asn
    210                 215                 220
His Thr Gly Ser Met His Phe Asp Ile Arg Pro Ala Pro Lys Trp Gly
225                 230                 235                 240
Thr Val Glu Val Arg Val Ser Asp Ala Thr Ser Asn Leu Arg Glu Leu
                245                 250                 255
Ala Ala Val Val Ala Leu Thr His Cys Leu Val Val His Tyr Asp Arg
            260                 265                 270
Met Ile Asp Arg Gly Glu Glu Leu Pro Val Leu Gln Pro Trp His Val
        275                 280                 285
Ala Glu Asn Lys Trp Arg Ala Ala Arg Tyr Gly Leu Glu Ala Leu Val
    290                 295                 300
Ile Thr Ser Arg Asp Thr Asp Glu Arg Trp Val Thr Gln Glu Leu Ala
305                 310                 315                 320
Glu Leu Val Asp Glu Leu Ala Pro Leu Ala Thr Glu Leu Gly Cys Leu
                325                 330                 335
Ala Glu Leu Gln Leu Val Ser Glu Ile Leu Glu Arg Gly Ala Gly Tyr
            340                 345                 350
Gln Arg Gln Arg Arg Ile His Asp Val Thr Gly Ser Trp Ile Pro Val
        355                 360                 365
Ile Asp Ala Ala Cys Arg Glu Met Glu Glu Met Val Pro
    370                 375                 380
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tcatcgcgca ccgcctgtcg acgatcgcgg gtgtggacac catcgtcacc ctccgcgacg      120
gcatggtcga cgaaataggt tcaccggacc agctcgccgc ctcgggtggc atctacgccg      180
aactcctgca gctcacggcg tcctcctcgg ccgctgaccg ggcccgtctg aagaggtacg      240
ggctcgtcgt cgacggtcac ggcgacgagg aggacgagga agaggactag tctgtctggc      300
atg cag ttc ccc acc ctc gac cag ctc aag gac cgt cgc acc cgc aag         348
Met Gln Phe Pro Thr Leu Asp Gln Leu Lys Asp Arg Arg Thr Arg Lys
1               5                   10                  15
tgg acg gtc tac gcc gac gac gtc ctg ccc ctg tgg atc gcg gag agt         396
Trp Thr Val Tyr Ala Asp Asp Val Leu Pro Leu Trp Ile Ala Glu Ser
            20                  25                  30
gac ttc ttc acc tgc ccg ccg gtg aag cag gcg atc gcg gac gcc atc         444
Asp Phe Phe Thr Cys Pro Pro Val Lys Gln Ala Ile Ala Asp Ala Ile
        35                  40                  45
gac cgg gag tcc ttc ggg tac acc ccg gcg acc tcc gac ctg ccg cag         492
Asp Arg Glu Ser Phe Gly Tyr Thr Pro Ala Thr Ser Asp Leu Pro Gln
    50                  55                  60
gcg gtc tcc gac ttc tac gcc gca cgt tac ggc tgg cgc ccg gac ccg         540
Ala Val Ser Asp Phe Tyr Ala Ala Arg Tyr Gly Trp Arg Pro Asp Pro
65                  70                  75                  80
gcg ctc atc gtc gcg gtc ccc gac gtc gtc cgt ggc ctg gcc ctc gcc         588
Ala Leu Ile Val Ala Val Pro Asp Val Val Arg Gly Leu Ala Leu Ala
                85                  90                  95
atc gag tac atg acg cgc ccg gac tcg ggt gtc atc gtg ccg gtg ccg         636
Ile Glu Tyr Met Thr Arg Pro Asp Ser Gly Val Ile Val Pro Val Pro
            100                 105                 110
gcg tac ccg ccg ttc ctg gag ctg ccg gag gcg acc cgc cgt ccg atg         684
Ala Tyr Pro Pro Phe Leu Glu Leu Pro Glu Ala Thr Arg Arg Pro Met
        115                 120                 125
cac cag atc gac gcc tac ggc ggg atc gac ctg ggg gac gtc gag aag         732
His Gln Ile Asp Ala Tyr Gly Gly Ile Asp Leu Gly Asp Val Glu Lys
    130                 135                 140
cag ttc gcg gcc ggc gcc ggc tcg atc ctc ctg tgc gcc ccg aac aac         780
Gln Phe Ala Ala Gly Ala Gly Ser Ile Leu Leu Cys Ala Pro Asn Asn
145                 150                 155                 160
ccc ctg ggg tac acg ttc gac gcg gag ttc ctg cgg gag ctg tgc gac         828
Pro Leu Gly Tyr Thr Phe Asp Ala Glu Phe Leu Arg Glu Leu Cys Asp
                165                 170                 175
ctg gcg gac cgt tac gac gcc cgc gtg ctc gtc gac gag atc cac gcc         876
Leu Ala Asp Arg Tyr Asp Ala Arg Val Leu Val Asp Glu Ile His Ala
            180                 185                 190
ccg ctg gtg ttc gac ggc acc cat gtg tgc gcc gcc gcc gtc agc gag         924
Pro Leu Val Phe Asp Gly Thr His Val Cys Ala Ala Ala Val Ser Glu
        195                 200                 205
```

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acc gcc gcg cgg gtg tgc gtc acc gtc acg gcg acg tcg aag gcg tgg        972
Thr Ala Ala Arg Val Cys Val Thr Val Thr Ala Thr Ser Lys Ala Trp
    210                 215                 220
aac atc gcg ggc ctc aag tgc gcg cag atg atc ttc tcc aac ccg gcg       1020
Asn Ile Ala Gly Leu Lys Cys Ala Gln Met Ile Phe Ser Asn Pro Ala
225                 230                 235                 240
gac atg gac acg tgg cgg tcg atg acc ggc gtg gcc aag gac ggc acc       1068
Asp Met Asp Thr Trp Arg Ser Met Thr Gly Val Ala Lys Asp Gly Thr
                245                 250                 255
tcc acc ctg ggc atc tgg gcg gcg atc gcc tgc tac cgg gag ggc ggc       1116
Ser Thr Leu Gly Ile Trp Ala Ala Ile Ala Cys Tyr Arg Glu Gly Gly
            260                 265                 270
gac tgc ctc gac gag cag gtc gcg tac ctg cgg gag aac cgc gac tgg       1164
Asp Cys Leu Asp Glu Gln Val Ala Tyr Leu Arg Glu Asn Arg Asp Trp
        275                 280                 285
ctg gcc gag gag ctg ccg cgc cgc gtg ccg ggg ctg cag gtg atc agc       1212
Leu Ala Glu Glu Leu Pro Arg Arg Val Pro Gly Leu Gln Val Ile Ser
    290                 295                 300
ccg gcg gcg acc tat ctc atg tgg atg gac ttc tcc ggc acc tcc atc       1260
Pro Ala Ala Thr Tyr Leu Met Trp Met Asp Phe Ser Gly Thr Ser Ile
305                 310                 315                 320
ggg cac ctg gag cgc ccg gcg gtg tgg ctg cgg gag aac gcg aag gtc       1308
Gly His Leu Glu Arg Pro Ala Val Trp Leu Arg Glu Asn Ala Lys Val
                325                 330                 335
gcc ctc aac gac ggc gtc gcc ttc ggc ccg gga ggc agc cac cac gcg       1356
Ala Leu Asn Asp Gly Val Ala Phe Gly Pro Gly Gly Ser His His Ala
            340                 345                 350
cgg ctg aac ttc gcc acg tcc cgg gag atc ctg gag gag gcc tgc gac       1404
Arg Leu Asn Phe Ala Thr Ser Arg Glu Ile Leu Glu Glu Ala Cys Asp
        355                 360                 365
cgg ctg ggg tct gca ttc gcc cgg tga tttccctacc ctggatttca             1451
Arg Leu Gly Ser Ala Phe Ala Arg
    370                 375
tgactgacga gcgatacgac gacccgtccg ccacgaccgg cccccagggt cccggactgt      1511
ccatgggtcc gctgggggtc ggcgccgaac cggagaagtc cccggtccgc ccccgtaccg      1571
acgccgaggg ctacctggtc gaaccggagt ccgagcagtt cgagaccccg accccggcgc      1631
ccggtgacgc cccctgggag cgccccgagc cggagtggta caaggaggcc gtgttctacg      1691
aggtcctggt gcgcgccttc tacgacccgg agggcaccgg                            1731
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<212>  PRT
<213>  Corynebacterium humireducens
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Met Gln Phe Pro Thr Leu Asp Gln Leu Lys Asp Arg Arg Thr Arg Lys
1               5                   10                  15
Trp Thr Val Tyr Ala Asp Asp Val Leu Pro Leu Trp Ile Ala Glu Ser
            20                  25                  30
Asp Phe Phe Thr Cys Pro Pro Val Lys Gln Ala Ile Ala Asp Ala Ile
        35                  40                  45
Asp Arg Glu Ser Phe Gly Tyr Thr Pro Ala Thr Ser Asp Leu Pro Gln
    50                  55                  60
Ala Val Ser Asp Phe Tyr Ala Ala Arg Tyr Gly Trp Arg Pro Asp Pro
65                  70                  75                  80
Ala Leu Ile Val Ala Val Pro Asp Val Val Arg Gly Leu Ala Leu Ala
                85                  90                  95
Ile Glu Tyr Met Thr Arg Pro Asp Ser Gly Val Ile Val Pro Val Pro
            100                 105                 110
Ala Tyr Pro Pro Phe Leu Glu Leu Pro Glu Ala Thr Arg Arg Pro Met
        115                 120                 125
His Gln Ile Asp Ala Tyr Gly Gly Ile Asp Leu Gly Asp Val Glu Lys
    130                 135                 140
Gln Phe Ala Ala Gly Ala Gly Ser Ile Leu Leu Cys Ala Pro Asn Asn
145                 150                 155                 160
Pro Leu Gly Tyr Thr Phe Asp Ala Glu Phe Leu Arg Glu Leu Cys Asp
                165                 170                 175
Leu Ala Asp Arg Tyr Asp Ala Arg Val Leu Val Asp Glu Ile His Ala
            180                 185                 190
Pro Leu Val Phe Asp Gly Thr His Val Cys Ala Ala Ala Val Ser Glu
        195                 200                 205
Thr Ala Ala Arg Val Cys Val Thr Val Thr Ala Thr Ser Lys Ala Trp
    210                 215                 220
Asn Ile Ala Gly Leu Lys Cys Ala Gln Met Ile Phe Ser Asn Pro Ala
225                 230                 235                 240
Asp Met Asp Thr Trp Arg Ser Met Thr Gly Val Ala Lys Asp Gly Thr
                245                 250                 255
Ser Thr Leu Gly Ile Trp Ala Ala Ile Ala Cys Tyr Arg Glu Gly Gly
            260                 265                 270
Asp Cys Leu Asp Glu Gln Val Ala Tyr Leu Arg Glu Asn Arg Asp Trp
```

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        275                 280                 285
Leu Ala Glu Glu Leu Pro Arg Arg Val Pro Gly Leu Gln Val Ile Ser
    290                 295                 300
Pro Ala Ala Thr Tyr Leu Met Trp Met Asp Phe Ser Gly Thr Ser Ile
305                 310                 315                 320
Gly His Leu Glu Arg Pro Ala Val Trp Leu Arg Glu Asn Ala Lys Val
                325                 330                 335
Ala Leu Asn Asp Gly Val Ala Phe Gly Pro Gly Gly Ser His His Ala
            340                 345                 350
Arg Leu Asn Phe Ala Thr Ser Arg Glu Ile Leu Glu Glu Ala Cys Asp
        355                 360                 365
Arg Leu Gly Ser Ala Phe Ala Arg
    370                 375
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<213>  Corynebacterium humireducens
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<222>  (301)..(1332)
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catgaagtcc cacccgggcg tcaccgccga cttcgccgag gcgctccgcg acgccggcgt      120
gaacatcgag ctaatctcca cctcggagat ccgcatctcg gtgctcaccc gcgaggccga      180
cctggacgcc gccgcccgtg ccctgcacga gaagttcgag ctcggcggcg acgccgaggc      240
caccgtctac gccggcaccg gccgctagac aatcccttcc acagaggagc tttcactctc      300
atg acc acc att gct gtc gtc ggt gcc acc ggc cag gtc ggc cgc gtg        348
Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Arg Val
1               5                  10                  15
atg cgc tcg atc ctg gag gag cgc aac ttc ccg gcc gac aag gtc cgt        396
Met Arg Ser Ile Leu Glu Glu Arg Asn Phe Pro Ala Asp Lys Val Arg
            20                  25                  30
ttc ttc gcg tcc ccg cgc tcc gcg ggc acc gtc atc gag ttc cgc ggt        444
Phe Phe Ala Ser Pro Arg Ser Ala Gly Thr Val Ile Glu Phe Arg Gly
        35                  40                  45
gag gac atc acc gtc gag gac ctc acc cag atc acc ccg gag tcc gtc        492
Glu Asp Ile Thr Val Glu Asp Leu Thr Gln Ile Thr Pro Glu Ser Val
    50                  55                  60
aag gac gtc gac atc gcc ctc ttc tcc gcc ggt ggt tcc acc tcc cgt        540
Lys Asp Val Asp Ile Ala Leu Phe Ser Ala Gly Gly Ser Thr Ser Arg
65                  70                  75                  80
gag tgg gcc ccg gtc ttc gcc gag gcc ggc gcg acc gtc atc gac aac        588
Glu Trp Ala Pro Val Phe Ala Glu Ala Gly Ala Thr Val Ile Asp Asn
                85                  90                  95
tcc tcc gcc tgg cgc aag gac gac gag gtc ccg ctc gtc gtc gcc gag        636
Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Val Val Ala Glu
            100                 105                 110
gtc aac ggc gag gag gcg aag aac ccg tcc aag ggc atc gtc gcc aac        684
Val Asn Gly Glu Glu Ala Lys Asn Pro Ser Lys Gly Ile Val Ala Asn
        115                 120                 125
ccg aac tgc acc acc atg gcc gcc atg ccg gtg ctc aag ccg ctg cac        732
Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
    130                 135                 140
gac gcc gcc ggc ctc atc cgc ctg cat gtc tcc tcc tac cag gcc gtc        780
Asp Ala Ala Gly Leu Ile Arg Leu His Val Ser Ser Tyr Gln Ala Val
145                 150                 155                 160
tcc ggc tcc ggc ctc gcc ggt gtg gag acc ctg gcg aag cag acc gcc        828
Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Thr Ala
                165                 170                 175
gag ctc ggt gag gac aac gtc aag ctg gtc cat gac ggt tcc gtc gag        876
Glu Leu Gly Glu Asp Asn Val Lys Leu Val His Asp Gly Ser Val Glu
            180                 185                 190
gcc ccc gcc gac ctg ggt ccc tac gtc gcc ccc atc gcg ttc aac gcc        924
Ala Pro Ala Asp Leu Gly Pro Tyr Val Ala Pro Ile Ala Phe Asn Ala
        195                 200                 205
ctg ccg ctg gcc ggc gcg ctg gtc gat gac ggc tcc ctg gag acg gat        972
Leu Pro Leu Ala Gly Ala Leu Val Asp Asp Gly Ser Leu Glu Thr Asp
    210                 215                 220
gag gag cag aag ctg cgc aac gag tcc cgc aag atc ctg gac atc ccg       1020
Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Asp Ile Pro
225                 230                 235                 240
ggt ctg cgc gtc gcc ggc acc tgc gtc cgc gtg ccg gtg ttc acc ggt       1068
Gly Leu Arg Val Ala Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
                245                 250                 255
cac acc ctg acc atc cac gcc gag ttc gag cgt ccg atc acc gtc gac       1116
His Thr Leu Thr Ile His Ala Glu Phe Glu Arg Pro Ile Thr Val Asp
            260                 265                 270
```

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gag gcc aag gcc ctg ctc gcc gac gcc ccg ggt gtc gag ctt gtc gac      1164
Glu Ala Lys Ala Leu Leu Ala Asp Ala Pro Gly Val Glu Leu Val Asp
        275                 280                 285
gtc ccg acc ccg ctg gag gcc gcc ggc aag gac acc tcc ctg gtc ggc      1212
Val Pro Thr Pro Leu Glu Ala Ala Gly Lys Asp Thr Ser Leu Val Gly
    290                 295                 300
cgt atc cgc cag gac cag tcc gtc gac gac aac aag ggc ctc gtg ctc      1260
Arg Ile Arg Gln Asp Gln Ser Val Asp Asp Asn Lys Gly Leu Val Leu
305                 310                 315                 320
gtc gtc tcc ggt gac aac ctg cgc aag ggc gcg gcg ctg aac acg gtg      1308
Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Val
                325                 330                 335
cag atc gcg gag ctg ctg gtg tag tccaccgcct ccactgatat cgggcccctc      1362
Gln Ile Ala Glu Leu Leu Val
            340
accatgttgt ggtgaggggc ccgttcttgt cggtggtctg gtaggggagg ccttcattct     1422
gtccagacaa ttcttgtggt gtcctggggc gtcggcatgc ggcgtcgggc gggtatcggc     1482
gttcccgttc ctcgtttggc ggttcactgc cggacaatgg aggattttct caggaacagg     1542
gatccctgct gatctcgtat ttcgccccgg aactccgctg gacgctcagc ttgtccccag     1602
aattggggtc tttccgcagc gaattgtgag                                      1632
<210>  28
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<212>  PRT
<213>  Corynebacterium humireducens
<400>  28
Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Arg Val
1               5                   10                  15
Met Arg Ser Ile Leu Glu Glu Arg Asn Phe Pro Ala Asp Lys Val Arg
            20                  25                  30
Phe Phe Ala Ser Pro Arg Ser Ala Gly Thr Val Ile Glu Phe Arg Gly
        35                  40                  45
Glu Asp Ile Thr Val Glu Asp Leu Thr Gln Ile Thr Pro Glu Ser Val
    50                  55                  60
Lys Asp Val Asp Ile Ala Leu Phe Ser Ala Gly Gly Ser Thr Ser Arg
65                  70                  75                  80
Glu Trp Ala Pro Val Phe Ala Glu Ala Gly Ala Thr Val Ile Asp Asn
                85                  90                  95
Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Val Val Ala Glu
            100                 105                 110
Val Asn Gly Glu Glu Ala Lys Asn Pro Ser Lys Gly Ile Val Ala Asn
        115                 120                 125
Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
    130                 135                 140
Asp Ala Ala Gly Leu Ile Arg Leu His Val Ser Ser Tyr Gln Ala Val
145                 150                 155                 160
Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Thr Ala
                165                 170                 175
Glu Leu Gly Glu Asp Asn Val Lys Leu Val His Asp Gly Ser Val Glu
            180                 185                 190
Ala Pro Ala Asp Leu Gly Pro Tyr Val Ala Pro Ile Ala Phe Asn Ala
        195                 200                 205
Leu Pro Leu Ala Gly Ala Leu Val Asp Asp Gly Ser Leu Glu Thr Asp
    210                 215                 220
Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Asp Ile Pro
225                 230                 235                 240
Gly Leu Arg Val Ala Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
                245                 250                 255
His Thr Leu Thr Ile His Ala Glu Phe Glu Arg Pro Ile Thr Val Asp
            260                 265                 270
Glu Ala Lys Ala Leu Leu Ala Asp Ala Pro Gly Val Glu Leu Val Asp
        275                 280                 285
Val Pro Thr Pro Leu Glu Ala Ala Gly Lys Asp Thr Ser Leu Val Gly
    290                 295                 300
Arg Ile Arg Gln Asp Gln Ser Val Asp Asp Asn Lys Gly Leu Val Leu
305                 310                 315                 320
Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Val
                325                 330                 335
Gln Ile Ala Glu Leu Leu Val
            340
<210>  29
<211>  1725
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1425)
<223>  gen brnE
<400>  29
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gatctcgttg gccttgcccg tggcaccgac ggcggtgagg gcgtcgagga cctcgcggga       60
ggcggcgtcg tcgagaagga cggaggccgg cagctccggg ccgtcctcac cgcagaggac      120
ggggacgagc agtgcgtcgg gggtcttcgg ggccttcttg gccagctcga cggcgggggt      180
ggtgccgcgg gcgggaaggg tgaaagtggg gttcgccatg gaaagtacct cctgagattg      240
acaagcgatg aacccagctt atagagatca cctctgggtc gtcggtgtag cgtgttcccc      300
atg acg tct ctc aat ttc acc gtg aac cgt acg agc acc ccg acg tcc         348
Met Thr Ser Leu Asn Phe Thr Val Asn Arg Thr Ser Thr Pro Thr Ser
1               5                  10                  15
gat gag gcg cgc gag gag att ctg cag aat ccg cgg ttc ggc aag aac         396
Asp Glu Ala Arg Glu Glu Ile Leu Gln Asn Pro Arg Phe Gly Lys Asn
            20                  25                  30
ttc acc gat cac atg gtc acc atc gag tgg tcc gag gac aag ggc tgg         444
Phe Thr Asp His Met Val Thr Ile Glu Trp Ser Glu Asp Lys Gly Trp
        35                  40                  45
cac gac gcc cgc gtg cgt ccc tac gag gcc atc ccg atg gat ccc gcg         492
His Asp Ala Arg Val Arg Pro Tyr Glu Ala Ile Pro Met Asp Pro Ala
    50                  55                  60
acc acg gtg ttc cac tac ggc cag gcg atc ttc gag ggc atc aag gcc         540
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
65                  70                  75                  80
tac cgt cag ccg gac ggc tcc atc gcc acc ttc cgc ccg gag cgc aac         588
Tyr Arg Gln Pro Asp Gly Ser Ile Ala Thr Phe Arg Pro Glu Arg Asn
                85                  90                  95
gcc gag cgc atg cag cgt tcc gcc gag cgc atg gcc atg ccg ccg ctg         636
Ala Glu Arg Met Gln Arg Ser Ala Glu Arg Met Ala Met Pro Pro Leu
            100                 105                 110
ccg acc gag gac ttc ctc gag acg ctc cgc ctg ctt gtc gac gtc gac         684
Pro Thr Glu Asp Phe Leu Glu Thr Leu Arg Leu Leu Val Asp Val Asp
        115                 120                 125
cgt gac tgg gtc ccc gcc gcc ggc ggc gag gcc agc ctc tac ctg cgt         732
Arg Asp Trp Val Pro Ala Ala Gly Gly Glu Ala Ser Leu Tyr Leu Arg
    130                 135                 140
ccc ttc atg atc tcc acc gag gtc tcc ctg ggc gtc agc ccg gcc aac         780
Pro Phe Met Ile Ser Thr Glu Val Ser Leu Gly Val Ser Pro Ala Asn
145                 150                 155                 160
cgg tac acc ttc ttc gtc atc gcc tcc ccg gtc ggg gcg tac ttc acc         828
Arg Tyr Thr Phe Phe Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
                165                 170                 175
ggt ggc gtc aag ccg gtc tcc gtg tgg ctg agc gag gac tac gtc cgt         876
Gly Gly Val Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
            180                 185                 190
gcc gcc ccg ggt ggc acc ggt gcc gcg aag ttc gcc ggc aac tac gcc         924
Ala Ala Pro Gly Gly Thr Gly Ala Ala Lys Phe Ala Gly Asn Tyr Ala
        195                 200                 205
gcc tcc ctg ctc gcg cag gcg cag gcg gag gag aag ggc tgc gac cag         972
Ala Ser Leu Leu Ala Gln Ala Gln Ala Glu Glu Lys Gly Cys Asp Gln
    210                 215                 220
gtc gtg tgg ctc gac gcc atc gag cac acc tac atc gag gag atg ggt        1020
Val Val Trp Leu Asp Ala Ile Glu His Thr Tyr Ile Glu Glu Met Gly
225                 230                 235                 240
ggc atg aac ctg ttc ttc gtg tac ggc tcg ggt gac gac gtc acc gtg        1068
Gly Met Asn Leu Phe Phe Val Tyr Gly Ser Gly Asp Asp Val Thr Val
                245                 250                 255
gcc acc ccc gag ctc tcc ggc tcc ctc ctg ccg ggc gtc acc cgc gac        1116
Ala Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Val Thr Arg Asp
            260                 265                 270
tcc ctc ctg cag gtc gcc cgc gat ctc ggc cac cgc acc gag gag cgg        1164
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly His Arg Thr Glu Glu Arg
        275                 280                 285
agg atc tcc aag ttc gac tgg cgc gac gac gtc gcc tcc ggt gcg atg        1212
Arg Ile Ser Lys Phe Asp Trp Arg Asp Asp Val Ala Ser Gly Ala Met
    290                 295                 300
acc gag gcc atg gcc tgc ggc aca gcc gcc gtg atc acc ccg gtc ggc        1260
Thr Glu Ala Met Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
305                 310                 315                 320
cgg gtc ctg tcc aac gac ggc gag ttc cag atc aat gac aac cag ccg        1308
Arg Val Leu Ser Asn Asp Gly Glu Phe Gln Ile Asn Asp Asn Gln Pro
                325                 330                 335
ggt gag gtc acc atg gcc atg cgc gag cgt ctc acc gac atc cag cgc        1356
Gly Glu Val Thr Met Ala Met Arg Glu Arg Leu Thr Asp Ile Gln Arg
            340                 345                 350
ggc ctg tac gag gac acc cac ggc tgg gtg cac acc ctc gtc ccg gct        1404
Gly Leu Tyr Glu Asp Thr His Gly Trp Val His Thr Leu Val Pro Ala
        355                 360                 365
gag gac cag ccg gcg gac tag tcggccagca gctcggcggc ggcccgcacc            1455
Glu Asp Gln Pro Ala Asp
    370
agcgggagcg ccgctagcgc gccggtgccc tggccggcgt tcatgtccag ggcgacgaga       1515
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ggcgtgagtt cgagggcctg cagcgcgatg aggtgcgcgg gctccggggt cagctgccct 1575
gcctggcacc agggggcggt gccgggggag agacgttccg cgaggtaggc ggcgacggtg 1635
acgggggcgc cgtcgagaag cacgggggtg cggcgtgccg cggcctgcgc gatgaaggcc 1695
accagtgcca ccaggtccgg ggaggcgatc 1725

<210> 30
<211> 374
<212> PRT
<213> Corynebacterium humireducens
<400> 30

Met Thr Ser Leu Asn Phe Thr Val Asn Arg Thr Ser Thr Pro Thr Ser
1 5 10 15
Asp Glu Ala Arg Glu Glu Ile Leu Gln Asn Pro Arg Phe Gly Lys Asn
20 25 30
Phe Thr Asp His Met Val Thr Ile Glu Trp Ser Glu Asp Lys Gly Trp
35 40 45
His Asp Ala Arg Val Arg Pro Tyr Glu Ala Ile Pro Met Asp Pro Ala
50 55 60
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
65 70 75 80
Tyr Arg Gln Pro Asp Gly Ser Ile Ala Thr Phe Arg Pro Glu Arg Asn
85 90 95
Ala Glu Arg Met Gln Arg Ser Ala Glu Arg Met Ala Met Pro Pro Leu
100 105 110
Pro Thr Glu Asp Phe Leu Glu Thr Leu Arg Leu Leu Val Asp Val Asp
115 120 125
Arg Asp Trp Val Pro Ala Ala Gly Gly Glu Ala Ser Leu Tyr Leu Arg
130 135 140
Pro Phe Met Ile Ser Thr Glu Val Ser Leu Gly Val Ser Pro Ala Asn
145 150 155 160
Arg Tyr Thr Phe Phe Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
165 170 175
Gly Gly Val Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
180 185 190
Ala Ala Pro Gly Gly Thr Gly Ala Ala Lys Phe Ala Gly Asn Tyr Ala
195 200 205
Ala Ser Leu Leu Ala Gln Ala Gln Ala Glu Glu Lys Gly Cys Asp Gln
210 215 220
Val Val Trp Leu Asp Ala Ile Glu His Thr Tyr Ile Glu Glu Met Gly
225 230 235 240
Gly Met Asn Leu Phe Phe Val Tyr Gly Ser Gly Asp Asp Val Thr Val
245 250 255
Ala Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Val Thr Arg Asp
260 265 270
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly His Arg Thr Glu Glu Arg
275 280 285
Arg Ile Ser Lys Phe Asp Trp Arg Asp Asp Val Ala Ser Gly Ala Met
290 295 300
Thr Glu Ala Met Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
305 310 315 320
Arg Val Leu Ser Asn Asp Gly Glu Phe Gln Ile Asn Asp Asn Gln Pro
325 330 335
Gly Glu Val Thr Met Ala Met Arg Glu Arg Leu Thr Asp Ile Gln Arg
340 345 350
Gly Leu Tyr Glu Asp Thr His Gly Trp Val His Thr Leu Val Pro Ala
355 360 365
Glu Asp Gln Pro Ala Asp
370

<210> 31
<211> 1296
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(996)
<223> gen brnF
<400> 31

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gcgcgccgat cccggtgaca tcgccgagct cgtcgagggc atgcgtctgt tcgccggtta 120
cgccgagtgg gcgcccggcc agctcgacgg ggagatcgac cgcggcgact ggttcgtcac 180
cccggcgctg cccaccgacg tcatcgtccc gggccgcacc gacctgtggg gcgacgtcat 240
gcgccgccag cagccgccgc tgccgctctt ctcgacgttc cccgccgacc tcatggacaa 300
ttg acc ccc gcg ttc cct gac gtc cgt gcc gga ctg cgg gac gcc tgg 348
Leu Thr Pro Ala Phe Pro Asp Val Arg Ala Gly Leu Arg Asp Ala Trp
1 5 10 15
gcc gtc gcg ctc ggg ctg gtc ccc ctg ggg ctg gcc ttc ggc ctg ctg 396
Ala Val Ala Leu Gly Leu Val Pro Leu Gly Leu Ala Phe Gly Leu Leu
20 25 30
atg acg cag gtg ggt ttc gcc tgg tgg tgg acg ccg gtc ttc tcg gtg 444

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Met Thr Gln Val Gly Phe Ala Trp Trp Trp Thr Pro Val Phe Ser Val
        35                  40                  45
ctc atc tac gcc ggg tcc atg gag ttc ctg gcg gtc aac ctg gtg ctc      492
Leu Ile Tyr Ala Gly Ser Met Glu Phe Leu Ala Val Asn Leu Val Leu
    50                  55                  60
gcc ggc gtc ggc ccc ctg tcg acg gcg ctg acc gcc ttc atg gtc aac      540
Ala Gly Val Gly Pro Leu Ser Thr Ala Leu Thr Ala Phe Met Val Asn
65                  70                  75                  80
ttc cgg cac atc ttc tac ggc ctc acc ttc ccc cgg cac ctc gtc cgg      588
Phe Arg His Ile Phe Tyr Gly Leu Thr Phe Pro Arg His Leu Val Arg
                85                  90                  95
ggc cgg gcc ggc cgt gct tac tcc acg tac tcg ctg acc gac gag tcc      636
Gly Arg Ala Gly Arg Ala Tyr Ser Thr Tyr Ser Leu Thr Asp Glu Ser
            100                 105                 110
tac gcc atc gcc tcc gcc cac cct ccg cgc tcc ggt acg cag gtg ctg      684
Tyr Ala Ile Ala Ser Ala His Pro Pro Arg Ser Gly Thr Gln Val Leu
        115                 120                 125
acg atc cag ctc ttc tgc cag gcg atg tgg gtg gtg ccc ggc atc atc      732
Thr Ile Gln Leu Phe Cys Gln Ala Met Trp Val Val Pro Gly Ile Ile
    130                 135                 140
ggg gcg ctc gtc ggt gag gtc atc ccg gcg ggc atc cag ggc atg gag      780
Gly Ala Leu Val Gly Glu Val Ile Pro Ala Gly Ile Gln Gly Met Glu
145                 150                 155                 160
ttc gca ctc gtc gca ctg ttc gtg gtg ctg gcg tgg gag acc ttc cgg      828
Phe Ala Leu Val Ala Leu Phe Val Val Leu Ala Trp Glu Thr Phe Arg
                165                 170                 175
ggc agc cgg gac ctc tcc ctg ccg ctg ctc gcc ggt ggc ctg gca ctc      876
Gly Ser Arg Asp Leu Ser Leu Pro Leu Leu Ala Gly Gly Leu Ala Leu
            180                 185                 190
gtt gcc ggc ctg gtg ctc ccg ggg cag atg ctc atg gtg gcg ctg agc      924
Val Ala Gly Leu Val Leu Pro Gly Gln Met Leu Met Val Ala Leu Ser
        195                 200                 205
gcc tac ttc ctc gtc ctc atc ggc cgg cac ctc tcc ccc gcc ctg gac      972
Ala Tyr Phe Leu Val Leu Ile Gly Arg His Leu Ser Pro Ala Leu Asp
    210                 215                 220
cgt cgc ctg gag tgg agg gtc tga tgtacgggct tcccgagggg gtcaccctca     1026
Arg Arg Leu Glu Trp Arg Val
225                 230
cccagacgtt ggcggtcctg ctgcccatcg gggtggtcac ggtggcgctg cgctggctgc     1086
ccttcgcctt tgtcagggcg ctgcgcgaca accagttctt cggtctgctc gcccggatga     1146
tgccggtggg agtgatgacc gtgctggtgg tgtacacgct cctcgggcag cgttcggcgc     1206
ccggtggcct ggcggcggcc ctcatcgggg tcgcggtgac cctggggctg cacgcctggc     1266
ggcgggactc tgggctctcg atcctcggag                                     1296
<210>  32
<211>  231
<212>  PRT
<213>  Corynebacterium humireducens
<400>  32
Leu Thr Pro Ala Phe Pro Asp Val Arg Ala Gly Leu Arg Asp Ala Trp
1               5                   10                  15
Ala Val Ala Leu Gly Leu Val Pro Leu Gly Leu Ala Phe Gly Leu Leu
            20                  25                  30
Met Thr Gln Val Gly Phe Ala Trp Trp Trp Thr Pro Val Phe Ser Val
        35                  40                  45
Leu Ile Tyr Ala Gly Ser Met Glu Phe Leu Ala Val Asn Leu Val Leu
    50                  55                  60
Ala Gly Val Gly Pro Leu Ser Thr Ala Leu Thr Ala Phe Met Val Asn
65                  70                  75                  80
Phe Arg His Ile Phe Tyr Gly Leu Thr Phe Pro Arg His Leu Val Arg
                85                  90                  95
Gly Arg Ala Gly Arg Ala Tyr Ser Thr Tyr Ser Leu Thr Asp Glu Ser
            100                 105                 110
Tyr Ala Ile Ala Ser Ala His Pro Pro Arg Ser Gly Thr Gln Val Leu
        115                 120                 125
Thr Ile Gln Leu Phe Cys Gln Ala Met Trp Val Val Pro Gly Ile Ile
    130                 135                 140
Gly Ala Leu Val Gly Glu Val Ile Pro Ala Gly Ile Gln Gly Met Glu
145                 150                 155                 160
Phe Ala Leu Val Ala Leu Phe Val Val Leu Ala Trp Glu Thr Phe Arg
                165                 170                 175
Gly Ser Arg Asp Leu Ser Leu Pro Leu Leu Ala Gly Gly Leu Ala Leu
            180                 185                 190
Val Ala Gly Leu Val Leu Pro Gly Gln Met Leu Met Val Ala Leu Ser
        195                 200                 205
Ala Tyr Phe Leu Val Leu Ile Gly Arg His Leu Ser Pro Ala Leu Asp
    210                 215                 220
Arg Arg Leu Glu Trp Arg Val
225                 230
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<210> 33
<211> 1200
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(900)
<223> gen cysE
<400> 33

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tggaccgcaa ggtcctcgac gacgtcatca ccgtcaccaa cgaggacgcc atcgagacct       60
cccgtcagct ggcggtcaag gacggcatcc tgggcggtat ctcctccggc ggcaacgtct      120
gggccgcgct ggagctggcg aagaaggagg agaacgcggg caagaccatc gtcaccgtcg      180
tcaccgacta cggcgagcgt tacgtctcca ccgtcctgta cgaggacatt cgcgactagg      240
aaacggctta ggccccgca gcgcccacca ggcgacgggc aagcaagtag actctgggcc       300
atg ctg ctg ttg aac atc gcg aag atg gtc cgg gag gac ctg cgc aac         348
Met Leu Leu Leu Asn Ile Ala Lys Met Val Arg Glu Asp Leu Arg Asn
1               5                  10                  15
gcc cgc gac cac gat ccc gcc gcc cgc ggc gac atc gag aac gcc gtc         396
Ala Arg Asp His Asp Pro Ala Ala Arg Gly Asp Ile Glu Asn Ala Val
            20                  25                  30
gtc tac tcg ggc ctg cac gcc atc tgg gca cac cgt gtc tcc cac tgg         444
Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val Ser His Trp
        35                  40                  45
atg tgg gag cgc ggt ctc cgc ggc ccc gcg cga atc ctc gcg cag ctc         492
Met Trp Glu Arg Gly Leu Arg Gly Pro Ala Arg Ile Leu Ala Gln Leu
    50                  55                  60
aac cgg ttc ttc acg ggc atc gag atc cac ccc ggt gcc acc atc ggc         540
Asn Arg Phe Phe Thr Gly Ile Glu Ile His Pro Gly Ala Thr Ile Gly
65                  70                  75                  80
cgc cgt ttc ttc atc gac cac ggc atg ggc atc gtc atc ggc gag acc         588
Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile Gly Glu Thr
                85                  90                  95
acc gag atc ggc gac ggc gtc atg ctc tac cac ggc gtc acc ctg ggt         636
Thr Glu Ile Gly Asp Gly Val Met Leu Tyr His Gly Val Thr Leu Gly
            100                 105                 110
ggt cag gtg ctc acg cag acc aag cgc cac ccg acc atc gag gac aac         684
Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Ile Glu Asp Asn
        115                 120                 125
gtc acc atc ggt gcc ggc gcc aag gtg ctc ggc ccg atc acc atc ggc         732
Val Thr Ile Gly Ala Gly Ala Lys Val Leu Gly Pro Ile Thr Ile Gly
    130                 135                 140
aag ggc tcc gcg atc ggc gcc aac gcc gtg gtg acc aag gac gtc ccg         780
Lys Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys Asp Val Pro
145                 150                 155                 160
gcg gac cac atc gcc acg ggc atc ccg gcg aag aac cgc ccg cgc cgc         828
Ala Asp His Ile Ala Thr Gly Ile Pro Ala Lys Asn Arg Pro Arg Arg
                165                 170                 175
cag tcc gag cgc atc aag ctc gtc gat ccg gac tac tac acc tcc aac         876
Gln Ser Glu Arg Ile Lys Leu Val Asp Pro Asp Tyr Tyr Thr Ser Asn
            180                 185                 190
gat ccg gtc gac tac agc atc tag acacaaggaa ggccccggtt tcccggggcc        930
Asp Pro Val Asp Tyr Ser Ile
        195
tttttgtgct tcacgacgtc ggcgcgtgcc cgacgtcacc cgacgaggtc gcggtactcc       990
tcgttcttgc tgatgaagtg ctcgaccgcg gaacagctcg ggcgcacccg cgccccctcc      1050
tcccgggccc agtcgagggc ctcgcggatg agcggggtgg acagcgcacg tccgcggtag      1110
gcctggtcca ccacggtgtg gtggaagtcc agtaggccac cgtggcggac gtaggaggcg      1170
tagccgacct cccggtcgtc cacggagatg                                       1200
```

<210> 34
<211> 199
<212> PRT
<213> Corynebacterium humireducens
<400> 34

```
Met Leu Leu Leu Asn Ile Ala Lys Met Val Arg Glu Asp Leu Arg Asn
1               5                  10                  15
Ala Arg Asp His Asp Pro Ala Ala Arg Gly Asp Ile Glu Asn Ala Val
            20                  25                  30
Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val Ser His Trp
        35                  40                  45
Met Trp Glu Arg Gly Leu Arg Gly Pro Ala Arg Ile Leu Ala Gln Leu
    50                  55                  60
Asn Arg Phe Phe Thr Gly Ile Glu Ile His Pro Gly Ala Thr Ile Gly
65                  70                  75                  80
Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile Gly Glu Thr
                85                  90                  95
Thr Glu Ile Gly Asp Gly Val Met Leu Tyr His Gly Val Thr Leu Gly
            100                 105                 110
Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Ile Glu Asp Asn
```

```
        115                 120                 125
Val Thr Ile Gly Ala Gly Ala Lys Val Leu Gly Pro Ile Thr Ile Gly
    130                 135                 140
Lys Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys Asp Val Pro
145                 150                 155                 160
Ala Asp His Ile Ala Thr Gly Ile Pro Ala Lys Asn Arg Pro Arg Arg
                165                 170                 175
Gln Ser Glu Arg Ile Lys Leu Val Asp Pro Asp Tyr Tyr Thr Ser Asn
            180                 185                 190
Asp Pro Val Asp Tyr Ser Ile
        195
<210>  35
<211>  1536
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1236)
<223>  gen cysK
<400>  35
cctccgggta cacccgtaca ggtgcacccg atgggcacat gaacgggggt aactttcctt       60
tacagatggg cattataacg cgacttcggg ggtaaacgga atcgaatccg ccgtaacttg      120
cgcattcaag accgttctga tcggaacaac ggcacccact gaaggggtga tatcccgcgc      180
cggagaccac ccccgcaacc ttggagaaac catgtggtct gccagggaca taccatcctg      240
tctactcaca tggtgtacgc tgacaccacc aacgtcagac gaagcaagga agcagtcacc      300
atg agc aag atc tac gac aac atc ctc gac acc atc gga aac acc ccg         348
Met Ser Lys Ile Tyr Asp Asn Ile Leu Asp Thr Ile Gly Asn Thr Pro
1               5                   10                  15
ctg gtg cgc ctc aac ggc ctc acc gag ggc ctc cag gcg gag gtg ctc         396
Leu Val Arg Leu Asn Gly Leu Thr Glu Gly Leu Gln Ala Glu Val Leu
            20                  25                  30
gtg aag gtc gag tcc ttc aac ccg gcg aac tcc gtc aag gac cgc atc         444
Val Lys Val Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
        35                  40                  45
ggc aag gcg atc atc gac gcc gcc gag gcc gac ggg tcc ctc cag ccg         492
Gly Lys Ala Ile Ile Asp Ala Ala Glu Ala Asp Gly Ser Leu Gln Pro
    50                  55                  60
ggc ggc acc atc gtg gag gcc acc tcc ggc aac acc ggc atc gcc ctc         540
Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu
65                  70                  75                  80
gcc ctc gtg ggc gcg gcc cgc ggc tac aac gtg atc ctc acc atg ccg         588
Ala Leu Val Gly Ala Ala Arg Gly Tyr Asn Val Ile Leu Thr Met Pro
                85                  90                  95
gag acc atg tcc aac gag cgt cgc gtc atg ctc cgc gcc tac ggc gct         636
Glu Thr Met Ser Asn Glu Arg Arg Val Met Leu Arg Ala Tyr Gly Ala
            100                 105                 110
cag atc gtc ctg acc ccg ggc gcg gcc ggc atg cag ggc gcc gtc gac         684
Gln Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Val Asp
        115                 120                 125
aag gcg aac gag atc gtc gcc gcc gag gac aac gcc atc ctc gcg aac         732
Lys Ala Asn Glu Ile Val Ala Ala Glu Asp Asn Ala Ile Leu Ala Asn
    130                 135                 140
cag ttc gcg cac ccg gcg aac ctg cgg atc cac cgc gag acc acc gcc         780
Gln Phe Ala His Pro Ala Asn Leu Arg Ile His Arg Glu Thr Thr Ala
145                 150                 155                 160
gag gag atc tgg aac gac acc gac ggc gag gtc gac atc ttc gtc gcg         828
Glu Glu Ile Trp Asn Asp Thr Asp Gly Glu Val Asp Ile Phe Val Ala
                165                 170                 175
ggc atc ggc acg ggc ggc acc gtc tcc ggc gtc ggc cag gtg ctc aag         876
Gly Ile Gly Thr Gly Gly Thr Val Ser Gly Val Gly Gln Val Leu Lys
            180                 185                 190
gag cgc aag ccg gag gtc cag atc tac gcc gtc gag ccg gcc gcg tcc         924
Glu Arg Lys Pro Glu Val Gln Ile Tyr Ala Val Glu Pro Ala Ala Ser
        195                 200                 205
ccg ctg ctg tcc gcc ggc aag gcg ggc ccg cac aag atc cag ggc atc         972
Pro Leu Leu Ser Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile
    210                 215                 220
ggc gcc aac ttc atc ccg gag gtc ctg gac cgc aag gtc ctc gac gac        1020
Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp
225                 230                 235                 240
gtc atc acc gtc acc aac gag gac gcc atc gag acc tcc cgt cag ctg        1068
Val Ile Thr Val Thr Asn Glu Asp Ala Ile Glu Thr Ser Arg Gln Leu
                245                 250                 255
gcg gtc aag gac ggc atc ctg ggc ggt atc tcc tcc ggc ggc aac gtc        1116
Ala Val Lys Asp Gly Ile Leu Gly Gly Ile Ser Ser Gly Gly Asn Val
            260                 265                 270
tgg gcc gcg ctg gag ctg gcg aag aag gag gag aac gcg ggc aag acc        1164
Trp Ala Ala Leu Glu Leu Ala Lys Lys Glu Glu Asn Ala Gly Lys Thr
```

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        275                 280                 285
atc gtc acc gtc gtc acc gac tac ggc gag cgt tac gtc tcc acc gtc      1212
Ile Val Thr Val Val Thr Asp Tyr Gly Glu Arg Tyr Val Ser Thr Val
    290                 295                 300
ctg tac gag gac att cgc gac tag gaaacggctt aggccccgc agcgcccacc      1266
Leu Tyr Glu Asp Ile Arg Asp
305                 310
aggcgacggg caagcaagta gactctgggc catgctgctg ttgaacatcg cgaagatggt     1326
ccgggaggac ctgcgcaacg cccgcgacca cgatcccgcc gcccgcggcg acatcgagaa     1386
cgccgtcgtc tactcgggcc tgcacgccat ctgggcacac cgtgtctccc actggatgtg     1446
ggagcgcggt ctccgcggcc ccgcgcgaat cctcgcgcag ctcaaccggt tcttcacggg     1506
catcgagatc cacccggtg ccaccatcgg                                       1536
<210>  36
<211>  311
<212>  PRT
<213>  Corynebacterium humireducens
<400>  36
Met Ser Lys Ile Tyr Asp Asn Ile Leu Asp Thr Ile Gly Asn Thr Pro
1               5                  10                  15
Leu Val Arg Leu Asn Gly Leu Thr Glu Gly Leu Gln Ala Glu Val Leu
            20                  25                  30
Val Lys Val Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
        35                  40                  45
Gly Lys Ala Ile Ile Asp Ala Ala Glu Ala Asp Gly Ser Leu Gln Pro
    50                  55                  60
Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu
65                  70                  75                  80
Ala Leu Val Gly Ala Ala Arg Gly Tyr Asn Val Ile Leu Thr Met Pro
                85                  90                  95


Glu Thr Met Ser Asn Glu Arg Arg Val Met Leu Arg Ala Tyr Gly Ala
            100                 105                 110
Gln Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Val Asp
        115                 120                 125
Lys Ala Asn Glu Ile Val Ala Ala Glu Asp Asn Ala Ile Leu Ala Asn
    130                 135                 140
Gln Phe Ala His Pro Ala Asn Leu Arg Ile His Arg Glu Thr Thr Ala
145                 150                 155                 160
Glu Glu Ile Trp Asn Asp Thr Asp Gly Glu Val Asp Ile Phe Val Ala
                165                 170                 175
Gly Ile Gly Thr Gly Gly Thr Val Ser Gly Val Gly Gln Val Leu Lys
            180                 185                 190
Glu Arg Lys Pro Glu Val Gln Ile Tyr Ala Val Glu Pro Ala Ala Ser
        195                 200                 205
Pro Leu Leu Ser Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile
    210                 215                 220
Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp
225                 230                 235                 240
Val Ile Thr Val Thr Asn Glu Asp Ala Ile Glu Thr Ser Arg Gln Leu
                245                 250                 255
Ala Val Lys Asp Gly Ile Leu Gly Gly Ile Ser Ser Gly Gly Asn Val
            260                 265                 270
Trp Ala Ala Leu Glu Leu Ala Lys Lys Glu Glu Asn Ala Gly Lys Thr
        275                 280                 285
Ile Val Thr Val Val Thr Asp Tyr Gly Glu Arg Tyr Val Ser Thr Val
    290                 295                 300
Leu Tyr Glu Asp Ile Arg Asp
305                 310
<210>  37
<211>  999
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(699)
<223>  gen gcvH

<400>  37
cagggagccg accagcgcca tcgtcgggct ccggggtctg gggcgccgcg cggcccgcga       60
gggcgccgag gtctacctcg acggcgaaca ggtcggcgtg gtcacctccg ggcagccggc      120
gccggtgctc ggctacccga tcgcactcgc ccgcctgcgc cccgacgtca ccgcggccgg      180
cacggcactg gaggtggaca tccgtgggag gcggcacccc ttcgagatcg tcgacctgcc      240
cttctaccgc cgcgccgcac gataacctga acccaccacc aacggaaagg ctcccccacc      300
atg gcc acc gag cac tcc ctg ccc ggg aac tac tcc tac tcc gag gac        348
Met Ala Thr Glu His Ser Leu Pro Gly Asn Tyr Ser Tyr Ser Glu Asp
1               5                  10                  15
cac gag tgg atc gac gcg acg ccc gag gac gcc gtc ggc gcg acc gtg        396
```

```
His Glu Trp Ile Asp Ala Thr Pro Glu Asp Ala Val Gly Ala Thr Val
            20                  25                  30
aag gtc ggc atc acc tcc gtg gcc acc gaa cgc ctc ggc gag gtc gtc        444
Lys Val Gly Ile Thr Ser Val Ala Thr Glu Arg Leu Gly Glu Val Val
        35                  40                  45
tac gcg gag ctc ccg cag gtc ggt gac gcc gtc acc gcc ggt gaa ccg        492
Tyr Ala Glu Leu Pro Gln Val Gly Asp Ala Val Thr Ala Gly Glu Pro
    50                  55                  60
tgc ggc gag gtc gag tcc acg aag tcg gtc tcc gac ctc tac gcg ccg        540
Cys Gly Glu Val Glu Ser Thr Lys Ser Val Ser Asp Leu Tyr Ala Pro
65                  70                  75                  80
gtc acg ggc acc gtc acc gag gtc aac gac gcg gtc cac gac gac tac        588
Val Thr Gly Thr Val Thr Glu Val Asn Asp Ala Val His Asp Asp Tyr
                85                  90                  95
gcc gtg atc aac gac gac ccc ttc ggc gcg ggc tgg ctc ttc gcc gtc        636
Ala Val Ile Asn Asp Asp Pro Phe Gly Ala Gly Trp Leu Phe Ala Val
            100                 105                 110
gag gtc gac gag gtc gga ccg ctc atg acc gcc gcc gag tac gcg gag        684
Glu Val Asp Glu Val Gly Pro Leu Met Thr Ala Ala Glu Tyr Ala Glu
        115                 120                 125
gcc aac ggc gtg tga ccgcccggga ccggtaccct ggtcccatca tgactgcacc        739
Ala Asn Gly Val
    130
ccgtgagccc ttcttccctg cggaccgttc catccgtgcc tccggcgagc ccccggagat      799
ccgttatctc ggcgtcgtcg actaccagga ggcctggaat ctgcaggccg agctggcgtc      859
gcaacgcgcg gccggggaga tcggtgacca gctcctcatc ctcgagcacc cgagcgtgta      919
caccgccggc aagcgcacgc agccggagga ccgccccacc aacggcctgc cggtcatcga      979
cgtcgaccgg ggtggccgca                                                 999
<210>  38
<211>  132
<212>  PRT
<213>  Corynebacterium humireducens
<400>  38
Met Ala Thr Glu His Ser Leu Pro Gly Asn Tyr Ser Tyr Ser Glu Asp
1               5                   10                  15
His Glu Trp Ile Asp Ala Thr Pro Glu Asp Ala Val Gly Ala Thr Val
            20                  25                  30
Lys Val Gly Ile Thr Ser Val Ala Thr Glu Arg Leu Gly Glu Val Val
        35                  40                  45
Tyr Ala Glu Leu Pro Gln Val Gly Asp Ala Val Thr Ala Gly Glu Pro
    50                  55                  60
Cys Gly Glu Val Glu Ser Thr Lys Ser Val Ser Asp Leu Tyr Ala Pro
65                  70                  75                  80
Val Thr Gly Thr Val Thr Glu Val Asn Asp Ala Val His Asp Asp Tyr
                85                  90                  95
Ala Val Ile Asn Asp Asp Pro Phe Gly Ala Gly Trp Leu Phe Ala Val
            100                 105                 110
Glu Val Asp Glu Val Gly Pro Leu Met Thr Ala Ala Glu Tyr Ala Glu
        115                 120                 125
Ala Asn Gly Val
    130
<210>  39
<211>  3462
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(3162)
<223>  gen gcvP
<400>  39
ctgggcaccg cggccatcga gaagcgtccg gtcgtggtga ccgatgacgg cgtcgactcg       60
atcgccatcc gccagatgtg ctacctgccg ttcacctacg accaccaggt catcgacggt      120
gccgacgccg gtcgcttcat caccaccatc aaggaccgcc tggagaccgc ggacttccag      180
tccgacctcg gcctctaagc tctcccgctg agagagaccg ccacctgacc ttcccggtcg      240
ggtggcggtt ttcttcttat aatcggaatc atccggtccc ccatcgagga gcgattccgc      300
atg gcc ctg cac ccg atc acc gat tcc gcc tcc tac ctg gcc cga cac        348
Met Ala Leu His Pro Ile Thr Asp Ser Ala Ser Tyr Leu Ala Arg His
1               5                   10                  15
ctc ggc ccc gac acc gcg gag gag cag gtc atg ctg ggg gcg ctg ggc        396
Leu Gly Pro Asp Thr Ala Glu Glu Gln Val Met Leu Gly Ala Leu Gly
            20                  25                  30
tac ggt tcc ctc gcc gag ctt gtc gac gcc gcc ctg ccc acc gac atc        444
Tyr Gly Ser Leu Ala Glu Leu Val Asp Ala Ala Leu Pro Thr Asp Ile
        35                  40                  45
cgc ctc acc gaa cct ctc ccg cgg cac gcg ccc ctc tcg gag acg gag        492
Arg Leu Thr Glu Pro Leu Pro Arg His Ala Pro Leu Ser Glu Thr Glu
    50                  55                  60
gcg cag gcg cga ctg cgg gag tac gcc tcg cgg aac acg gtg ctc cgt        540
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Ala Gln Ala Arg Leu Arg Glu Tyr Ala Ser Arg Asn Thr Val Leu Arg
65                  70                  75                  80
tcc ttt tac ggg cag ggt ttc tcc gac acg gtc act ccc ccg gtg atc      588
Ser Phe Tyr Gly Gln Gly Phe Ser Asp Thr Val Thr Pro Pro Val Ile
                85                  90                  95
cgc cgc ggg gtg ctc gag gcc ccg ggc tgg tac acc gcg tac acg ccg      636
Arg Arg Gly Val Leu Glu Ala Pro Gly Trp Tyr Thr Ala Tyr Thr Pro
            100                 105                 110
tac cag ccg gag atc tcg cag ggc cgc ctc gag gcg ctg ctc aac ttc      684
Tyr Gln Pro Glu Ile Ser Gln Gly Arg Leu Glu Ala Leu Leu Asn Phe
        115                 120                 125
cag acg atg gtc tcc gag ctc acc ggc ctg ccg gtg gcg aac gcc tcg      732
Gln Thr Met Val Ser Glu Leu Thr Gly Leu Pro Val Ala Asn Ala Ser
    130                 135                 140
ctc ctc gac gag gct tcc gcc acc gcc gaa gcc gtc ggc ctc atg tcg      780
Leu Leu Asp Glu Ala Ser Ala Thr Ala Glu Ala Val Gly Leu Met Ser
145                 150                 155                 160
cgg gcg cag agg aag ggg cgg cgg gtg ctt ctc gac gcc cgc ctc cac      828
Arg Ala Gln Arg Lys Gly Arg Arg Val Leu Leu Asp Ala Arg Leu His
                165                 170                 175
ccc cag gtc ctc gcc gtc gct gcg gag cgg gcc cgg gcg atc gac ctg      876
Pro Gln Val Leu Ala Val Ala Ala Glu Arg Ala Arg Ala Ile Asp Leu
            180                 185                 190
gag gtc gcc gtc gag gac ctg tcc ggc ccg ctg gtg ggt gag gat ctc      924
Glu Val Ala Val Glu Asp Leu Ser Gly Pro Leu Val Gly Glu Asp Leu
        195                 200                 205
tgc ggc gtc gtc atc gcc tac ccc ggc acg gag ggc gac atc gcc gat      972
Cys Gly Val Val Ile Ala Tyr Pro Gly Thr Glu Gly Asp Ile Ala Asp
    210                 215                 220
ccc cgc ccg gtc atc gag gcc gtg cac gca cgc ggg ggt ctg gcc acc     1020
Pro Arg Pro Val Ile Glu Ala Val His Ala Arg Gly Gly Leu Ala Thr
225                 230                 235                 240

gtg gtc acc gat ccc ctg tcg ctg ctc ctg ctc gag tcg ccg ggt gag     1068
Val Val Thr Asp Pro Leu Ser Leu Leu Leu Leu Glu Ser Pro Gly Glu
                245                 250                 255
atg ggg gcg gac atc gcg gtg ggc tcc tcg cag cgt ttc ggc gtg ccc     1116
Met Gly Ala Asp Ile Ala Val Gly Ser Ser Gln Arg Phe Gly Val Pro
            260                 265                 270
ctg ttc tac ggt ggc ccg cac gcc gcg tac atg gcc gtc agt gac gcc     1164
Leu Phe Tyr Gly Gly Pro His Ala Ala Tyr Met Ala Val Ser Asp Ala
        275                 280                 285
ctc aag cgc cag atc ccc ggc cgc ctg gtg ggc gtg tcc gtc gac gcc     1212
Leu Lys Arg Gln Ile Pro Gly Arg Leu Val Gly Val Ser Val Asp Ala
    290                 295                 300
gag ggc gcc ccc gcc tac cgg ctc gcg ctg cag acc cgg gag cag cac     1260
Glu Gly Ala Pro Ala Tyr Arg Leu Ala Leu Gln Thr Arg Glu Gln His
305                 310                 315                 320
atc cgt cgc gag cgg gcg acg tcg aac atc tgc acc gcg cag gcg ctg     1308
Ile Arg Arg Glu Arg Ala Thr Ser Asn Ile Cys Thr Ala Gln Ala Leu
                325                 330                 335
ctg gcg gtc acc gcc ggc atg tac gcc gtc tac cac ggt ccc gag ggg     1356
Leu Ala Val Thr Ala Gly Met Tyr Ala Val Tyr His Gly Pro Glu Gly
            340                 345                 350
ttg cgt gcc atc gcg gag cgc gtg cac ggt ctg gcc tgt gac ttc gcg     1404
Leu Arg Ala Ile Ala Glu Arg Val His Gly Leu Ala Cys Asp Phe Ala
        355                 360                 365
gcg gcc gtc cgc gcc gcc ggc ggg acg gtg ctg cac gac gcc ttc ttc     1452
Ala Ala Val Arg Ala Ala Gly Gly Thr Val Leu His Asp Ala Phe Phe
    370                 375                 380
gac acc gtc gcg gtg cgg gtg gag gct gca cga ccg atc gtc ggc acg     1500
Asp Thr Val Ala Val Arg Val Glu Ala Ala Arg Pro Ile Val Gly Thr
385                 390                 395                 400
ctc gcg gag gcg ggc tac ctc gtg cgt gcc gtg gac ggc acg acc gtc     1548
Leu Ala Glu Ala Gly Tyr Leu Val Arg Ala Val Asp Gly Thr Thr Val
                405                 410                 415
ggc gtg agc ttc ggt gag tcg gcg gag gag ggg gac gtc gag aag ctc     1596
Gly Val Ser Phe Gly Glu Ser Ala Glu Glu Gly Asp Val Glu Lys Leu
            420                 425                 430
gcc gcc gtc ttc ggc gcc tcc ctg acg gcg ggc acc cgc tgc atc ccc     1644
Ala Ala Val Phe Gly Ala Ser Leu Thr Ala Gly Thr Arg Cys Ile Pro
        435                 440                 445
gcg tcc gtg gcg cgg cag acg ccg acg ctg acg cac ccg gtc ttc tcc     1692
Ala Ser Val Ala Arg Gln Thr Pro Thr Leu Thr His Pro Val Phe Ser
    450                 455                 460
acg ctc cac tcc gag acg cag atg atg cgc tac ctg cgc acg ctc tcg     1740
Thr Leu His Ser Glu Thr Gln Met Met Arg Tyr Leu Arg Thr Leu Ser
465                 470                 475                 480
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gac cgg gat ctc gcg ctc gac cgc acg atg atc ccg ctg ggt tcg tgc      1788
Asp Arg Asp Leu Ala Leu Asp Arg Thr Met Ile Pro Leu Gly Ser Cys
                485                 490                 495
acg atg aag ctc aac ccg acc gcc ggg ctg gag acg atc acg tgg ccg      1836
Thr Met Lys Leu Asn Pro Thr Ala Gly Leu Glu Thr Ile Thr Trp Pro
            500                 505                 510
gag ttc gcc gac atg cac ccc ttc gcc ccc gac gac cag gcc gcg ggc      1884
Glu Phe Ala Asp Met His Pro Phe Ala Pro Asp Asp Gln Ala Ala Gly
        515                 520                 525
tgg ctg gcg ctc atc gcg gag ctg gag ggc tgg ctc gcg gag ctc acc      1932
Trp Leu Ala Leu Ile Ala Glu Leu Glu Gly Trp Leu Ala Glu Leu Thr
    530                 535                 540
gga tac gcg aag gtg tcc gtg cag ccc aac gcg ggt tcc cag ggg gag      1980
Gly Tyr Ala Lys Val Ser Val Gln Pro Asn Ala Gly Ser Gln Gly Glu
545                 550                 555                 560
ctg gcc gga ctg ctg gcc atc cgc cgc tac cac gtg gcc aac ggg gac      2028
Leu Ala Gly Leu Leu Ala Ile Arg Arg Tyr His Val Ala Asn Gly Asp
                565                 570                 575
atg gac cgt gat atc tgc ctg gtc ccg gcc tcg gcg cac ggc acg aac      2076
Met Asp Arg Asp Ile Cys Leu Val Pro Ala Ser Ala His Gly Thr Asn
            580                 585                 590
gcg gcg tcg gcg acg ctg gcg cac ctg cgg gtc gtg gtg gtc ggc acc      2124
Ala Ala Ser Ala Thr Leu Ala His Leu Arg Val Val Val Val Gly Thr
        595                 600                 605
gcc ggg gac ggc tcc atc gac atg gac gac ctc gac gcg aaa ctc gcc      2172
Ala Gly Asp Gly Ser Ile Asp Met Asp Asp Leu Asp Ala Lys Leu Ala
    610                 615                 620
gag cac ggc ccg cag gtg gcc gcg atc atg atc acc tac ccc tcc acg      2220
Glu His Gly Pro Gln Val Ala Ala Ile Met Ile Thr Tyr Pro Ser Thr
625                 630                 635                 640
cac ggc gtc ttc gag gac acc gtg cgc gag gtg tgc gac agg gtg cac      2268
His Gly Val Phe Glu Asp Thr Val Arg Glu Val Cys Asp Arg Val His
                645                 650                 655

gcg gtc ggc ggg cag gtc tac atc gac ggc gcg aac ctc aac gcc ctg      2316
Ala Val Gly Gly Gln Val Tyr Ile Asp Gly Ala Asn Leu Asn Ala Leu
            660                 665                 670
acc ggc ctg gcg ctg ctg ggc cgc atc ggc ggc gac gtc tcc cac ctc      2364
Thr Gly Leu Ala Leu Leu Gly Arg Ile Gly Gly Asp Val Ser His Leu
        675                 680                 685
aac ctg cac aag acg ttc acc atc ccg cac ggc ggc ggt ggc ccg ggc      2412
Asn Leu His Lys Thr Phe Thr Ile Pro His Gly Gly Gly Gly Pro Gly
    690                 695                 700
gtg ggc ccg gtg tgc gtc gcg gag cac ctc gtc ccc ttc ctg ccg gcg      2460
Val Gly Pro Val Cys Val Ala Glu His Leu Val Pro Phe Leu Pro Ala
705                 710                 715                 720
gac ccg acc tcc ctc gac ggc gcc acc ccg gcg gcg gtc ggc acc ggc      2508
Asp Pro Thr Ser Leu Asp Gly Ala Thr Pro Ala Ala Val Gly Thr Gly
                725                 730                 735
gtg ccc gtc tct gcg acg cgc cac ggc tcg gcg ggc gtc ctg cag atc      2556
Val Pro Val Ser Ala Thr Arg His Gly Ser Ala Gly Val Leu Gln Ile
            740                 745                 750
tcc tgg gcg tac atc gcc atg atg ggc acc gac ggc ctc acc cgc gcc      2604
Ser Trp Ala Tyr Ile Ala Met Met Gly Thr Asp Gly Leu Thr Arg Ala
        755                 760                 765
agc gcc gcg gcg atc ctc agc gcg aac tac gtc gcc cac cgc ctg ggc      2652
Ser Ala Ala Ala Ile Leu Ser Ala Asn Tyr Val Ala His Arg Leu Gly
    770                 775                 780
gag gcc ttc ccg gtg ctc tac acc ggc cgc aac ggc ctg gtg gcg cac      2700
Glu Ala Phe Pro Val Leu Tyr Thr Gly Arg Asn Gly Leu Val Ala His
785                 790                 795                 800
gag tgc atc ctc gac ctg cgc gac ctg acg agg cag acc ggc gtc acc      2748
Glu Cys Ile Leu Asp Leu Arg Asp Leu Thr Arg Gln Thr Gly Val Thr
                805                 810                 815
gcc acg gac gtg gcc aaa cgc ctc atc gac ttc ggc ttc cac gcc ccc      2796
Ala Thr Asp Val Ala Lys Arg Leu Ile Asp Phe Gly Phe His Ala Pro
            820                 825                 830
acg ctc tcc ttc ccc gtc gcc ggt acc ctc atg gtc gag ccg acc gag      2844
Thr Leu Ser Phe Pro Val Ala Gly Thr Leu Met Val Glu Pro Thr Glu
        835                 840                 845
tcc gag gac ctc gcc gag ctc gac cgc ttc atc gag gcg atg ctc acc      2892
Ser Glu Asp Leu Ala Glu Leu Asp Arg Phe Ile Glu Ala Met Leu Thr
    850                 855                 860
atc cgc gcg gag atc gac gag atc agc ggc ggc gac atc gcc tac gag      2940
Ile Arg Ala Glu Ile Asp Glu Ile Ser Gly Gly Asp Ile Ala Tyr Glu
865                 870                 875                 880
gac tcc gtc ctc cac cac gcg ccg ttc acc gcg tgg agc gtg tcc cgc      2988
Asp Ser Val Leu His His Ala Pro Phe Thr Ala Trp Ser Val Ser Arg
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                885                 890                 895
gac gac tgg gac cac gcc ttc acc cgt gag cag gcg gcc tgg ccg gtc      3036
Asp Asp Trp Asp His Ala Phe Thr Arg Glu Gln Ala Ala Trp Pro Val
            900                 905                 910
ccc ggt ctg cgc cgc acc aag tac ttc ccg ccg gtc cgc cgc ctc aac      3084
Pro Gly Leu Arg Arg Thr Lys Tyr Phe Pro Pro Val Arg Arg Leu Asn
        915                 920                 925
gag gcc tac ggt gac cgc cac ctc gtg tgc gcc tgc ccg ccg ccc gag      3132
Glu Ala Tyr Gly Asp Arg His Leu Val Cys Ala Cys Pro Pro Pro Glu
    930                 935                 940
gcc ttc gac ctt tcc gag gag aac cag tga ccgacctgcg taccagcccc        3182
Ala Phe Asp Leu Ser Glu Glu Asn Gln
945                 950
ctccacgagc gtcatgtgga gctcggggcc tccttcaccc ccttcggccc gtggaacatg    3242
cccctgcgct acggcaacga gctcgacgag caccgcgccg tccgttccac cgccgggctc    3302
ttcgacctct cgcacatggg tgagatccgc gtgtggggcg cacaggccgc ggagttcctc    3362
gaccatgcgc tgctctccgc cttctccacg ctccccgtgg gtaaggcgcg gtactccatg    3422
cttgtcgacg ccaccggtgc catcctcgac gacctcctca                          3462
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<213>  Corynebacterium humireducens
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Leu Gly Pro Asp Thr Ala Glu Glu Gln Val Met Leu Gly Ala Leu Gly
            20                  25                  30
Tyr Gly Ser Leu Ala Glu Leu Val Asp Ala Ala Leu Pro Thr Asp Ile
        35                  40                  45
Arg Leu Thr Glu Pro Leu Pro Arg His Ala Pro Leu Ser Glu Thr Glu
    50                  55                  60
Ala Gln Ala Arg Leu Arg Glu Tyr Ala Ser Arg Asn Thr Val Leu Arg
65                  70                  75                  80
Ser Phe Tyr Gly Gln Gly Phe Ser Asp Thr Val Thr Pro Pro Val Ile
                85                  90                  95

Arg Arg Gly Val Leu Glu Ala Pro Gly Trp Tyr Thr Ala Tyr Thr Pro
            100                 105                 110
Tyr Gln Pro Glu Ile Ser Gln Gly Arg Leu Glu Ala Leu Leu Asn Phe
        115                 120                 125
Gln Thr Met Val Ser Glu Leu Thr Gly Leu Pro Val Ala Asn Ala Ser
    130                 135                 140
Leu Leu Asp Glu Ala Ser Ala Thr Ala Glu Ala Val Gly Leu Met Ser
145                 150                 155                 160
Arg Ala Gln Arg Lys Gly Arg Arg Val Leu Leu Asp Ala Arg Leu His
                165                 170                 175
Pro Gln Val Leu Ala Val Ala Ala Glu Arg Ala Arg Ala Ile Asp Leu
            180                 185                 190
Glu Val Ala Val Glu Asp Leu Ser Gly Pro Leu Val Gly Glu Asp Leu
        195                 200                 205
Cys Gly Val Val Ile Ala Tyr Pro Gly Thr Glu Gly Asp Ile Ala Asp
    210                 215                 220
Pro Arg Pro Val Ile Glu Ala Val His Ala Arg Gly Gly Leu Ala Thr
225                 230                 235                 240
Val Val Thr Asp Pro Leu Ser Leu Leu Leu Leu Glu Ser Pro Gly Glu
                245                 250                 255
Met Gly Ala Asp Ile Ala Val Gly Ser Ser Gln Arg Phe Gly Val Pro
            260                 265                 270
Leu Phe Tyr Gly Gly Pro His Ala Ala Tyr Met Ala Val Ser Asp Ala
        275                 280                 285
Leu Lys Arg Gln Ile Pro Gly Arg Leu Val Gly Val Ser Val Asp Ala
    290                 295                 300
Glu Gly Ala Pro Ala Tyr Arg Leu Ala Leu Gln Thr Arg Glu Gln His
305                 310                 315                 320
Ile Arg Arg Glu Arg Ala Thr Ser Asn Ile Cys Thr Ala Gln Ala Leu
                325                 330                 335
Leu Ala Val Thr Ala Gly Met Tyr Ala Val Tyr His Gly Pro Glu Gly
            340                 345                 350
Leu Arg Ala Ile Ala Glu Arg Val His Gly Leu Ala Cys Asp Phe Ala
        355                 360                 365
Ala Ala Val Arg Ala Ala Gly Gly Thr Val Leu His Asp Ala Phe Phe
    370                 375                 380
Asp Thr Val Ala Val Arg Val Glu Ala Ala Arg Pro Ile Val Gly Thr
385                 390                 395                 400
Leu Ala Glu Ala Gly Tyr Leu Val Arg Ala Val Asp Gly Thr Thr Val
                405                 410                 415
Gly Val Ser Phe Gly Glu Ser Ala Glu Glu Gly Asp Val Glu Lys Leu
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            420                 425                 430
Ala Ala Val Phe Gly Ala Ser Leu Thr Ala Gly Thr Arg Cys Ile Pro
        435                 440                 445
Ala Ser Val Ala Arg Gln Thr Pro Thr Leu Thr His Pro Val Phe Ser
    450                 455                 460
Thr Leu His Ser Glu Thr Gln Met Met Arg Tyr Leu Arg Thr Leu Ser
465                 470                 475                 480
Asp Arg Asp Leu Ala Leu Asp Arg Thr Met Ile Pro Leu Gly Ser Cys
                485                 490                 495
Thr Met Lys Leu Asn Pro Thr Ala Gly Leu Glu Thr Ile Thr Trp Pro
            500                 505                 510
Glu Phe Ala Asp Met His Pro Phe Ala Pro Asp Asp Gln Ala Ala Gly
        515                 520                 525
Trp Leu Ala Leu Ile Ala Glu Leu Glu Gly Trp Leu Ala Glu Leu Thr
    530                 535                 540
Gly Tyr Ala Lys Val Ser Val Gln Pro Asn Ala Gly Ser Gln Gly Glu
545                 550                 555                 560
Leu Ala Gly Leu Leu Ala Ile Arg Arg Tyr His Val Ala Asn Gly Asp
                565                 570                 575
Met Asp Arg Asp Ile Cys Leu Val Pro Ala Ser Ala His Gly Thr Asn
            580                 585                 590
Ala Ala Ser Ala Thr Leu Ala His Leu Arg Val Val Val Val Gly Thr
        595                 600                 605
Ala Gly Asp Gly Ser Ile Asp Met Asp Asp Leu Asp Ala Lys Leu Ala
    610                 615                 620
Glu His Gly Pro Gln Val Ala Ala Ile Met Ile Thr Tyr Pro Ser Thr
625                 630                 635                 640
His Gly Val Phe Glu Asp Thr Val Arg Glu Val Cys Asp Arg Val His
                645                 650                 655
Ala Val Gly Gly Gln Val Tyr Ile Asp Gly Ala Asn Leu Asn Ala Leu
            660                 665                 670
Thr Gly Leu Ala Leu Leu Gly Arg Ile Gly Gly Asp Val Ser His Leu
        675                 680                 685
Asn Leu His Lys Thr Phe Thr Ile Pro His Gly Gly Gly Gly Pro Gly
    690                 695                 700


Val Gly Pro Val Cys Val Ala Glu His Leu Val Pro Phe Leu Pro Ala
705                 710                 715                 720
Asp Pro Thr Ser Leu Asp Gly Ala Thr Pro Ala Ala Val Gly Thr Gly
                725                 730                 735
Val Pro Val Ser Ala Thr Arg His Gly Ser Ala Gly Val Leu Gln Ile
            740                 745                 750
Ser Trp Ala Tyr Ile Ala Met Met Gly Thr Asp Gly Leu Thr Arg Ala
        755                 760                 765
Ser Ala Ala Ala Ile Leu Ser Ala Asn Tyr Val Ala His Arg Leu Gly
    770                 775                 780
Glu Ala Phe Pro Val Leu Tyr Thr Gly Arg Asn Gly Leu Val Ala His
785                 790                 795                 800
Glu Cys Ile Leu Asp Leu Arg Asp Leu Thr Arg Gln Thr Gly Val Thr
                805                 810                 815
Ala Thr Asp Val Ala Lys Arg Leu Ile Asp Phe Gly Phe His Ala Pro
            820                 825                 830
Thr Leu Ser Phe Pro Val Ala Gly Thr Leu Met Val Glu Pro Thr Glu
        835                 840                 845
Ser Glu Asp Leu Ala Glu Leu Asp Arg Phe Ile Glu Ala Met Leu Thr
    850                 855                 860
Ile Arg Ala Glu Ile Asp Glu Ile Ser Gly Gly Asp Ile Ala Tyr Glu
865                 870                 875                 880
Asp Ser Val Leu His His Ala Pro Phe Thr Ala Trp Ser Val Ser Arg
                885                 890                 895
Asp Asp Trp Asp His Ala Phe Thr Arg Glu Gln Ala Ala Trp Pro Val
            900                 905                 910
Pro Gly Leu Arg Arg Thr Lys Tyr Phe Pro Pro Val Arg Arg Leu Asn
        915                 920                 925
Glu Ala Tyr Gly Asp Arg His Leu Val Cys Ala Cys Pro Pro Pro Glu
    930                 935                 940
Ala Phe Asp Leu Ser Glu Glu Asn Gln
945                 950
<210>  41
<211>  1704
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1404)
<223>  gen gcvT
<400>  41
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cggcggcgac atcgcctacg aggactccgt cctccaccac gcgccgttca ccgcgtggag     120
cgtgtcccgc gacgactggg accacgcctt cacccgtgag caggcggcct ggccggtccc     180
cggtctgcgc cgcaccaagt acttcccgcc ggtccgccgc ctcaacgagg cctacggtga     240
ccgccacctc gtgtgcgcct gcccgccgcc cgaggccttc gacctttccg aggagaacca     300
gtg acc gac ctg cgt acc agc ccc ctc cac gag cgt cat gtg gag ctc        348
Val Thr Asp Leu Arg Thr Ser Pro Leu His Glu Arg His Val Glu Leu
1               5                  10                  15
ggg gcc tcc ttc acc ccc ttc ggc ccg tgg aac atg ccc ctg cgc tac       396
Gly Ala Ser Phe Thr Pro Phe Gly Pro Trp Asn Met Pro Leu Arg Tyr
            20                  25                  30
ggc aac gag ctc gac gag cac cgc gcc gtc cgt tcc acc gcc ggg ctc       444
Gly Asn Glu Leu Asp Glu His Arg Ala Val Arg Ser Thr Ala Gly Leu
        35                  40                  45
ttc gac ctc tcg cac atg ggt gag atc cgc gtg tgg ggc gca cag gcc       492
Phe Asp Leu Ser His Met Gly Glu Ile Arg Val Trp Gly Ala Gln Ala
    50                  55                  60
gcg gag ttc ctc gac cat gcg ctg ctc tcc gcc ttc tcc acg ctc ccc       540
Ala Glu Phe Leu Asp His Ala Leu Leu Ser Ala Phe Ser Thr Leu Pro
65                  70                  75                  80
gtg ggt aag gcg cgg tac tcc atg ctt gtc gac gcc acc ggt gcc atc       588
Val Gly Lys Ala Arg Tyr Ser Met Leu Val Asp Ala Thr Gly Ala Ile
                85                  90                  95
ctc gac gac ctc ctc acc tac cgc ctc gcc ggg gac gag ttc ctg gtg       636
Leu Asp Asp Leu Leu Thr Tyr Arg Leu Ala Gly Asp Glu Phe Leu Val
            100                 105                 110
gtc ccc aac gcg gcg aac acg gag acc gtg tgg gag gag ttc cgg gcc       684
Val Pro Asn Ala Ala Asn Thr Glu Thr Val Trp Glu Glu Phe Arg Ala
        115                 120                 125
cgc gcc gcc ggc ttc gac gtg gag ctg gcc gac gag tcc gcc gac act       732
Arg Ala Ala Gly Phe Asp Val Glu Leu Ala Asp Glu Ser Ala Asp Thr
    130                 135                 140
gcg ctg ctg gct gtg cag ggc ccc cgc gcc gag cag atc atc gcc gac       780
Ala Leu Leu Ala Val Gln Gly Pro Arg Ala Glu Gln Ile Ile Ala Asp
145                 150                 155                 160
ctc gtc gcc ggg gac gac gag tcg gtc gtg cgc acg atg aag ttc tac       828
Leu Val Ala Gly Asp Asp Glu Ser Val Val Arg Thr Met Lys Phe Tyr
                165                 170                 175
tcg gcg gcc ccg ttg acg gtg gcg ggc gtc gat acg ctg ctc gcc cgc       876
Ser Ala Ala Pro Leu Thr Val Ala Gly Val Asp Thr Leu Leu Ala Arg
            180                 185                 190
acc ggc tac acc ggg gag gac ggc ttc gag ctc tac gtc tcc ggc gcg       924
Thr Gly Tyr Thr Gly Glu Asp Gly Phe Glu Leu Tyr Val Ser Gly Ala
        195                 200                 205
gac gcc gct gaa ctg tgg gac gcg ctg ctc aac gcc ggc gcc gcc tac       972
Asp Ala Ala Glu Leu Trp Asp Ala Leu Leu Asn Ala Gly Ala Ala Tyr
    210                 215                 220
gac atg ctg ccc gcc gga ctg gcg gcg cgg gac tcc ctg cgc ctg gag      1020
Asp Met Leu Pro Ala Gly Leu Ala Ala Arg Asp Ser Leu Arg Leu Glu
225                 230                 235                 240
gcc ggg ctc ccc ctc tac ggg cag gag ctc acc cgc gac atc acg ccg      1068
Ala Gly Leu Pro Leu Tyr Gly Gln Glu Leu Thr Arg Asp Ile Thr Pro
                245                 250                 255
gtg gag gcc ggg atg gcc cgc gcc ttc gcc tcg aag gag ggg gac ttc      1116
Val Glu Ala Gly Met Ala Arg Ala Phe Ala Ser Lys Glu Gly Asp Phe
            260                 265                 270
gtc ggc cgc gac gcc ctc gtc ggc agg gag ccg acc agc gcc atc gtc      1164
Val Gly Arg Asp Ala Leu Val Gly Arg Glu Pro Thr Ser Ala Ile Val
        275                 280                 285
ggg ctc cgg ggt ctg ggg cgc cgc gcg gcc cgc gag ggc gcc gag gtc      1212
Gly Leu Arg Gly Leu Gly Arg Arg Ala Ala Arg Glu Gly Ala Glu Val
    290                 295                 300
tac ctc gac ggc gaa cag gtc ggc gtg gtc acc tcc ggg cag ccg gcg      1260
Tyr Leu Asp Gly Glu Gln Val Gly Val Val Thr Ser Gly Gln Pro Ala
305                 310                 315                 320
ccg gtg ctc ggc tac ccg atc gca ctc gcc cgc ctg cgc ccc gac gtc      1308
Pro Val Leu Gly Tyr Pro Ile Ala Leu Ala Arg Leu Arg Pro Asp Val
                325                 330                 335
acc gcg gcc ggc acg gca ctg gag gtg gac atc cgt ggg agg cgg cac      1356
Thr Ala Ala Gly Thr Ala Leu Glu Val Asp Ile Arg Gly Arg Arg His
            340                 345                 350
ccc ttc gag atc gtc gac ctg ccc ttc tac cgc cgc gcc gca cga taa      1404
Pro Phe Glu Ile Val Asp Leu Pro Phe Tyr Arg Arg Ala Ala Arg
        355                 360                 365
cctgaaccca ccaccaacgg aaaggctccc ccaccatggc caccgagcac tccctgcccg     1464
ggaactactc ctactccgag gaccacgagt ggatcgacgc gacgcccgag gacgccgtcg     1524
gcgcgaccgt gaaggtcggc atcacctccg tggccaccga acgcctcggc gaggtcgtct     1584
acgcggagct cccgcaggtc ggtgacgccg tcaccgccgg tgaaccgtgc ggcgaggtcg     1644
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agtccacgaa gtcggtctcc gacctctacg cgccggtcac gggcaccgtc accgaggtca 1704

<210> 42
<211> 367
<212> PRT
<213> Corynebacterium humireducens
<400> 42

Val Thr Asp Leu Arg Thr Ser Pro Leu His Glu Arg His Val Glu Leu
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Gly Ala Ser Phe Thr Pro Phe Gly Pro Trp Asn Met Pro Leu Arg Tyr
20 25 30
Gly Asn Glu Leu Asp Glu His Arg Ala Val Arg Ser Thr Ala Gly Leu
35 40 45
Phe Asp Leu Ser His Met Gly Glu Ile Arg Val Trp Gly Ala Gln Ala
50 55 60
Ala Glu Phe Leu Asp His Ala Leu Leu Ser Ala Phe Ser Thr Leu Pro
65 70 75 80
Val Gly Lys Ala Arg Tyr Ser Met Leu Val Asp Ala Thr Gly Ala Ile
85 90 95
Leu Asp Asp Leu Leu Thr Tyr Arg Leu Ala Gly Asp Glu Phe Leu Val
100 105 110
Val Pro Asn Ala Ala Asn Thr Glu Thr Val Trp Glu Glu Phe Arg Ala
115 120 125
Arg Ala Ala Gly Phe Asp Val Glu Leu Ala Asp Glu Ser Ala Asp Thr
130 135 140
Ala Leu Leu Ala Val Gln Gly Pro Arg Ala Glu Gln Ile Ile Ala Asp
145 150 155 160
Leu Val Ala Gly Asp Asp Glu Ser Val Val Arg Thr Met Lys Phe Tyr
165 170 175
Ser Ala Ala Pro Leu Thr Val Ala Gly Val Asp Thr Leu Leu Ala Arg
180 185 190
Thr Gly Tyr Thr Gly Glu Asp Gly Phe Glu Leu Tyr Val Ser Gly Ala
195 200 205
Asp Ala Ala Glu Leu Trp Asp Ala Leu Leu Asn Ala Gly Ala Ala Tyr
210 215 220
Asp Met Leu Pro Ala Gly Leu Ala Ala Arg Asp Ser Leu Arg Leu Glu
225 230 235 240
Ala Gly Leu Pro Leu Tyr Gly Gln Glu Leu Thr Arg Asp Ile Thr Pro
245 250 255
Val Glu Ala Gly Met Ala Arg Ala Phe Ala Ser Lys Glu Gly Asp Phe
260 265 270
Val Gly Arg Asp Ala Leu Val Gly Arg Glu Pro Thr Ser Ala Ile Val
275 280 285
Gly Leu Arg Gly Leu Gly Arg Arg Ala Ala Arg Glu Gly Ala Glu Val
290 295 300
Tyr Leu Asp Gly Glu Gln Val Gly Val Val Thr Ser Gly Gln Pro Ala
305 310 315 320
Pro Val Leu Gly Tyr Pro Ile Ala Leu Ala Arg Leu Arg Pro Asp Val
325 330 335
Thr Ala Ala Gly Thr Ala Leu Glu Val Asp Ile Arg Gly Arg Arg His
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Pro Phe Glu Ile Val Asp Leu Pro Phe Tyr Arg Arg Ala Ala Arg
355 360 365

<210> 43
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<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1599)
<223> gen glyA
<400> 43

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gaggagcggt cgaaatccac gtagggggtg gcgtccttgg gccgagacat gcgtcccatt 180
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tgtgggcggt atgctgtcca cgaatgccgt gtacccctag aaaggctggc tgtaacgccc 300
atg acc gct gag tct tct gat ctc cgt tac cag gaa ctg tcc gtc ctc 348
Met Thr Ala Glu Ser Ser Asp Leu Arg Tyr Gln Glu Leu Ser Val Leu
1 5 10 15
gac ccg gag gtc cac gcc gcc atc ggc ggt gag atc gcc cgt cag cgt 396
Asp Pro Glu Val His Ala Ala Ile Gly Gly Glu Ile Ala Arg Gln Arg
20 25 30
gac ttc ctc gag atg atc gcg tcc gag aac ttc gtc ccc cgt gcc gtc 444
Asp Phe Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ala Val
35 40 45
ctg cag gca cag ggt tcg gtg ttc acc aac aag tac gcc gag ggc tac 492
Leu Gln Ala Gln Gly Ser Val Phe Thr Asn Lys Tyr Ala Glu Gly Tyr
50 55 60

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ccg ggg cgt cgt tac tac ggt ggc tgc gag aac gcc gac atc gtc gag        540
Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Asn Ala Asp Ile Val Glu
65                  70                  75                  80
gac ctg gcc cgc gac cgc gcc aag gcc ctg ttc ggc gcc gag ttc gcc        588
Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala
                85                  90                  95
aac gtc cag ccg cac tcc ggc gcc cag gcc aac gcc gcc gtc ctg cac        636
Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu His
            100                 105                 110
gcg ctg gcc gac gcc ggc gac aag atc atg ggt ctg tcc ctg gcc cac        684
Ala Leu Ala Asp Ala Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His
        115                 120                 125
ggt ggt cac ctg acc cac ggc atg aag ctc aac ttc tcc ggc aag ctc        732
Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu
    130                 135                 140
tac gac gtc gtc gcc tac gag gtc gac ccg gag acc cac cgc atc gac        780
Tyr Asp Val Val Ala Tyr Glu Val Asp Pro Glu Thr His Arg Ile Asp
145                 150                 155                 160
atg gac cgc gtc cgc gag cag gcc ctg gcc gag cgc ccg aag gtc ctc        828
Met Asp Arg Val Arg Glu Gln Ala Leu Ala Glu Arg Pro Lys Val Leu
                165                 170                 175
atc gcc ggc tgg tcc gcg tac ccg cgc acc ctc gac ttc gag gcg ttc        876
Ile Ala Gly Trp Ser Ala Tyr Pro Arg Thr Leu Asp Phe Glu Ala Phe
            180                 185                 190
cgc tcc atc gcc gac gag gtc ggc gcg tac ctg tgg acc gac atg gcg        924
Arg Ser Ile Ala Asp Glu Val Gly Ala Tyr Leu Trp Thr Asp Met Ala
        195                 200                 205
cac ttc gcc ggc ctc gtc gcc gcc gac ctg cac ccg tcc ccg gtc ccg        972
His Phe Ala Gly Leu Val Ala Ala Asp Leu His Pro Ser Pro Val Pro
    210                 215                 220
cac tcc gac gtc gtc tcc acc acc gtc cac aag acg ctg ggt ggc ccg       1020
His Ser Asp Val Val Ser Thr Thr Val His Lys Thr Leu Gly Gly Pro
225                 230                 235                 240
cgt tcc ggc ctg atc gtc gcg aag cag gag tgg gcc aag aag ctc aac       1068
Arg Ser Gly Leu Ile Val Ala Lys Gln Glu Trp Ala Lys Lys Leu Asn
                245                 250                 255
tcc gcc gtc ttc ccg ggc cag cag ggt ggt ccg ctc atg cac gcc atc       1116
Ser Ala Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His Ala Ile
            260                 265                 270

gcc gcc aag gcc gtg gca ctg aag gtc gcc ggc acc gac gag ttc aag       1164
Ala Ala Lys Ala Val Ala Leu Lys Val Ala Gly Thr Asp Glu Phe Lys
        275                 280                 285
gac cgt cag gcc cgc acc atc gag ggt gcc aag atc ctg gcc gag cgt       1212
Asp Arg Gln Ala Arg Thr Ile Glu Gly Ala Lys Ile Leu Ala Glu Arg
    290                 295                 300
ctc acc gcc gct gac gcg aag gcc gcc ggc atc gac gtc ctc acc ggt       1260
Leu Thr Ala Ala Asp Ala Lys Ala Ala Gly Ile Asp Val Leu Thr Gly
305                 310                 315                 320
ggc acc gac gtg cac ctg gtc ctc gct gac ctg cgc aac tcc gag atg       1308
Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser Glu Met
                325                 330                 335
gac ggc cag cag gcc gaa gac ctc ctc cac gag gtc ggc atc acc gtc       1356
Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile Thr Val
            340                 345                 350
aac cgc aac gcc gtc ccg aac gac ccg cgc ccg ccg atg gtc acc tcc       1404
Asn Arg Asn Ala Val Pro Asn Asp Pro Arg Pro Pro Met Val Thr Ser
        355                 360                 365
ggc ctg cgc atc ggc acc ccg gcc ctg gcc acc cgt ggt ttc gac gcc       1452
Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe Asp Ala
    370                 375                 380
gcc gcc ttc acc gag gtc gcc gac atc atc ggc acc gcc ctg gtc aac       1500
Ala Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu Val Asn
385                 390                 395                 400
ggc aag aac gcc gac atc gag gca ctg cgt gcc cgc gtc gcg aag ctg       1548
Gly Lys Asn Ala Asp Ile Glu Ala Leu Arg Ala Arg Val Ala Lys Leu
                405                 410                 415
acc gac cag tac ccg ctg tac gag ggt ctg gag gag tgg aag atc aac       1596
Thr Asp Gln Tyr Pro Leu Tyr Glu Gly Leu Glu Glu Trp Lys Ile Asn
            420                 425                 430
tag gtcttcccgc cctccccgtg cgcgtcctcg tcatagacaa cctcgattcc            1649
ttcacctgga atctcgtcgc ctacgtcgag gacgtcaccg gtgtcgcccc cgaggtgatc     1709
accaacaacg aacccggatg ggatgtcgac cgcgtcgcca cctacgacgc cgtcatcatc     1769
tccccgggcc ccggccgccc ggagcgtgag aaggacatcg gcatgtgcct cgatgtcctg     1829
cgcgacgggc gtgtcccgat tctgggggtc tgcctcgggc accaggccct cgcccacgcg     1889
tggggcggca                                                           1899
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<211>  432
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<212> PRT
<213> Corynebacterium humireducens
<400> 44

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Met Thr Ala Glu Ser Ser Asp Leu Arg Tyr Gln Glu Leu Ser Val Leu
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Asp Pro Glu Val His Ala Ala Ile Gly Gly Glu Ile Ala Arg Gln Arg
            20                  25                  30
Asp Phe Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ala Val
        35                  40                  45
Leu Gln Ala Gln Gly Ser Val Phe Thr Asn Lys Tyr Ala Glu Gly Tyr
    50                  55                  60
Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Asn Ala Asp Ile Val Glu
65                  70                  75                  80
Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala
                85                  90                  95
Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu His
            100                 105                 110
Ala Leu Ala Asp Ala Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His
        115                 120                 125
Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu
    130                 135                 140
Tyr Asp Val Val Ala Tyr Glu Val Asp Pro Glu Thr His Arg Ile Asp
145                 150                 155                 160
Met Asp Arg Val Arg Glu Gln Ala Leu Ala Glu Arg Pro Lys Val Leu
                165                 170                 175
Ile Ala Gly Trp Ser Ala Tyr Pro Arg Thr Leu Asp Phe Glu Ala Phe
            180                 185                 190
Arg Ser Ile Ala Asp Glu Val Gly Ala Tyr Leu Trp Thr Asp Met Ala
        195                 200                 205
His Phe Ala Gly Leu Val Ala Ala Asp Leu His Pro Ser Pro Val Pro
    210                 215                 220
His Ser Asp Val Val Ser Thr Thr Val His Lys Thr Leu Gly Gly Pro
225                 230                 235                 240
Arg Ser Gly Leu Ile Val Ala Lys Gln Glu Trp Ala Lys Lys Leu Asn
                245                 250                 255
Ser Ala Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His Ala Ile
            260                 265                 270


Ala Ala Lys Ala Val Ala Leu Lys Val Ala Gly Thr Asp Glu Phe Lys
        275                 280                 285
Asp Arg Gln Ala Arg Thr Ile Glu Gly Ala Lys Ile Leu Ala Glu Arg
    290                 295                 300
Leu Thr Ala Ala Asp Ala Lys Ala Ala Gly Ile Asp Val Leu Thr Gly
305                 310                 315                 320
Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser Glu Met
                325                 330                 335
Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile Thr Val
            340                 345                 350
Asn Arg Asn Ala Val Pro Asn Asp Pro Arg Pro Pro Met Val Thr Ser
        355                 360                 365
Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe Asp Ala
    370                 375                 380
Ala Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu Val Asn
385                 390                 395                 400
Gly Lys Asn Ala Asp Ile Glu Ala Leu Arg Ala Arg Val Ala Lys Leu
                405                 410                 415
Thr Asp Gln Tyr Pro Leu Tyr Glu Gly Leu Glu Glu Trp Lys Ile Asn
            420                 425                 430
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<210> 45
<211> 1932
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1632)
<223> gen hom
<400> 45

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gcggcgtgcg cggacgagat ccccgccagt gggatcacca ggcacgccac gcaggccgtg      60
agtgcacggg tgatccgacg gcgggacatg ctgactcctg tcactggcag aggcatgggg     120
gtggtgagga cagattaatc gtctgaacgc aatatgtcca gagatgtgac ttatcttatg     180
gagtgtcgtg accccggagt ctgaggaagt ggccgaatcc cggtagggtg gtcacggaaa     240
tctgtcctca gtctgcccgt ccccgacggg cacggaccca cgaccatgtg caggagaacc     300
atg acc gtc act cag cag ccc agc ttc aac ccc ggc aag gga gcc ggc       348
Met Thr Val Thr Gln Gln Pro Ser Phe Asn Pro Gly Lys Gly Ala Gly
1               5                  10                  15
gag ccg gtg ggc gtc gcc att ctc ggc cac ggc acc gtc gga tct gag       396
Glu Pro Val Gly Val Ala Ile Leu Gly His Gly Thr Val Gly Ser Glu
```

```
                20                  25                  30
gtg ctg cgc ctg atg ggc gag tac tcc gac gcg ctc gcg cac cgc atc        444
Val Leu Arg Leu Met Gly Glu Tyr Ser Asp Ala Leu Ala His Arg Ile
        35                  40                  45
ggc ggt ccg ctc gag ctc aag ggt gtg gcc gtg tcc gac ctc tcc aag        492
Gly Gly Pro Leu Glu Leu Lys Gly Val Ala Val Ser Asp Leu Ser Lys
    50                  55                  60
ccg cgc gag ggc gtg gac cgt gag ctg ctc acc gat gac gcg ctg agc        540
Pro Arg Glu Gly Val Asp Arg Glu Leu Leu Thr Asp Asp Ala Leu Ser
65                  70                  75                  80
ctc atc aac cgc gac gac gtc gac atc gtc gtc gag gtc atc ggc ggc        588
Leu Ile Asn Arg Asp Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
                85                  90                  95
atc gag tac ccg cgt gag ctg gtc ctg gcc gcc ctg cgc gcc ggc aag        636
Ile Glu Tyr Pro Arg Glu Leu Val Leu Ala Ala Leu Arg Ala Gly Lys
            100                 105                 110
tcc gtc gtc acc gcc aac aag gcc ctc gtc gcc gcg cac gcc gac gag        684
Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ala Asp Glu
        115                 120                 125
ctt gcc gac gcc gcc gac gcc gcc aac gtc gac ctc tac ttc gag gcc        732
Leu Ala Asp Ala Ala Asp Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala
    130                 135                 140
gcc gtc gcc gcc gcc atc ccg gtc gtc ggc atg ctg cgt cgt tcc ctc        780
Ala Val Ala Ala Ala Ile Pro Val Val Gly Met Leu Arg Arg Ser Leu
145                 150                 155                 160
gcc ggc gac aac atc ctg cgt atc tcc ggc atc gtc aac ggc acc acc        828
Ala Gly Asp Asn Ile Leu Arg Ile Ser Gly Ile Val Asn Gly Thr Thr
                165                 170                 175
aac ttc atc ctc gac gcg atg gag tcc acc ggc gcc agc tac gac gac        876
Asn Phe Ile Leu Asp Ala Met Glu Ser Thr Gly Ala Ser Tyr Asp Asp
            180                 185                 190
gcg ctc gcc gag gcc acc cgt ctg ggc tac gcc gag gcc gac ccg acc        924
Ala Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr
        195                 200                 205
gcc gac gtc gag ggc cac gac gcc gcc tcc aag gcc gcc atc ctc gcc        972
Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala
    210                 215                 220
tcc ctg ggc ttc cac acc cgc gtc aag ttc gac gac gtc agc tgc gag       1020
Ser Leu Gly Phe His Thr Arg Val Lys Phe Asp Asp Val Ser Cys Glu
225                 230                 235                 240

ggc atc tcc aag gtc acc gcc gag gac atc gag gcc gcc cgc gac gcc       1068
Gly Ile Ser Lys Val Thr Ala Glu Asp Ile Glu Ala Ala Arg Asp Ala
                245                 250                 255
ggc tac gtg atc aag ctg ctc gcc atc tgt gag cgc gtc acc gac aag       1116
Gly Tyr Val Ile Lys Leu Leu Ala Ile Cys Glu Arg Val Thr Asp Lys
            260                 265                 270
gac ggc gtg gag tcc gtc gcc agc cgc gtc cac ccg acc ctc gtt ccg       1164
Asp Gly Val Glu Ser Val Ala Ser Arg Val His Pro Thr Leu Val Pro
        275                 280                 285
gtc gac cac ccg ctg gcc tcg gtc aac cag tcc tac aac gcc atc ttc       1212
Val Asp His Pro Leu Ala Ser Val Asn Gln Ser Tyr Asn Ala Ile Phe
    290                 295                 300
gtc gag gcc gag gca gcc ggt cgc ctg atg ttc tac ggc aac ggt gcc       1260
Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala
305                 310                 315                 320
ggt ggc gcc ccg acc gcc tcc gcc gtc ctc ggt gac ctc gtc ggc gcc       1308
Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Leu Val Gly Ala
                325                 330                 335
gcc cgc aac aag gtc cac ggt ggc cgc gcc ccg ggc gag aac acc tac       1356
Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Asn Thr Tyr
            340                 345                 350
gcg aac ctg ccg atc gcc gac ctc ggc gac gtg cgc acc cgc tac cac       1404
Ala Asn Leu Pro Ile Ala Asp Leu Gly Asp Val Arg Thr Arg Tyr His
        355                 360                 365
atc gac atg gag gtc gag gac cgc acc ggt gtc ctc gcc gag ctg tcc       1452
Ile Asp Met Glu Val Glu Asp Arg Thr Gly Val Leu Ala Glu Leu Ser
    370                 375                 380
gcg atc ttc gcc acc cac gac atc tcc ctc aag acc gtc cgc cag gag       1500
Ala Ile Phe Ala Thr His Asp Ile Ser Leu Lys Thr Val Arg Gln Glu
385                 390                 395                 400
gag gcc ggc gac cac gcc cgc ctc atc gtc gtc acg cat tcc gca cgt       1548
Glu Ala Gly Asp His Ala Arg Leu Ile Val Val Thr His Ser Ala Arg
                405                 410                 415
gag gcc gac ctg gcc gcc acc gtc gag gac ctg aag aag gcc ccg gcg       1596
Glu Ala Asp Leu Ala Ala Thr Val Glu Asp Leu Lys Lys Ala Pro Ala
            420                 425                 430
gtc aag tcc gtc gac agc gtc ctg cga ctc atc tag ggagcgttga            1642
```

```
Val Lys Ser Val Asp Ser Val Leu Arg Leu Ile
        435                 440
gctgtgagca tccagcttga ggtgggcacc cgggccaccg tcaccgtccc cggctcctcc     1702
gcgaacctgg gccccggatt cgacaccctc ggcctggccg tgggcatcta cgacaccgtc     1762
gaggtcgagg tcatcgagtc gggcctcgag gtcgaggtct tcggcgaggg cgaggacgac     1822
ctgccccgcg acggttccca cctggtggtc aaggccatcc ggtcgggcct caacgccgcc     1882
cacgccgagg ccccgggcct gcgcgtggtg tgcaccaacg ccatcccgca                1932
<210>  46
<211>  443
<212>  PRT
<213>  Corynebacterium humireducens
<400>  46
Met Thr Val Thr Gln Gln Pro Ser Phe Asn Pro Gly Lys Gly Ala Gly
1               5                  10                  15
Glu Pro Val Gly Val Ala Ile Leu Gly His Gly Thr Val Gly Ser Glu
            20                  25                  30
Val Leu Arg Leu Met Gly Glu Tyr Ser Asp Ala Leu Ala His Arg Ile
        35                  40                  45
Gly Gly Pro Leu Glu Leu Lys Gly Val Ala Val Ser Asp Leu Ser Lys
    50                  55                  60
Pro Arg Glu Gly Val Asp Arg Glu Leu Leu Thr Asp Asp Ala Leu Ser
65                  70                  75                  80
Leu Ile Asn Arg Asp Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
                85                  90                  95
Ile Glu Tyr Pro Arg Glu Leu Val Leu Ala Ala Leu Arg Ala Gly Lys
            100                 105                 110
Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ala Asp Glu
        115                 120                 125
Leu Ala Asp Ala Ala Asp Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala
    130                 135                 140
Ala Val Ala Ala Ala Ile Pro Val Val Gly Met Leu Arg Arg Ser Leu
145                 150                 155                 160
Ala Gly Asp Asn Ile Leu Arg Ile Ser Gly Ile Val Asn Gly Thr Thr
                165                 170                 175
Asn Phe Ile Leu Asp Ala Met Glu Ser Thr Gly Ala Ser Tyr Asp Asp
            180                 185                 190
Ala Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr
        195                 200                 205
Ala Asp Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala
    210                 215                 220

Ser Leu Gly Phe His Thr Arg Val Lys Phe Asp Asp Val Ser Cys Glu
225                 230                 235                 240
Gly Ile Ser Lys Val Thr Ala Glu Asp Ile Glu Ala Ala Arg Asp Ala
                245                 250                 255
Gly Tyr Val Ile Lys Leu Leu Ala Ile Cys Glu Arg Val Thr Asp Lys
            260                 265                 270
Asp Gly Val Glu Ser Val Ala Ser Arg Val His Pro Thr Leu Val Pro
        275                 280                 285
Val Asp His Pro Leu Ala Ser Val Asn Gln Ser Tyr Asn Ala Ile Phe
    290                 295                 300
Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala
305                 310                 315                 320
Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Leu Val Gly Ala
                325                 330                 335
Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Asn Thr Tyr
            340                 345                 350
Ala Asn Leu Pro Ile Ala Asp Leu Gly Asp Val Arg Thr Arg Tyr His
        355                 360                 365
Ile Asp Met Glu Val Glu Asp Arg Thr Gly Val Leu Ala Glu Leu Ser
    370                 375                 380
Ala Ile Phe Ala Thr His Asp Ile Ser Leu Lys Thr Val Arg Gln Glu
385                 390                 395                 400
Glu Ala Gly Asp His Ala Arg Leu Ile Val Val Thr His Ser Ala Arg
                405                 410                 415
Glu Ala Asp Leu Ala Ala Thr Val Glu Asp Leu Lys Lys Ala Pro Ala
            420                 425                 430
Val Lys Ser Val Asp Ser Val Leu Arg Leu Ile
        435                 440
<210>  47
<211>  1644
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1344)
<223>  gen lipA
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<400> 47

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gcggggtgac catgcacggg ctgagcctga actgctcgaa cacgctcgag cactacgggc      60
acatcgtggc gtgcggcatc gacgacgccg acgtcaccac cctcagcatg gaactggggc     120
gcgacgtcag cgtcggggag gtcacggcac cgcttgtcga cgccctcctg gccgccctcg     180
ccggtgaact cgccgtcgcg gaccacacct tcggatcggc gcccgatccg acgaagattc     240
ccgcgaaaac gcgctgacct ctaagtttat ccctatcagt agaaagagta tggtggcgtt     300
gtg act atc gca cct gaa gga cgc aag ctg ctc cgg gtg gag aag cgc       348
Val Thr Ile Ala Pro Glu Gly Arg Lys Leu Leu Arg Val Glu Lys Arg
1               5                  10                  15
aat gcg cag acc ccc atc gag acg aag ccc cgt tgg atc cgc aac gcg       396
Asn Ala Gln Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Ala
            20                  25                  30
gtg aag acc ggc ccc gag tac gag gac atg aag aag aag gtg gcg ggc       444
Val Lys Thr Gly Pro Glu Tyr Glu Asp Met Lys Lys Lys Val Ala Gly
        35                  40                  45
gcc tcc ctg cac acc gtc tgt cag gag gcg ggc tgc ccc aac atc cac       492
Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
    50                  55                  60
gag tgc tgg gag tcc cgc gag gcg acg ttt ctc atc ggc ggc gcc aac       540
Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
65                  70                  75                  80
tgc tcc cgc cgc tgc gac ttc tgc cag atc aac tcc gcg aag ccg gag       588
Cys Ser Arg Arg Cys Asp Phe Cys Gln Ile Asn Ser Ala Lys Pro Glu
                85                  90                  95
ccg ctg gac cgc gac gag ccg cgc cgc gtg gcc gag tcc gtc cgc gag       636
Pro Leu Asp Arg Asp Glu Pro Arg Arg Val Ala Glu Ser Val Arg Glu
            100                 105                 110
atg ggc ctg aac tac tcc acc atc acc ggc gtg acc cgc gac gac ctc       684
Met Gly Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
        115                 120                 125
gag gac gag ggt gcc tgg ctc tac gcg gag gtc gtc cgc cag atc cac       732
Glu Asp Glu Gly Ala Trp Leu Tyr Ala Glu Val Val Arg Gln Ile His
    130                 135                 140
gag ctc aac ccg aac acc ggc gtc gag aac ctc gtg ccc gac ttc tcc       780
Glu Leu Asn Pro Asn Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
145                 150                 155                 160
ggc cgt tcc gag ctg ctg gag cag gtc ttc gag tcc cgc ccc gag gtg       828
Gly Arg Ser Glu Leu Leu Glu Gln Val Phe Glu Ser Arg Pro Glu Val
                165                 170                 175
ttc gcc cac aac ctg gag acc gtg ccg cgc atc ttc aag cgc atc cgc       876
Phe Ala His Asn Leu Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
            180                 185                 190

ccg gcc ttc cgc tac gag cgt tcc ctc gac gtg atc cgc cag gcc cac       924
Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala His
        195                 200                 205
gac tac ggg ctg atc acc aag tcg aac ctc atc ctc ggc atg ggc gag       972
Asp Tyr Gly Leu Ile Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
    210                 215                 220
acc ctc gac gag atc cgt gag gcc ctc acc gac ctg cac agc gcc ggc      1020
Thr Leu Asp Glu Ile Arg Glu Ala Leu Thr Asp Leu His Ser Ala Gly
225                 230                 235                 240
tgc gac atc atc acc atc acg cag tac ctg cgc ccc ggc ccg atg tac      1068
Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Met Tyr
                245                 250                 255
cac ccg atc gac cgc tgg gtg aag ccg gag gag ttc gtc gag cac aag      1116
His Pro Ile Asp Arg Trp Val Lys Pro Glu Glu Phe Val Glu His Lys
            260                 265                 270
gac ttc gcc gag gag ctc ggc ttc ggt gcc gtc atg tcc ggc ccg ctg      1164
Asp Phe Ala Glu Glu Leu Gly Phe Gly Ala Val Met Ser Gly Pro Leu
        275                 280                 285
gtc cgt tcc tcc tac cgt gcg gga cgt ctc tac tcg cag gcg atg gcc      1212
Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ser Gln Ala Met Ala
    290                 295                 300
gcc cgc ggc cgg gag atc ccc gac cac ctc aag cac ctg gcc gag acc      1260
Ala Arg Gly Arg Glu Ile Pro Asp His Leu Lys His Leu Ala Glu Thr
305                 310                 315                 320
tcg cag ggc agc acc gac cag gag gcc acc acc ctc ctg gcc aag tac      1308
Ser Gln Gly Ser Thr Asp Gln Glu Ala Thr Thr Leu Leu Ala Lys Tyr
                325                 330                 335
ggc ccc tcc cag gac aca ccg gtc acc tca cgt tag gcacccaccg            1354
Gly Pro Ser Gln Asp Thr Pro Val Thr Ser Arg
            340                 345
gaccctgacc taaagtagag gccatggcag acgacaagca gaaggcggca gcaaaggccg     1414
cgaaggcaga ggcacgggcc gccaagcggg cgaagagcaa ggagacgcgc gcccagctct     1474
ggcaggcgtt caacatccag cgcaagcagg acaagatgct cgtcccgctg atggtgctct     1534
ccgtcgtggg tgtggccgcg ctcctcttcc tcatcggcct ggcctggggc ggccagtggt     1594
tcacgctcat cctgggtatc ttcctgggtg ccgtcctggc gatgtacatc                1644
```

<210> 48
<211> 347
<212> PRT
<213> Corynebacterium humireducens
<400> 48

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Val Thr Ile Ala Pro Glu Gly Arg Lys Leu Leu Arg Val Glu Lys Arg
1               5                  10                  15
Asn Ala Gln Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Ala
            20                  25                  30
Val Lys Thr Gly Pro Glu Tyr Glu Asp Met Lys Lys Lys Val Ala Gly
        35                  40                  45
Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
    50                  55                  60
Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
65                  70                  75                  80
Cys Ser Arg Arg Cys Asp Phe Cys Gln Ile Asn Ser Ala Lys Pro Glu
                85                  90                  95
Pro Leu Asp Arg Asp Glu Pro Arg Arg Val Ala Glu Ser Val Arg Glu
            100                 105                 110
Met Gly Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
        115                 120                 125
Glu Asp Glu Gly Ala Trp Leu Tyr Ala Glu Val Val Arg Gln Ile His
    130                 135                 140
Glu Leu Asn Pro Asn Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
145                 150                 155                 160
Gly Arg Ser Glu Leu Leu Glu Gln Val Phe Glu Ser Arg Pro Glu Val
                165                 170                 175
Phe Ala His Asn Leu Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
            180                 185                 190
Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala His
        195                 200                 205
Asp Tyr Gly Leu Ile Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
    210                 215                 220
Thr Leu Asp Glu Ile Arg Glu Ala Leu Thr Asp Leu His Ser Ala Gly
225                 230                 235                 240
Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Met Tyr
                245                 250                 255
His Pro Ile Asp Arg Trp Val Lys Pro Glu Glu Phe Val Glu His Lys
            260                 265                 270
Asp Phe Ala Glu Glu Leu Gly Phe Gly Ala Val Met Ser Gly Pro Leu
        275                 280                 285
Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ser Gln Ala Met Ala
    290                 295                 300

Ala Arg Gly Arg Glu Ile Pro Asp His Leu Lys His Leu Ala Glu Thr
305                 310                 315                 320
Ser Gln Gly Ser Thr Asp Gln Glu Ala Thr Thr Leu Leu Ala Lys Tyr
                325                 330                 335
Gly Pro Ser Gln Asp Thr Pro Val Thr Ser Arg
            340                 345
```

<210> 49
<211> 1389
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1089)
<223> gen lipB
<400> 49

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gaaggtcggc atcacctccg tggccaccga acgcctcggc gaggtcgtct acgcggagct       60
cccgcaggtc ggtgacgccg tcaccgccgg tgaaccgtgc ggcgaggtcg agtccacgaa      120
gtcggtctcc gacctctacg cgccggtcac gggcaccgtc accgaggtca acgacgcggt      180
ccacgacgac tacgccgtga tcaacgacga ccccttcggc gcgggctggc tcttcgccgt      240
cgaggtcgac gaggtcggac cgctcatgac cgccgccgag tacgcggagg ccaacggcgt      300
gtg acc gcc cgg gac cgg tac cct ggt ccc atc atg act gca ccc cgt         348
Val Thr Ala Arg Asp Arg Tyr Pro Gly Pro Ile Met Thr Ala Pro Arg
1               5                  10                  15
gag ccc ttc ttc cct gcg gac cgt tcc atc cgt gcc tcc ggc gag ccc       396
Glu Pro Phe Phe Pro Ala Asp Arg Ser Ile Arg Ala Ser Gly Glu Pro
            20                  25                  30
ccg gag atc cgt tat ctc ggc gtc gtc gac tac cag gag gcc tgg aat       444
Pro Glu Ile Arg Tyr Leu Gly Val Val Asp Tyr Gln Glu Ala Trp Asn
        35                  40                  45
ctg cag gcc gag ctg gcg tcg caa cgc gcg gcc ggg gag atc ggt gac       492
Leu Gln Ala Glu Leu Ala Ser Gln Arg Ala Ala Gly Glu Ile Gly Asp
    50                  55                  60
cag ctc ctc atc ctc gag cac ccg agc gtg tac acc gcc ggc aag cgc       540
```

```
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
65                  70                  75                  80
acg cag ccg gag gac cgc ccc acc aac ggc ctg ccg gtc atc gac gtc        588
Thr Gln Pro Glu Asp Arg Pro Thr Asn Gly Leu Pro Val Ile Asp Val
                85                  90                  95
gac cgg ggt ggc cgc atc acc tgg cac ggc gag gga cag ctg gtg gtc        636
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Glu Gly Gln Leu Val Val
            100                 105                 110
tac ccg atc atc aaa ctg gcc gac ccg gtg gac gtc gtg gac tat gtc        684
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Val Asp Val Val Asp Tyr Val
        115                 120                 125
cgc cgc ctc gag gag gcg gtg atc gcg acg gtg cgg gag gtg ggc gtc        732
Arg Arg Leu Glu Glu Ala Val Ile Ala Thr Val Arg Glu Val Gly Val
    130                 135                 140
ggc aat gcg ggt cgc atc gac ggc cgc tcc gga gtc tgg gtc ccc gcc        780
Gly Asn Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala
145                 150                 155                 160
gac ggg acc cga cgc gac cgg aag gtg gcg gcg ctc ggc atc cgt gtc        828
Asp Gly Thr Arg Arg Asp Arg Lys Val Ala Ala Leu Gly Ile Arg Val
                165                 170                 175
acc cgc ggg gtg acc atg cac ggg ctg agc ctg aac tgc tcg aac acg        876
Thr Arg Gly Val Thr Met His Gly Leu Ser Leu Asn Cys Ser Asn Thr
            180                 185                 190
ctc gag cac tac ggg cac atc gtg gcg tgc ggc atc gac gac gcc gac        924
Leu Glu His Tyr Gly His Ile Val Ala Cys Gly Ile Asp Asp Ala Asp
        195                 200                 205
gtc acc acc ctc agc atg gaa ctg ggg cgc gac gtc agc gtc ggg gag        972
Val Thr Thr Leu Ser Met Glu Leu Gly Arg Asp Val Ser Val Gly Glu
    210                 215                 220
gtc acg gca ccg ctt gtc gac gcc ctc ctg gcc gcc ctc gcc ggt gaa       1020
Val Thr Ala Pro Leu Val Asp Ala Leu Leu Ala Ala Leu Ala Gly Glu
225                 230                 235                 240
ctc gcc gtc gcg gac cac acc ttc gga tcg gcg ccc gat ccg acg aag       1068
Leu Ala Val Ala Asp His Thr Phe Gly Ser Ala Pro Asp Pro Thr Lys
                245                 250                 255
att ccc gcg aaa acg cgc tga cctctaagtt tatccctatc agtagaaaga          1119
Ile Pro Ala Lys Thr Arg
            260
gtatggtggc gttgtgacta tcgcacctga aggacgcaag ctgctccggg tggagaagcg     1179
caatgcgcag acccccatcg agacgaagcc ccgttggatc cgcaacgcgg tgaagaccgg     1239
ccccgagtac gaggacatga agaagaaggt ggcgggcgcc tccctgcaca ccgtctgtca     1299
ggaggcgggc tgccccaaca tccacgagtg ctgggagtcc cgcgaggcga cgtttctcat     1359
cggcggcgcc aactgctccc gccgctgcga                                      1389

<210>  50
<211>  262
<212>  PRT
<213>  Corynebacterium humireducens
<400>  50
Val Thr Ala Arg Asp Arg Tyr Pro Gly Pro Ile Met Thr Ala Pro Arg
1                   5                  10                  15
Glu Pro Phe Phe Pro Ala Asp Arg Ser Ile Arg Ala Ser Gly Glu Pro
            20                  25                  30
Pro Glu Ile Arg Tyr Leu Gly Val Val Asp Tyr Gln Glu Ala Trp Asn
        35                  40                  45
Leu Gln Ala Glu Leu Ala Ser Gln Arg Ala Ala Gly Glu Ile Gly Asp
    50                  55                  60
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
65                  70                  75                  80
Thr Gln Pro Glu Asp Arg Pro Thr Asn Gly Leu Pro Val Ile Asp Val
                85                  90                  95
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Glu Gly Gln Leu Val Val
            100                 105                 110
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Val Asp Val Val Asp Tyr Val
        115                 120                 125
Arg Arg Leu Glu Glu Ala Val Ile Ala Thr Val Arg Glu Val Gly Val
    130                 135                 140
Gly Asn Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala
145                 150                 155                 160
Asp Gly Thr Arg Arg Asp Arg Lys Val Ala Ala Leu Gly Ile Arg Val
                165                 170                 175
Thr Arg Gly Val Thr Met His Gly Leu Ser Leu Asn Cys Ser Asn Thr
            180                 185                 190
Leu Glu His Tyr Gly His Ile Val Ala Cys Gly Ile Asp Asp Ala Asp
        195                 200                 205
Val Thr Thr Leu Ser Met Glu Leu Gly Arg Asp Val Ser Val Gly Glu
    210                 215                 220
Val Thr Ala Pro Leu Val Asp Ala Leu Leu Ala Ala Leu Ala Gly Glu
```

```
225                 230                 235                 240
Leu Ala Val Ala Asp His Thr Phe Gly Ser Ala Pro Asp Pro Thr Lys
                245                 250                 255
Ile Pro Ala Lys Thr Arg
            260
<210>  51
<211>  2010
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ggccatcggc ctcttctagg tcgaccccgg aagcatctgc ttatcgacgc cccggccccc      180
ggtcggggcg ttcgtcgttg cggcaccaca gtcccgccac cgtcccaccg cccccacggg      240
ggcgggatcc ttttgtgggg ggcggtgaca cgggggaaac ggtcacctat ccttggtggc      300
gtg act gaa cat tat gac gtt gtt gta ctc ggt gcg ggc ccc ggt ggc         348
Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
1               5                   10                  15
tac gtc gcc gcc atc cgc gca gcc cag ctc ggc aag aag gtt gct gtc         396
Tyr Val Ala Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
            20                  25                  30
gtc gag aag cag tac tgg ggc gga gtc tgc ctc aac gtg ggc tgc atc         444
Val Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
        35                  40                  45
ccc tcg aag gcg ctg atc aag aac gcc gag atc gcc cac atc ttc acg         492
Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Thr
    50                  55                  60
cac gag aag aag acg ttc ggc atc aac ggc gac gtc tcc ttc aac tac         540
His Glu Lys Lys Thr Phe Gly Ile Asn Gly Asp Val Ser Phe Asn Tyr
65                  70                  75                  80
gag gac gcc cac aag cgc tcc cgt cag gtg tcg gag aag atc gtc ggc         588
Glu Asp Ala His Lys Arg Ser Arg Gln Val Ser Glu Lys Ile Val Gly
                85                  90                  95
ggc gtc cac tac ctg atg aag aag aac aag atc acc gag atc gac ggc         636
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
            100                 105                 110
ttc gga acc ttc agg gac gcc aag acc atc gag gtc agc gag ggc aag         684
Phe Gly Thr Phe Arg Asp Ala Lys Thr Ile Glu Val Ser Glu Gly Lys
        115                 120                 125
gac gcc ggc aag gtc gtc acc ttc gac gac tgc atc atc gcc acc ggc         732
Asp Ala Gly Lys Val Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    130                 135                 140
tcc gtg gtc aac agc ctc cgt ggc gtc gag ttc tcc gag aac gtc gtc         780
Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
145                 150                 155                 160
tcc tac gag gag cag atc ctc aac ccg gtc gcc ccg gag aag atg gtc         828
Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Glu Lys Met Val
                165                 170                 175
atc gtc ggt gcc ggc gcc atc ggc atg gag ttc gcc tac gtg ctc tcc         876
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Ser
            180                 185                 190
aac tac ggc gtc gac gtc acc gtc atc gag tac atg gac cgt gtc ctg         924
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Tyr Met Asp Arg Val Leu
        195                 200                 205
ccg aac gag gac gag gac gtc tcc aag gtc atc gcc aag gcc tac aag         972
Pro Asn Glu Asp Glu Asp Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
    210                 215                 220
aag atg ggc gtc acg ctc ctc ccg ggc cac gcc acc acc gcc gtg cgc        1020
Lys Met Gly Val Thr Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
225                 230                 235                 240
gac aac ggc gac tcc gtc gag gtc gac tac cag aag aag ggc tcg gac        1068
Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                245                 250                 255
aag acc gag acc atc gtc gcc gac cgc gtc ctc gtc tcc gtc ggc ttc        1116
Lys Thr Glu Thr Ile Val Ala Asp Arg Val Leu Val Ser Val Gly Phe
            260                 265                 270
cgc ccg cgt gtc gag ggc ttc ggc ctg gag aac acc ggc gtc gag ctc        1164
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Glu Leu
        275                 280                 285
acc gag cgc ggt gcc atc gcc atc gac gac ttc atg cgc acc aac gtc        1212
Thr Glu Arg Gly Ala Ile Ala Ile Asp Asp Phe Met Arg Thr Asn Val
    290                 295                 300
gag cac atc tac gcc atc ggt gac gtc acc gcc aag ctg cag ctg gcc        1260
Glu His Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
```

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305                 310                 315                 320
cac gtc gcc gag gcg cag ggc atc gtc gcc gcc gag acc atc gcc ggc      1308
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                325                 330                 335
gcc gag acc cac gag ctg ggc gac tac atg atg atg ccg cgc gcc acc      1356
Ala Glu Thr His Glu Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            340                 345                 350
ttc tgt aac ccg cag gtc gcg tcc ttc ggc tac acc gag gcg cag gcc      1404
Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Ala Gln Ala
        355                 360                 365
aag gag aag tgg ccg gac cgc gag atc aag gtc gcg tcc ttc ccg ttc      1452
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    370                 375                 380
tcc gcg aac ggc aag gcc gtc ggc ctg gcc gag acc gag ggc ttc gcc      1500
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Glu Gly Phe Ala
385                 390                 395                 400
aag atc gtc gcc gac gcc gag tac ggc gag ctg ctg ggc ggc cac ctg      1548
Lys Ile Val Ala Asp Ala Glu Tyr Gly Glu Leu Leu Gly Gly His Leu
                405                 410                 415
gtc ggc gcc aac gcg tcc gag ctg ctc aac gag ctg gtc ctc gcg cag      1596
Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
            420                 425                 430
aac tac gat ctc acc acc gag gag atc agc cgc gcg gtc cac atc cac      1644
Asn Tyr Asp Leu Thr Thr Glu Glu Ile Ser Arg Ala Val His Ile His
        435                 440                 445
ccg acc ctg tcg gag gcc gtc aag gag gcc gca cac ggc atc gac ggc      1692
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Asp Gly
    450                 455                 460
cac atg atc aac ttc tag tccccccggaa aaaggggcct cccggctggg            1740
His Met Ile Asn Phe
465
aggccccttt tctcatgctt tccgacgccc ccggggcgtc gccaagcgcc tagttgtagg    1800
gcgcgaccga cgaccggtgg gcgtcgatgg tgatctcctc gtggatcggc gggaacgcgc    1860
gctgcgcgca gttctcccgc gggcacacgc ggcagccggc gccgatcggg gtggcgctgg    1920
acaggtcggc gaggttgagt ccctgcgcgt agaccgtgcg gtcggcgtgg cgggcctcgc    1980
agcccaggcc gatggcgaag agcttgccgg                                     2010
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            20                  25                  30
Val Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
        35                  40                  45
Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Thr
    50                  55                  60
His Glu Lys Lys Thr Phe Gly Ile Asn Gly Asp Val Ser Phe Asn Tyr
65                  70                  75                  80
Glu Asp Ala His Lys Arg Ser Arg Gln Val Ser Glu Lys Ile Val Gly
                85                  90                  95
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
            100                 105                 110
Phe Gly Thr Phe Arg Asp Ala Lys Thr Ile Glu Val Ser Glu Gly Lys
        115                 120                 125
Asp Ala Gly Lys Val Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    130                 135                 140
Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
145                 150                 155                 160
Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Glu Lys Met Val
                165                 170                 175
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Ser
            180                 185                 190
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Tyr Met Asp Arg Val Leu
        195                 200                 205
Pro Asn Glu Asp Glu Asp Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
    210                 215                 220
Lys Met Gly Val Thr Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
225                 230                 235                 240
Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                245                 250                 255
Lys Thr Glu Thr Ile Val Ala Asp Arg Val Leu Val Ser Val Gly Phe
            260                 265                 270
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Glu Leu
        275                 280                 285
Thr Glu Arg Gly Ala Ile Ala Ile Asp Asp Phe Met Arg Thr Asn Val
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    290                 295                 300
Glu His Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
305                 310                 315                 320
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                325                 330                 335
Ala Glu Thr His Glu Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            340                 345                 350
Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Ala Gln Ala
        355                 360                 365
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    370                 375                 380
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Glu Gly Phe Ala
385                 390                 395                 400
Lys Ile Val Ala Asp Ala Glu Tyr Gly Glu Leu Leu Gly Gly His Leu
                405                 410                 415
Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
            420                 425                 430
Asn Tyr Asp Leu Thr Thr Glu Glu Ile Ser Arg Ala Val His Ile His
        435                 440                 445
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Asp Gly
    450                 455                 460
His Met Ile Asn Phe
465
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ggtgagggcg gaggccagtg cgaacagcac ggccagcaga ttgctgtgca cctcatccac      180
cttagtgaac gggggccttt ccgcagggcc gggacccgcc cactcgacta ctcggacgac      240
cccggctccg ggtacgatga agcagaactt tggcacccca gacgaaaggc ggcctacacg      300
gtg gct ctg atc gtt cag aaa tat gga ggc tcc tcc ctg gag acc gcg         348
Val Ala Leu Ile Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Thr Ala
1               5                  10                  15
gag cgg atc cgc gct gtc gcc gaa cgg atc gtc gcc acg aaa aag gcc         396
Glu Arg Ile Arg Ala Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
            20                  25                  30
ggc aac gac gtc gtc gtg gtc tgc tcc gcg atg ggc gac acc acg gac         444
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
        35                  40                  45
gaa ctc ctg gac ctc gcc gcc cag gtg aac ccg gtt ccg ccg gcc cgt         492
Glu Leu Leu Asp Leu Ala Ala Gln Val Asn Pro Val Pro Pro Ala Arg
    50                  55                  60
gag atg gac atg ctg ctc acc gcg ggt gag cgc atc tcc aac gcg ctg         540
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65                  70                  75                  80
gtc gcg atg gcg atc tcc tcg ctc ggc gcg aag gcg cag tcc ttc acc         588
Val Ala Met Ala Ile Ser Ser Leu Gly Ala Lys Ala Gln Ser Phe Thr
                85                  90                  95
ggc tcg cag gcc ggt gtg ctc acc acc gag cgt cac ggc aac gcc cgc         636
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
            100                 105                 110
atc gtc gac gtc acc ccg gac cgc gtc cgc gag gcg ctg gac gag ggc         684
Ile Val Asp Val Thr Pro Asp Arg Val Arg Glu Ala Leu Asp Glu Gly
        115                 120                 125
aac atc tgc atc gtc gcc ggt ttc cag ggc atc aac aag gac acc cgc         732
Asn Ile Cys Ile Val Ala Gly Phe Gln Gly Ile Asn Lys Asp Thr Arg
    130                 135                 140
gac gtc acc acc ctg ggt cgt ggc ggt tcc gac acc aca gcg gtg gcc         780
Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145                 150                 155                 160
ctg gcg gcg gcg ctc aac gcc gac gtg tgc gag atc tac tcc gac gtc         828
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
                165                 170                 175
gac ggc gtc tac acc gcc gat ccg cgc atc gtc ccg aac gcg cag aag         876
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
            180                 185                 190
ctc gag aag ctc tcc ttc gag gag atg ctc gag ctg gcg gcc gtc ggt         924
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
        195                 200                 205
tcg aag atc ctg gtg ctg cgt gcc gtc gag tac gca cgt gcc ttc aat         972
Ser Lys Ile Leu Val Leu Arg Ala Val Glu Tyr Ala Arg Ala Phe Asn
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gtt ccc ctg cga gtt cgc tcg tct tac agc aat gac acc ggc acc ctg      1020
Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Thr Gly Thr Leu
225                 230                 235                 240
atc gcc ggt tcg atg gag gat atc ccc gtg gaa gaa gca gtt ctc act      1068
Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
                245                 250                 255
ggc gtt gcc acc gac aag tcc gag gcc aag gtc acc atc ctg ggt att      1116
Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Ile Leu Gly Ile
            260                 265                 270
ccc gac aag ccg ggc gag gcg gcc acc gtc ttc cgc gcc gtc gcg gac      1164
Pro Asp Lys Pro Gly Glu Ala Ala Thr Val Phe Arg Ala Val Ala Asp
        275                 280                 285
gcg gag atc aac atc gac atg gtc ctg cag aac gtc tcc tcc ctg gag      1212
Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Leu Glu
    290                 295                 300
gac ggc acg acc gac atc acc ttc acc tgc ccg cgt gcc gac ggc ccc      1260
Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Pro
305                 310                 315                 320
cgc gcc atc gag ctg ctc aag aag atg cag gcg aag agc ggc tgg tcc      1308
Arg Ala Ile Glu Leu Leu Lys Lys Met Gln Ala Lys Ser Gly Trp Ser
                325                 330                 335
aac gtg ctc tac gac gac cag gtg ggc aag gtc tcc ctc gtg ggt gcc      1356
Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
            340                 345                 350
ggc atg aag tcc cac ccg ggc gtc acc gcc gac ttc gcc gag gcg ctc      1404
Gly Met Lys Ser His Pro Gly Val Thr Ala Asp Phe Ala Glu Ala Leu
        355                 360                 365
cgc gac gcc ggc gtg aac atc gag cta atc tcc acc tcg gag atc cgc      1452
Arg Asp Ala Gly Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
    370                 375                 380
atc tcg gtg ctc acc cgc gag gcc gac ctg gac gcc gcc gcc cgt gcc      1500
Ile Ser Val Leu Thr Arg Glu Ala Asp Leu Asp Ala Ala Ala Arg Ala
385                 390                 395                 400
ctg cac gag aag ttc gag ctc ggc ggc gac gcc gag gcc acc gtc tac      1548
Leu His Glu Lys Phe Glu Leu Gly Gly Asp Ala Glu Ala Thr Val Tyr
                405                 410                 415
gcc ggc acc ggc cgc tag acaatccctt ccacagagga gctttcactc             1596
Ala Gly Thr Gly Arg
            420
tcatgaccac cattgctgtc gtcggtgcca ccggccaggt cggccgcgtg atgcgctcga     1656
tcctggagga gcgcaacttc ccggccgaca aggtccgttt cttcgcgtcc ccgcgctccg     1716
cgggcaccgt catcgagttc cgcggtgagg acatcaccgt cgaggacctc acccagatca     1776
ccccggagtc cgtcaaggac gtcgacatcg ccctcttctc cgccggtggt tccacctccc     1836
gtgagtgggc cccggtcttc gccgaggccg                                      1866
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Glu Arg Ile Arg Ala Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
            20                  25                  30
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
        35                  40                  45
Glu Leu Leu Asp Leu Ala Ala Gln Val Asn Pro Val Pro Pro Ala Arg
    50                  55                  60
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65                  70                  75                  80
Val Ala Met Ala Ile Ser Ser Leu Gly Ala Lys Ala Gln Ser Phe Thr
                85                  90                  95
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
            100                 105                 110
Ile Val Asp Val Thr Pro Asp Arg Val Arg Glu Ala Leu Asp Glu Gly
        115                 120                 125
Asn Ile Cys Ile Val Ala Gly Phe Gln Gly Ile Asn Lys Asp Thr Arg
    130                 135                 140
Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145                 150                 155                 160
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
                165                 170                 175
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
            180                 185                 190
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
        195                 200                 205
Ser Lys Ile Leu Val Leu Arg Ala Val Glu Tyr Ala Arg Ala Phe Asn
    210                 215                 220
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Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Thr Gly Thr Leu
225                 230                 235                 240
Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
                245                 250                 255
Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Ile Leu Gly Ile
            260                 265                 270
Pro Asp Lys Pro Gly Glu Ala Ala Thr Val Phe Arg Ala Val Ala Asp
        275                 280                 285
Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Leu Glu
    290                 295                 300
Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Pro
305                 310                 315                 320
Arg Ala Ile Glu Leu Leu Lys Lys Met Gln Ala Lys Ser Gly Trp Ser
                325                 330                 335
Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
            340                 345                 350
Gly Met Lys Ser His Pro Gly Val Thr Ala Asp Phe Ala Glu Ala Leu
        355                 360                 365
Arg Asp Ala Gly Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
    370                 375                 380
Ile Ser Val Leu Thr Arg Glu Ala Asp Leu Asp Ala Ala Ala Arg Ala
385                 390                 395                 400
Leu His Glu Lys Phe Glu Leu Gly Gly Asp Ala Glu Ala Thr Val Tyr
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Ala Gly Thr Gly Arg
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tcctgctgct caaggagggc cgcgtcctgg cctccggacc cgtcgacgag acgctgacct      180
cggggaacct gtcggcactc tacgacctgc cggtgtcgtt ggagaaggtc cacggacgct      240
ggttcgcgct ctgcatataa ttcccggatg ctgccgggaa agtgaaccgc ttggtctata      300
gtg gcc gac atg acc cac gga ctt tct ggt ttc tcg tct cgt tcc atc          348
Val Ala Asp Met Thr His Gly Leu Ser Gly Phe Ser Ser Arg Ser Ile
1               5                   10                  15
cat gcc gga tac gag cct gac agc ctc tac ggc ccg atc aac acg ccg         396
His Ala Gly Tyr Glu Pro Asp Ser Leu Tyr Gly Pro Ile Asn Thr Pro
            20                  25                  30
atc tac gcg tcg acc acc ttc gcg cag gac ggc ctc aac gag ctg cgc         444
Ile Tyr Ala Ser Thr Thr Phe Ala Gln Asp Gly Leu Asn Glu Leu Arg
        35                  40                  45

ggt ggc ttc gag tac acc cgc tgc ggc aac ccc acg atc gac gcc ctc         492
Gly Gly Phe Glu Tyr Thr Arg Cys Gly Asn Pro Thr Ile Asp Ala Leu
    50                  55                  60
gaa aag acc gtc gca gcc ctg gaa ggc gca cag tac ggc cgc gcg ttc         540
Glu Lys Thr Val Ala Ala Leu Glu Gly Ala Gln Tyr Gly Arg Ala Phe
65                  70                  75                  80
tcc tcc ggc atg gcc gcc acc gac gtc atc ctg cgt atc ctc ctg cgc         588
Ser Ser Gly Met Ala Ala Thr Asp Val Ile Leu Arg Ile Leu Leu Arg
                85                  90                  95
ccc ggt gac cac ctc atc ctc ggc cac gac gcc tac ggc ggc acc tgg         636
Pro Gly Asp His Leu Ile Leu Gly His Asp Ala Tyr Gly Gly Thr Trp
            100                 105                 110
cgc ctc atc gac cag gcc ttc ggc cag tgg ggc gtc gag tac acc gtc         684
Arg Leu Ile Asp Gln Ala Phe Gly Gln Trp Gly Val Glu Tyr Thr Val
        115                 120                 125
gtc gac acc acc gac gtt gcc gcc gtc gag gcc gcc ctc cgc ccg aac         732
Val Asp Thr Thr Asp Val Ala Ala Val Glu Ala Ala Leu Arg Pro Asn
    130                 135                 140
acc aag ctc atc tgg ctg gag acc ccg acc aac ccg gcc ctg tcc atc         780
Thr Lys Leu Ile Trp Leu Glu Thr Pro Thr Asn Pro Ala Leu Ser Ile
145                 150                 155                 160
acc gac atc gcc gcc atc gcc gcg atc aag cag cag gcc gcc ctc gtc         828
Thr Asp Ile Ala Ala Ile Ala Ala Ile Lys Gln Gln Ala Ala Leu Val
                165                 170                 175
gtg gac aac acc ttc gcg tcc ccg tac ctg cag cag ccg ctc gcc ctc         876
Val Asp Asn Thr Phe Ala Ser Pro Tyr Leu Gln Gln Pro Leu Ala Leu
            180                 185                 190
ggc gcg gac cac gtc ctg cac tcc gcc acc aag tac ctc ggc ggt cac         924
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Gly Ala Asp His Val Leu His Ser Ala Thr Lys Tyr Leu Gly Gly His
        195                 200                 205
tcc gac gtc gtc ggc ggc ctc gtg gtg acc aac tgc gcc gag ttc gac      972
Ser Asp Val Val Gly Gly Leu Val Val Thr Asn Cys Ala Glu Phe Asp
    210                 215                 220
gag cag ctc ctc tgg ttc cag ggc ggc gtc ggc ccc atc ccg tcc ccc     1020
Glu Gln Leu Leu Trp Phe Gln Gly Gly Val Gly Pro Ile Pro Ser Pro
225                 230                 235                 240
ttc gac gcc tac ctc acc gcc cgc ggc atc aag acc ctg gcc gtg cgc     1068
Phe Asp Ala Tyr Leu Thr Ala Arg Gly Ile Lys Thr Leu Ala Val Arg
                245                 250                 255
atg gag cgc cac tgc gac aac gcc gag gcc atc gcc gcg cac ctc gag     1116
Met Glu Arg His Cys Asp Asn Ala Glu Ala Ile Ala Ala His Leu Glu
            260                 265                 270
gcc tcc gac cag gtc gcg acc gtg ctc tac ccc ggc ctc gag tcc cac     1164
Ala Ser Asp Gln Val Ala Thr Val Leu Tyr Pro Gly Leu Glu Ser His
        275                 280                 285
ccg ggc cac gag gtg gcc aag cgc cag atg aag cgc ttc ggc ggc atg     1212
Pro Gly His Glu Val Ala Lys Arg Gln Met Lys Arg Phe Gly Gly Met
    290                 295                 300
atc tcc gtg cgc ttc cgc tcc gag gag gcc gcc cgc gtc ttc tgc ctg     1260
Ile Ser Val Arg Phe Arg Ser Glu Glu Ala Ala Arg Val Phe Cys Leu
305                 310                 315                 320
aac acc cga ctg atc tgt ctg gcc gag tct ctc ggc ggc gtc gag tcg     1308
Asn Thr Arg Leu Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser
                325                 330                 335
ctc gtc gag cac ccg gcc acc atg acc cac cag tcc gcc acc ggc tcc     1356
Leu Val Glu His Pro Ala Thr Met Thr His Gln Ser Ala Thr Gly Ser
            340                 345                 350
cag ctg gag gtc ccg cgt gac ctg gtg cgc atc tcc atc ggc atc gag     1404
Gln Leu Glu Val Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu
        355                 360                 365
gac gtc gag gac ctc atc gcg gac atc gac gtc gcc ctc cag gcc gtc     1452
Asp Val Glu Asp Leu Ile Ala Asp Ile Asp Val Ala Leu Gln Ala Val
    370                 375                 380
gcg gcc gcg gag gcg gcc gct gag gcc tcc gtc gac gcc tga              1494
Ala Ala Ala Glu Ala Ala Ala Glu Ala Ser Val Asp Ala
385                 390                 395
gtgatgaccg ccccgcacac ggtcgagagg acatgtgcgg gacggctcct cccgggcggc    1554
gcagtgtcga gacgggtact cctcccgaac atgtgagccc gcccctggct ccggcccccc    1614
cagggcagcc ggatcgccgc cacaccgacc accatgagcg ccaggcccac cgcctggacc    1674
agggtggtcg gtttcctctt cgcccccagc agcccgaagt ggtcgatgag gaggctgccg    1734
accatcatgc cgagcaggat cgtcatgacg gtcagacccg tgccgatgac gggggagagg    1794
<210>  56
<211>  397
<212>  PRT
<213>  Corynebacterium humireducens
<400>  56
Val Ala Asp Met Thr His Gly Leu Ser Gly Phe Ser Ser Arg Ser Ile
1               5                   10                  15


His Ala Gly Tyr Glu Pro Asp Ser Leu Tyr Gly Pro Ile Asn Thr Pro
            20                  25                  30
Ile Tyr Ala Ser Thr Thr Phe Ala Gln Asp Gly Leu Asn Glu Leu Arg
        35                  40                  45
Gly Gly Phe Glu Tyr Thr Arg Cys Gly Asn Pro Thr Ile Asp Ala Leu
    50                  55                  60
Glu Lys Thr Val Ala Ala Leu Glu Gly Ala Gln Tyr Gly Arg Ala Phe
65                  70                  75                  80
Ser Ser Gly Met Ala Ala Thr Asp Val Ile Leu Arg Ile Leu Leu Arg
                85                  90                  95
Pro Gly Asp His Leu Ile Leu Gly His Asp Ala Tyr Gly Gly Thr Trp
            100                 105                 110
Arg Leu Ile Asp Gln Ala Phe Gly Gln Trp Gly Val Glu Tyr Thr Val
        115                 120                 125
Val Asp Thr Thr Asp Val Ala Ala Val Glu Ala Ala Leu Arg Pro Asn
    130                 135                 140
Thr Lys Leu Ile Trp Leu Glu Thr Pro Thr Asn Pro Ala Leu Ser Ile
145                 150                 155                 160
Thr Asp Ile Ala Ala Ile Ala Ala Ile Lys Gln Gln Ala Ala Leu Val
                165                 170                 175
Val Asp Asn Thr Phe Ala Ser Pro Tyr Leu Gln Gln Pro Leu Ala Leu
            180                 185                 190
Gly Ala Asp His Val Leu His Ser Ala Thr Lys Tyr Leu Gly Gly His
        195                 200                 205
Ser Asp Val Val Gly Gly Leu Val Val Thr Asn Cys Ala Glu Phe Asp
    210                 215                 220
```

```
Glu Gln Leu Leu Trp Phe Gln Gly Gly Val Gly Pro Ile Pro Ser Pro
225                 230                 235                 240
Phe Asp Ala Tyr Leu Thr Ala Arg Gly Ile Lys Thr Leu Ala Val Arg
                245                 250                 255
Met Glu Arg His Cys Asp Asn Ala Glu Ala Ile Ala Ala His Leu Glu
            260                 265                 270
Ala Ser Asp Gln Val Ala Thr Val Leu Tyr Pro Gly Leu Glu Ser His
        275                 280                 285
Pro Gly His Glu Val Ala Lys Arg Gln Met Lys Arg Phe Gly Gly Met
    290                 295                 300
Ile Ser Val Arg Phe Arg Ser Glu Glu Ala Ala Arg Val Phe Cys Leu
305                 310                 315                 320
Asn Thr Arg Leu Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser
                325                 330                 335
Leu Val Glu His Pro Ala Thr Met Thr His Gln Ser Ala Thr Gly Ser
            340                 345                 350
Gln Leu Glu Val Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu
        355                 360                 365
Asp Val Glu Asp Leu Ile Ala Asp Ile Asp Val Ala Leu Gln Ala Val
    370                 375                 380
Ala Ala Ala Glu Ala Ala Ala Glu Ala Ser Val Asp Ala
385                 390                 395
<210>  57
<211>  1581
<212>  ADN
<213>  Corynebacterium humireducens
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<222>  (301)..(1281)
<223>  gen metF
<400>  57
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tcgatcaggg cgggtttccg gatgtgtgga acctggggaa atgaaactga accgcttggt     120
ccatttttgt ccgaaaatcg gccctcgggg gtgaattata ttcatgctag ggtggggtta     180
tcgccgcagg tcacgcggca aaccggaaat agcaccttta ggaaaattac ccgccgcaaa     240
ccgttggctt gctacattca cagccacttg cccaacggga tgtctgaagg aggaaaacac     300
atg aac gca aac gcg ccg cag tac agc gcc aag cgt cga ttc tcc gcc       348
Met Asn Ala Asn Ala Pro Gln Tyr Ser Ala Lys Arg Arg Phe Ser Ala
1               5                   10                  15
tcc gcc ccg ttg gac acc ttc gat ccc gag gaa tgg cgc cag gcc ccc       396
Ser Ala Pro Leu Asp Thr Phe Asp Pro Glu Glu Trp Arg Gln Ala Pro
            20                  25                  30
gtg ccg gag cgc acc tcc ctc tcc ttc gag gtc atg ccc ccg cgc cac       444
Val Pro Glu Arg Thr Ser Leu Ser Phe Glu Val Met Pro Pro Arg His
        35                  40                  45
gac gcg gac gag gcc aag atc gac gaa ctg ctg gac acg ctg cag tcc       492
Asp Ala Asp Glu Ala Lys Ile Asp Glu Leu Leu Asp Thr Leu Gln Ser
    50                  55                  60
tac aac ccg gac tac atc tcc gtc acc agc tcc cgg aac tcc ggc tgg       540
Tyr Asn Pro Asp Tyr Ile Ser Val Thr Ser Ser Arg Asn Ser Gly Trp
65                  70                  75                  80
ctc gag ggc acc gcg aag ttc atc gcg aag atc agc gcc cag acc cgc       588
Leu Glu Gly Thr Ala Lys Phe Ile Ala Lys Ile Ser Ala Gln Thr Arg
                85                  90                  95
atc ccg acg gtc gcc cac ctg gcc tgc acc gcc ggc acc cgc gag gag       636
Ile Pro Thr Val Ala His Leu Ala Cys Thr Ala Gly Thr Arg Glu Glu
            100                 105                 110
ctc atc ggc tgg atc aac cgg ctc atg gac tcc ggc gtc cgc ggc ctg       684
Leu Ile Gly Trp Ile Asn Arg Leu Met Asp Ser Gly Val Arg Gly Leu
        115                 120                 125
ctc gcc ctc cgc ggc gac ctc gca gaa gga cag acc ggt atg cct gag       732
Leu Ala Leu Arg Gly Asp Leu Ala Glu Gly Gln Thr Gly Met Pro Glu
    130                 135                 140
ggt tac ctc aag cac gcg acc gac ctc atc aac ctc atc cag gag atc       780
Gly Tyr Leu Lys His Ala Thr Asp Leu Ile Asn Leu Ile Gln Glu Ile
145                 150                 155                 160
gag gag gag cag gtc gcc cgc ttc ggc gcc ggc cgc ctc gcc atc ggc       828
Glu Glu Glu Gln Val Ala Arg Phe Gly Ala Gly Arg Leu Ala Ile Gly
                165                 170                 175
gtc gcc gcc tac ccc agc ggc cac gag gag tcg acc agc cgc gac gag       876
Val Ala Ala Tyr Pro Ser Gly His Glu Glu Ser Thr Ser Arg Asp Glu
            180                 185                 190
gac atc gac gtc ctc ctg gcc aag cag cgc ctg ggc gcc gac ttc gcc       924
Asp Ile Asp Val Leu Leu Ala Lys Gln Arg Leu Gly Ala Asp Phe Ala
        195                 200                 205
atc acc cag ctc ttc ttc gac gcc gag gac tac ctc cgc ttc ctg gag       972
Ile Thr Gln Leu Phe Phe Asp Ala Glu Asp Tyr Leu Arg Phe Leu Glu
    210                 215                 220
```

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cgc gcc cgc ctg gca ggc gtc cgc atc ccg ctc atc ccc ggc atc atg      1020
Arg Ala Arg Leu Ala Gly Val Arg Ile Pro Leu Ile Pro Gly Ile Met
225                 230                 235                 240
ccg atg acg agc gtc gcg aga cta cgt cga atg gga cag ctc tcc ggc      1068
Pro Met Thr Ser Val Ala Arg Leu Arg Arg Met Gly Gln Leu Ser Gly
                245                 250                 255
ctt acc gtc ccc gac cgg ctg atc agc cga ctg gag gcg gca ggc ccg      1116
Leu Thr Val Pro Asp Arg Leu Ile Ser Arg Leu Glu Ala Ala Gly Pro
            260                 265                 270
gag agc gag tac cag acg ggc ctc gac ctc acg gcc gag ctc gcg cag      1164
Glu Ser Glu Tyr Gln Thr Gly Leu Asp Leu Thr Ala Glu Leu Ala Gln
        275                 280                 285
acc atc ctg gac gcc ggt gcc ggg ggg atg cac gtg tac acg ttc aac      1212
Thr Ile Leu Asp Ala Gly Ala Gly Gly Met His Val Tyr Thr Phe Asn
    290                 295                 300
cgg ccg gac acc acc acc gaa ctg ctg gac cgc atc ggc atc acc ccc      1260
Arg Pro Asp Thr Thr Thr Glu Leu Leu Asp Arg Ile Gly Ile Thr Pro
305                 310                 315                 320
gac cct cgg gtt agg gag tga ggcgggagac cgccgccgct gcatctcatg          1311
Asp Pro Arg Val Arg Glu
                325
ttgatagcga cctgctgcac gcaccgggag cccccgaagc agaccaggtt gtacacccaa     1371
gattttccga aaggcctccc ttttcatgtc ttccaccgct ttccccacct tcaccatcga     1431
gggctacccg cgcgtcggcg ccaaccgcga gctcaagaag gccctcgagt ccttctgggc     1491
cggccgcatc gacgaggaga ccttcatctc ctccgcgcac tccatccgcc tggagaacta     1551
cgcccgtctg cgtgacctcg gcctggacca                                      1581
<210>  58
<211>  326
<212>  PRT
<213>  Corynebacterium humireducens
<400>  58
Met Asn Ala Asn Ala Pro Gln Tyr Ser Ala Lys Arg Arg Phe Ser Ala
1               5                   10                  15
Ser Ala Pro Leu Asp Thr Phe Asp Pro Glu Glu Trp Arg Gln Ala Pro
            20                  25                  30
Val Pro Glu Arg Thr Ser Leu Ser Phe Glu Val Met Pro Pro Arg His
        35                  40                  45
Asp Ala Asp Glu Ala Lys Ile Asp Glu Leu Leu Asp Thr Leu Gln Ser
    50                  55                  60
Tyr Asn Pro Asp Tyr Ile Ser Val Thr Ser Ser Arg Asn Ser Gly Trp
65                  70                  75                  80
Leu Glu Gly Thr Ala Lys Phe Ile Ala Lys Ile Ser Ala Gln Thr Arg
                85                  90                  95
Ile Pro Thr Val Ala His Leu Ala Cys Thr Ala Gly Thr Arg Glu Glu
            100                 105                 110
Leu Ile Gly Trp Ile Asn Arg Leu Met Asp Ser Gly Val Arg Gly Leu
        115                 120                 125
Leu Ala Leu Arg Gly Asp Leu Ala Glu Gly Gln Thr Gly Met Pro Glu
    130                 135                 140
Gly Tyr Leu Lys His Ala Thr Asp Leu Ile Asn Leu Ile Gln Glu Ile
145                 150                 155                 160
Glu Glu Glu Gln Val Ala Arg Phe Gly Ala Gly Arg Leu Ala Ile Gly
                165                 170                 175
Val Ala Ala Tyr Pro Ser Gly His Glu Glu Ser Thr Ser Arg Asp Glu
            180                 185                 190
Asp Ile Asp Val Leu Leu Ala Lys Gln Arg Leu Gly Ala Asp Phe Ala
        195                 200                 205
Ile Thr Gln Leu Phe Phe Asp Ala Glu Asp Tyr Leu Arg Phe Leu Glu
    210                 215                 220
Arg Ala Arg Leu Ala Gly Val Arg Ile Pro Leu Ile Pro Gly Ile Met
225                 230                 235                 240

Pro Met Thr Ser Val Ala Arg Leu Arg Arg Met Gly Gln Leu Ser Gly
                245                 250                 255
Leu Thr Val Pro Asp Arg Leu Ile Ser Arg Leu Glu Ala Ala Gly Pro
            260                 265                 270
Glu Ser Glu Tyr Gln Thr Gly Leu Asp Leu Thr Ala Glu Leu Ala Gln
        275                 280                 285
Thr Ile Leu Asp Ala Gly Ala Gly Gly Met His Val Tyr Thr Phe Asn
    290                 295                 300
Arg Pro Asp Thr Thr Thr Glu Leu Leu Asp Arg Ile Gly Ile Thr Pro
305                 310                 315                 320
Asp Pro Arg Val Arg Glu
                325
<210>  59
<211>  1695
<212>  ADN
<213>  Corynebacterium humireducens
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<220>
<221> CDS
<222> (301)..(1395)
<223> gen metX
<400> 59

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tccgcctgtc ggtgggcatc gagaagatca ccgacatcat cgccgacctg gagaacgccc       60
tgaacgccgt ctaagagaca gcttggtcca catacattca cgtcccccac ctggggagac      120
gtggatgtcg gcgacccttc tgtttgcgtg gtcacgcgcg gaaacctacc ctttcaggag      180
accgtgccga atgtaggcac cgaggacgac aaactgtccc ccgggacccc caccagacca      240
ctaggacggt gagtttccat ctctaccctc aacctggccc cccagggcga actcgcgcag      300
gtg cgc atc ggt gat ctc cac acg gag gcc ggt ggc gtc atc aac gac         348
Val Arg Ile Gly Asp Leu His Thr Glu Ala Gly Gly Val Ile Asn Asp
1               5                  10                  15
gtc acc atc gcc tac cgc cgc tgg ggc gag ttc cgg gga gac ccg gac         396
Val Thr Ile Ala Tyr Arg Arg Trp Gly Glu Phe Arg Gly Asp Pro Asp
            20                  25                  30
ggg atg aac aac ctc gtg ctc atc gaa cac gcc ctc acc ggc gac acc         444
Gly Met Asn Asn Leu Val Leu Ile Glu His Ala Leu Thr Gly Asp Thr
        35                  40                  45
aac gtc gcc gac tgg tgg tgt gac ctg ctc ggc ccc ggc cgg gcg ctc         492
Asn Val Ala Asp Trp Trp Cys Asp Leu Leu Gly Pro Gly Arg Ala Leu
    50                  55                  60
gac acc gac gcg tgg tgc atc gtg tgc acc aac gtc atc ggc ggc tgc         540
Asp Thr Asp Ala Trp Cys Ile Val Cys Thr Asn Val Ile Gly Gly Cys
65                  70                  75                  80
cag ggc tcg acc ggc ccc gcc tcc gaa cac ccc gac ggc ggc cgc tgg         588
Gln Gly Ser Thr Gly Pro Ala Ser Glu His Pro Asp Gly Gly Arg Trp
                85                  90                  95
gga tcc cgc ttc ccg gcg atc tcc atc cgc gac cag gtc acc gcg gag         636
Gly Ser Arg Phe Pro Ala Ile Ser Ile Arg Asp Gln Val Thr Ala Glu
            100                 105                 110
aag cag ttc ctc gac gcc ctc ggc gtc tcc cgc atc cac gcc gtc ctc         684
Lys Gln Phe Leu Asp Ala Leu Gly Val Ser Arg Ile His Ala Val Leu
        115                 120                 125
ggc ggt tcc atg ggc ggt gcc cgc acc ctc gag tgg gcg atg atg tac         732
Gly Gly Ser Met Gly Gly Ala Arg Thr Leu Glu Trp Ala Met Met Tyr
    130                 135                 140
ccg gac aag gtc aac gcc gtg tgc gtc atc gcc gtc tcc gcc cgg gcc         780
Pro Asp Lys Val Asn Ala Val Cys Val Ile Ala Val Ser Ala Arg Ala
145                 150                 155                 160
agc gcc tgg cag atc ggc atc cag tcc gcg cag atc tcc gcc atc gag         828
Ser Ala Trp Gln Ile Gly Ile Gln Ser Ala Gln Ile Ser Ala Ile Glu
                165                 170                 175
cgt gac ccc gcc tgg cag ggc ggc gac ttc tac gac acc ggt gcc tcc         876
Arg Asp Pro Ala Trp Gln Gly Gly Asp Phe Tyr Asp Thr Gly Ala Ser
            180                 185                 190
ccc gac gcc ggc ctc gcc gcc gcc cgc cgc atc gcc cac ctc acc tac         924
Pro Asp Ala Gly Leu Ala Ala Ala Arg Arg Ile Ala His Leu Thr Tyr
        195                 200                 205
cgc ggt gag cag gag ctc gac gag cgt ttc ggc gcc gcc cgc cag gac         972
Arg Gly Glu Gln Glu Leu Asp Glu Arg Phe Gly Ala Ala Arg Gln Asp
    210                 215                 220

ggg gag aac ccg ctg ggc acc ttc cgg gac ccc gcc cag cgt ttc gcc        1020
Gly Glu Asn Pro Leu Gly Thr Phe Arg Asp Pro Ala Gln Arg Phe Ala
225                 230                 235                 240
gtc gag agc tac ctg cag tac cac ggc cgc aag ctg gtc gag cgt ttc        1068
Val Glu Ser Tyr Leu Gln Tyr His Gly Arg Lys Leu Val Glu Arg Phe
                245                 250                 255
gac gcc ggc agc tac gtc acc ctc acc gag gcc ctc aac cgg cac aac        1116
Asp Ala Gly Ser Tyr Val Thr Leu Thr Glu Ala Leu Asn Arg His Asn
            260                 265                 270
atc ggc cgg ggc cgc ggg ggc ctg aac aag gcg ctg gcg gcc tgc acg        1164
Ile Gly Arg Gly Arg Gly Gly Leu Asn Lys Ala Leu Ala Ala Cys Thr
        275                 280                 285
gtg ccg acg atg atc gtc ggc gtc gac acg gac atc ctg tac ccg tac        1212
Val Pro Thr Met Ile Val Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr
    290                 295                 300
cac cag cag gag cac ctc tcc cgc aac gtc ggt gag ctg atg ggc atc        1260
His Gln Gln Glu His Leu Ser Arg Asn Val Gly Glu Leu Met Gly Ile
305                 310                 315                 320
gcc cgg atc tcc tcc cct gtc ggc cac gac gcc ttc ctg gcg gag ttc        1308
Ala Arg Ile Ser Ser Pro Val Gly His Asp Ala Phe Leu Ala Glu Phe
                325                 330                 335
cgg cag atg gac cgc atc ctc cgg cgc ttc ttc gtc ctc agc gtg ctg        1356
Arg Gln Met Asp Arg Ile Leu Arg Arg Phe Phe Val Leu Ser Val Leu
            340                 345                 350
gac gag gac gcc cag gag gac gac ggc tac ctc atc tag caacccgaac        1405
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Asp Glu Asp Ala Gln Glu Asp Asp Gly Tyr Leu Ile
        355                 360
gtgccgcgag ggggctccca gccatcggtt gggagccccc tcgcggcacg tttcgcgggg     1465
tcacgagccc agcgcgtcca ccgaggccgc caggaacgcc atcgtccccc cgaggacggt     1525
gcagaaggcg gcgtcgaaac gccgggagcg cacggcgaac accccgacga tgcgggagtc     1585
gcacgcgtag cgcaccacgg ccagccacat gagtgagacg ccgagcacga acgtcgcgcg     1645
gcgccagtgc tcggtgagcg cgaagacgct cgccacgacc acgccgagca                1695
<210>  60
<211>  364
<212>  PRT
<213>  Corynebacterium humireducens
<400>  60
Val Arg Ile Gly Asp Leu His Thr Glu Ala Gly Gly Val Ile Asn Asp
1               5                  10                  15
Val Thr Ile Ala Tyr Arg Arg Trp Gly Glu Phe Arg Gly Asp Pro Asp
            20                  25                  30
Gly Met Asn Asn Leu Val Leu Ile Glu His Ala Leu Thr Gly Asp Thr
        35                  40                  45
Asn Val Ala Asp Trp Trp Cys Asp Leu Leu Gly Pro Gly Arg Ala Leu
    50                  55                  60
Asp Thr Asp Ala Trp Cys Ile Val Cys Thr Asn Val Ile Gly Gly Cys
65                  70                  75                  80
Gln Gly Ser Thr Gly Pro Ala Ser Glu His Pro Asp Gly Gly Arg Trp
                85                  90                  95
Gly Ser Arg Phe Pro Ala Ile Ser Ile Arg Asp Gln Val Thr Ala Glu
            100                 105                 110
Lys Gln Phe Leu Asp Ala Leu Gly Val Ser Arg Ile His Ala Val Leu
        115                 120                 125
Gly Gly Ser Met Gly Gly Ala Arg Thr Leu Glu Trp Ala Met Met Tyr
    130                 135                 140
Pro Asp Lys Val Asn Ala Val Cys Val Ile Ala Val Ser Ala Arg Ala
145                 150                 155                 160
Ser Ala Trp Gln Ile Gly Ile Gln Ser Ala Gln Ile Ser Ala Ile Glu
                165                 170                 175
Arg Asp Pro Ala Trp Gln Gly Gly Asp Phe Tyr Asp Thr Gly Ala Ser
            180                 185                 190
Pro Asp Ala Gly Leu Ala Ala Ala Arg Arg Ile Ala His Leu Thr Tyr
        195                 200                 205
Arg Gly Glu Gln Glu Leu Asp Glu Arg Phe Gly Ala Ala Arg Gln Asp
    210                 215                 220
Gly Glu Asn Pro Leu Gly Thr Phe Arg Asp Pro Ala Gln Arg Phe Ala
225                 230                 235                 240
Val Glu Ser Tyr Leu Gln Tyr His Gly Arg Lys Leu Val Glu Arg Phe
                245                 250                 255
Asp Ala Gly Ser Tyr Val Thr Leu Thr Glu Ala Leu Asn Arg His Asn
            260                 265                 270
Ile Gly Arg Gly Arg Gly Gly Leu Asn Lys Ala Leu Ala Ala Cys Thr
        275                 280                 285
Val Pro Thr Met Ile Val Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr
    290                 295                 300
His Gln Gln Glu His Leu Ser Arg Asn Val Gly Glu Leu Met Gly Ile
305                 310                 315                 320

Ala Arg Ile Ser Ser Pro Val Gly His Asp Ala Phe Leu Ala Glu Phe
                325                 330                 335
Arg Gln Met Asp Arg Ile Leu Arg Arg Phe Phe Val Leu Ser Val Leu
            340                 345                 350
Asp Glu Asp Ala Gln Glu Asp Asp Gly Tyr Leu Ile
        355                 360
<210>  61
<211>  1872
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1572)
<223>  gen metY
<400>  61
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gacgcctcga gcccaccggc ttcatcgacc acgtcggccg ggactacatt ttcgagacgc      120
tgcccaccgg ggtgcgggcc tacgccaacc gctaccaggc ccggcacgga cgctggccgg      180
acggggtgcc gcgcgaggtg gtcgagccct gacgcggacg gggtggaccc cgagctcatg      240
cccgcggcgg gtacatttgc attcaggtat tccgtcgccc cgaaaggtgt ctgcatcacc      300
atg cac aac cag acc aag ctc atc cac tcc ggc tat gtc ccg ggc aac         348
Met His Asn Gln Thr Lys Leu Ile His Ser Gly Tyr Val Pro Gly Asn
1               5                  10                  15
aag gac ccc cga cag gtg ccg atc gtg cag tcc acg acc tac acc ttc        396
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Lys Asp Pro Arg Gln Val Pro Ile Val Gln Ser Thr Thr Tyr Thr Phe
            20                  25                  30
gac tcc tcc gag gac atc gcg gcg gtg ttc gat gag ccg acc cac gcg        444
Asp Ser Ser Glu Asp Ile Ala Ala Val Phe Asp Glu Pro Thr His Ala
        35                  40                  45
ctg atc tac tcc cgc ttc gcc aac ccg acc gtc atg gcg gtg gag acg        492
Leu Ile Tyr Ser Arg Phe Ala Asn Pro Thr Val Met Ala Val Glu Thr
    50                  55                  60
aag atc gcc gag ctg gag ggc ggt gcc gcg gcg atg gcg acc tcc tcc        540
Lys Ile Ala Glu Leu Glu Gly Gly Ala Ala Ala Met Ala Thr Ser Ser
65                  70                  75                  80
ggc cag gcc gcg acc gcg ctg tcg atc atg aac gtc tgc tcg gcg ggt        588
Gly Gln Ala Ala Thr Ala Leu Ser Ile Met Asn Val Cys Ser Ala Gly
                85                  90                  95
gac tcc ttc gtg gcc tcc tcc gag atc tac ggc ggc acc ctc aac ctc        636
Asp Ser Phe Val Ala Ser Ser Glu Ile Tyr Gly Gly Thr Leu Asn Leu
            100                 105                 110
ttc cac acg acg ctc aag cgt ttc ggc atc gag gtc atc tac gtc gac        684
Phe His Thr Thr Leu Lys Arg Phe Gly Ile Glu Val Ile Tyr Val Asp
        115                 120                 125
cag gac gcc tcc gag gag gag atc gcc gcc gcc ttc aag ccg aac acg        732
Gln Asp Ala Ser Glu Glu Glu Ile Ala Ala Ala Phe Lys Pro Asn Thr
    130                 135                 140
aag gca ctg ttc ggt gag acc atc ggc aac ccg gcg atg agc gtg ctg        780
Lys Ala Leu Phe Gly Glu Thr Ile Gly Asn Pro Ala Met Ser Val Leu
145                 150                 155                 160
gac atc gag aag ttc gcc cgc atc gcc cac ggt cag ggc gtg ccg ctc        828
Asp Ile Glu Lys Phe Ala Arg Ile Ala His Gly Gln Gly Val Pro Leu
                165                 170                 175
atc gtc gac tcc acc ttc gcc acc ccg atg ctg tgc cgc ccc atc gag        876
Ile Val Asp Ser Thr Phe Ala Thr Pro Met Leu Cys Arg Pro Ile Glu
            180                 185                 190
cac ggc gcc gac gtg gtc atc cac tcc acc tcc aag tac atg gac ggc        924
His Gly Ala Asp Val Val Ile His Ser Thr Ser Lys Tyr Met Asp Gly
        195                 200                 205
cac gcg ctg cag gtc ggc ggc atg atc gtc gac gcc ggc acc ttc gac        972
His Ala Leu Gln Val Gly Gly Met Ile Val Asp Ala Gly Thr Phe Asp
    210                 215                 220
tac acc aac ggc aag ttc ccg ggc ttc acc gag ccg gac gag tcc tac       1020
Tyr Thr Asn Gly Lys Phe Pro Gly Phe Thr Glu Pro Asp Glu Ser Tyr
225                 230                 235                 240
cac ggc gtc gtg tac acc aag gac tac gcc gtt gcc ccc ttc atc atc       1068
His Gly Val Val Tyr Thr Lys Asp Tyr Ala Val Ala Pro Phe Ile Ile
                245                 250                 255
aag gcc cgc atg cag ctg cag cgt gat ttc ggc gcc tac ccg tcc gcg       1116
Lys Ala Arg Met Gln Leu Gln Arg Asp Phe Gly Ala Tyr Pro Ser Ala
            260                 265                 270
cac tcc gcc ttc atg ctc aac cac tcc ctc gag agc ctc gac gtg cgc       1164
His Ser Ala Phe Met Leu Asn His Ser Leu Glu Ser Leu Asp Val Arg
        275                 280                 285
atg cag cgc cac tgc gag aac gca cag agg gtc gcc gag tac ctc gag       1212
Met Gln Arg His Cys Glu Asn Ala Gln Arg Val Ala Glu Tyr Leu Glu
    290                 295                 300
ggc cgc aag gac gtg ctt gtc gac gtc cgc tac ccc gga ctc gac tcc       1260
Gly Arg Lys Asp Val Leu Val Asp Val Arg Tyr Pro Gly Leu Asp Ser
305                 310                 315                 320
tcc ccg tac cgc gag ctg gcg aag aag tac ctc agc ggc aac tcc ggc       1308
Ser Pro Tyr Arg Glu Leu Ala Lys Lys Tyr Leu Ser Gly Asn Ser Gly
                325                 330                 335
gtg ctg tgc atc gac atc aag ggg ggc cgc gag gcc ggc gtg aag ttc       1356
Val Leu Cys Ile Asp Ile Lys Gly Gly Arg Glu Ala Gly Val Lys Phe
            340                 345                 350
atg gac gcc ctc gag ctg gtc acc cgc cag gtg cac gtc gcc gac gcc       1404
Met Asp Ala Leu Glu Leu Val Thr Arg Gln Val His Val Ala Asp Ala
        355                 360                 365
cgt tcc tgc gtg ctg cac ccg gcg tcg acc acg cac cgc cag gtg ccg       1452
Arg Ser Cys Val Leu His Pro Ala Ser Thr Thr His Arg Gln Val Pro
    370                 375                 380
gac gag cag ctg ccg tcc gtc ggc atc acc ccg ggt ctg gtg cgc atc       1500
Asp Glu Gln Leu Pro Ser Val Gly Ile Thr Pro Gly Leu Val Arg Ile
385                 390                 395                 400
tcc gtc ggc ctg gag aac gtc gac gac atc atc gcc gac atc gag cag       1548
Ser Val Gly Leu Glu Asn Val Asp Asp Ile Ile Ala Asp Ile Glu Gln
                405                 410                 415
gcc ctg gag aag tcc cag gcc taa gttcgcttat cgacgccgcc ccggtccctc      1602
Ala Leu Glu Lys Ser Gln Ala
            420
atgtgggacc ggggcggtgg ctttcggggg atggctgcac tttcaccccg actgggtgcg     1662
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tgtcgacaac ggggtttggg ggacagcgat gagggtataa gtgcagacac ggagaaggcc 1722
cggacactgt gggaggtgtc cgggccttgg gggcgtcgat aagcggtgtc tctagaactc 1782
cggcagcggc agaacagtga gggagaacat cgcgacgatg gccatgacca gcgggatggc 1842
gatcatgatc ggggcggcga tagccgggtt 1872

<210> 62
<211> 423
<212> PRT
<213> Corynebacterium humireducens
<400> 62

Met His Asn Gln Thr Lys Leu Ile His Ser Gly Tyr Val Pro Gly Asn
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Lys Asp Pro Arg Gln Val Pro Ile Val Gln Ser Thr Thr Tyr Thr Phe
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Asp Ser Ser Glu Asp Ile Ala Ala Val Phe Asp Glu Pro Thr His Ala
35 40 45
Leu Ile Tyr Ser Arg Phe Ala Asn Pro Thr Val Met Ala Val Glu Thr
50 55 60
Lys Ile Ala Glu Leu Glu Gly Gly Ala Ala Ala Met Ala Thr Ser Ser
65 70 75 80
Gly Gln Ala Ala Thr Ala Leu Ser Ile Met Asn Val Cys Ser Ala Gly
85 90 95
Asp Ser Phe Val Ala Ser Ser Glu Ile Tyr Gly Gly Thr Leu Asn Leu
100 105 110
Phe His Thr Thr Leu Lys Arg Phe Gly Ile Glu Val Ile Tyr Val Asp
115 120 125
Gln Asp Ala Ser Glu Glu Glu Ile Ala Ala Ala Phe Lys Pro Asn Thr
130 135 140
Lys Ala Leu Phe Gly Glu Thr Ile Gly Asn Pro Ala Met Ser Val Leu
145 150 155 160
Asp Ile Glu Lys Phe Ala Arg Ile Ala His Gly Gln Gly Val Pro Leu
165 170 175
Ile Val Asp Ser Thr Phe Ala Thr Pro Met Leu Cys Arg Pro Ile Glu
180 185 190
His Gly Ala Asp Val Val Ile His Ser Thr Ser Lys Tyr Met Asp Gly
195 200 205
His Ala Leu Gln Val Gly Gly Met Ile Val Asp Ala Gly Thr Phe Asp
210 215 220
Tyr Thr Asn Gly Lys Phe Pro Gly Phe Thr Glu Pro Asp Glu Ser Tyr
225 230 235 240
His Gly Val Val Tyr Thr Lys Asp Tyr Ala Val Ala Pro Phe Ile Ile
245 250 255
Lys Ala Arg Met Gln Leu Gln Arg Asp Phe Gly Ala Tyr Pro Ser Ala
260 265 270
His Ser Ala Phe Met Leu Asn His Ser Leu Glu Ser Leu Asp Val Arg
275 280 285
Met Gln Arg His Cys Glu Asn Ala Gln Arg Val Ala Glu Tyr Leu Glu
290 295 300
Gly Arg Lys Asp Val Leu Val Asp Val Arg Tyr Pro Gly Leu Asp Ser
305 310 315 320
Ser Pro Tyr Arg Glu Leu Ala Lys Lys Tyr Leu Ser Gly Asn Ser Gly
325 330 335
Val Leu Cys Ile Asp Ile Lys Gly Gly Arg Glu Ala Gly Val Lys Phe
340 345 350
Met Asp Ala Leu Glu Leu Val Thr Arg Gln Val His Val Ala Asp Ala
355 360 365

Arg Ser Cys Val Leu His Pro Ala Ser Thr Thr His Arg Gln Val Pro
370 375 380
Asp Glu Gln Leu Pro Ser Val Gly Ile Thr Pro Gly Leu Val Arg Ile
385 390 395 400
Ser Val Gly Leu Glu Asn Val Asp Asp Ile Ile Ala Asp Ile Glu Gln
405 410 415
Ala Leu Glu Lys Ser Gln Ala
420

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<222> (301)..(3714)
<223> gen pyc
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ggcgcccgtc ccgcggagtg cggaaatgga ccgcaccggg tccaccacct gcagataccc 180
cctgtgacta ggggatactc ccccgaagac aaccctcttt cttgcgatac tgtggtgtgc 240

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cagagagctc acccgctctc agacacaccc ccgacatgac gttcggaaag gaaccccacc      300
gtg gcc aca acc act ctg cca gcc ttc aca aag gtg ctg gtc gcc aac          348
Val Ala Thr Thr Thr Leu Pro Ala Phe Thr Lys Val Leu Val Ala Asn
1               5                  10                  15
cgc ggc gag atc gcc gtc cgc gcc ttc cgt gcc gcc ttc gag acc ggt          396
Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Phe Glu Thr Gly
            20                  25                  30
gcc tcc acc gtc gcg gtc tac ccg aag gag gac cgc aac tcg cac cac          444
Ala Ser Thr Val Ala Val Tyr Pro Lys Glu Asp Arg Asn Ser His His
        35                  40                  45
cgc tcc ttc gcc tcc gag gcc gtg cgc atc ggc acc gag gga tcg ccg          492
Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro
    50                  55                  60
gtc aag gcg tac ctc gac atc gac gag atc atc cgc gcc gcc aag aag          540
Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Arg Ala Ala Lys Lys
65                  70                  75                  80
acc cac gcc gac gcc gtc tac ccc ggc tac ggt ttc ctc tcc gag aac          588
Thr His Ala Asp Ala Val Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn
                85                  90                  95
gcc cag ctc gcc cgc gag tgc gcc gag aac ggc ctc acc ttc atc ggc          636
Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Leu Thr Phe Ile Gly
            100                 105                 110
ccg ccg ccg gag gtc ctc gac ctg acc ggc gac aag tcc gcc gcc gtc          684
Pro Pro Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Ala Ala Val
        115                 120                 125
gag gcc gcc cgg aag gcc gga ctc ccg gtc ctg cag gac tcc gag ccg          732
Glu Ala Ala Arg Lys Ala Gly Leu Pro Val Leu Gln Asp Ser Glu Pro
    130                 135                 140
tcc acc gac atc gac gag ctc gtc gag atg tcg aag gac ttc acc ttc          780
Ser Thr Asp Ile Asp Glu Leu Val Glu Met Ser Lys Asp Phe Thr Phe
145                 150                 155                 160
ccg atc ttc gtc aag gcc gtc gcc ggt ggc ggt gga cgt ggc atg cgc          828
Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg
                165                 170                 175
ttc atc gag aag ccc gag gac gtc gcc cag ctg gcc acc gag gcc tcc          876
Phe Ile Glu Lys Pro Glu Asp Val Ala Gln Leu Ala Thr Glu Ala Ser
            180                 185                 190
cgc gag gcg gag gcc gcc ttc ggt gac ggt cat gtc tac ctc gag cgt          924
Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly His Val Tyr Leu Glu Arg
        195                 200                 205
gcg gtg ctc aac ccg cag cac atc gag gtc cag atc ctc gcc gac cac          972
Ala Val Leu Asn Pro Gln His Ile Glu Val Gln Ile Leu Ala Asp His
    210                 215                 220
acc ggc gac gtc atc cac ctc tac gag cgt gac tgc tcc ctg cag cgc         1020
Thr Gly Asp Val Ile His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg
225                 230                 235                 240
cgc cac cag aag gtc gtg gag atc gcc ccg gcc cag cac ctc gac cca         1068
Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro
                245                 250                 255
gcc ctg cgc gac cag atc tgc gcc gac gcc gtg aag ttc tgc cgc tcc         1116
Ala Leu Arg Asp Gln Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser
            260                 265                 270
atc ggc tac gtg tgc gcc ggc acc gtc gag ttc ctc gtc gac gag aac         1164
Ile Gly Tyr Val Cys Ala Gly Thr Val Glu Phe Leu Val Asp Glu Asn
        275                 280                 285
ggc aac cac gtc ttc atc gag atg aac ccg cgc atc cag gtc gag cac         1212
Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His
    290                 295                 300
acc atc acc gag gag gtc acc tcc gtc gac ctg gtc aag gcg cag atg         1260
Thr Ile Thr Glu Glu Val Thr Ser Val Asp Leu Val Lys Ala Gln Met
305                 310                 315                 320
aac atc gcc gcc ggc gcg acc ctc aag gac ctc ggc ctc acg cag gag         1308
Asn Ile Ala Ala Gly Ala Thr Leu Lys Asp Leu Gly Leu Thr Gln Glu
                325                 330                 335
tcc atc aag ctc cac ggc gcg gcc ctg cag tgc cgc atc acc acc gag         1356
Ser Ile Lys Leu His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu
            340                 345                 350
gac ccg gcc aac aac ttc cgc ccg gac acc ggc acc atc acc gcg tac         1404
Asp Pro Ala Asn Asn Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr
        355                 360                 365
cgc tcc ccg ggt ggc gcg ggc gtg cgt ctc gac ggc gcc gcg tcc ctc         1452
Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Ser Leu
    370                 375                 380
ggc ggc gag atc tcc ccg aac ttc gac tcc ctg ctg gtc aag atg acc         1500
Gly Gly Glu Ile Ser Pro Asn Phe Asp Ser Leu Leu Val Lys Met Thr
385                 390                 395                 400
tgc cgc ggc gcc gac ttc gcc acc gcc gtc gcc cgt gcc cag cgc gcg         1548
Cys Arg Gly Ala Asp Phe Ala Thr Ala Val Ala Arg Ala Gln Arg Ala
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                405                 410                 415
ctc aac gag ttc acc atc tcg ggc gtg gcc acc aac atc ggc ttc ctc      1596
Leu Asn Glu Phe Thr Ile Ser Gly Val Ala Thr Asn Ile Gly Phe Leu
            420                 425                 430
cgc gcc ctg ctg cgc gag gag gac ttc cag acc cgc cgc atc tcc acc      1644
Arg Ala Leu Leu Arg Glu Glu Asp Phe Gln Thr Arg Arg Ile Ser Thr
        435                 440                 445
aac ttc atc ggc gag cac ctc cac ctg ctg tcc gcc ccg ccg gcc gac      1692
Asn Phe Ile Gly Glu His Leu His Leu Leu Ser Ala Pro Pro Ala Asp
    450                 455                 460
gac gag gcc ggc cgc atc ctc aac tac ctc gcg gac gtc acc gtc aac      1740
Asp Glu Ala Gly Arg Ile Leu Asn Tyr Leu Ala Asp Val Thr Val Asn
465                 470                 475                 480
cgt ccg cac ggc aag cgc ccc acc gag atc cgt ccg gtg acc aag ctg      1788
Arg Pro His Gly Lys Arg Pro Thr Glu Ile Arg Pro Val Thr Lys Leu
                485                 490                 495
ccg gcc cgc gac gac agc ccg ctg ccg cgc ggt tcc cgc gac gtc ctg      1836
Pro Ala Arg Asp Asp Ser Pro Leu Pro Arg Gly Ser Arg Asp Val Leu
            500                 505                 510
cgt gac ctg ggc ccg cag aag ttc gcc gag cag ctg cgc aac cag gac      1884
Arg Asp Leu Gly Pro Gln Lys Phe Ala Glu Gln Leu Arg Asn Gln Asp
        515                 520                 525
gcc ctg gcc gtc acc gac acc acg ttc cgt gac gcg cac cag tcg ctg      1932
Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His Gln Ser Leu
    530                 535                 540
ctg gcc acc cgc atc cgt tcc tcc gcg ctc gtc gcc gcc gcc gag cac      1980
Leu Ala Thr Arg Ile Arg Ser Ser Ala Leu Val Ala Ala Ala Glu His
545                 550                 555                 560
gtc ggc cgc ctg acc ccg gag ctg ctc tcc gtc gag gcg tgg ggc ggt      2028
Val Gly Arg Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly
                565                 570                 575
gcg acc tac gac gtc gcg atg cgt ttc ctc cac gag gac ccg tgg gag      2076
Ala Thr Tyr Asp Val Ala Met Arg Phe Leu His Glu Asp Pro Trp Glu
            580                 585                 590
cgt ctc gac gac ctg cgc cgc gcc atg ccg aac gtc aac atc cag atg      2124
Arg Leu Asp Asp Leu Arg Arg Ala Met Pro Asn Val Asn Ile Gln Met
        595                 600                 605
ctg ctg cgc ggc cgc aac acc gtc ggc tac acc tcc tac ccg gac agc      2172
Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Ser Tyr Pro Asp Ser
    610                 615                 620
gtc ggc cag gcc ttc gtc aag gag gcc gcc gac tcc ggc gtc gac atc      2220
Val Gly Gln Ala Phe Val Lys Glu Ala Ala Asp Ser Gly Val Asp Ile
625                 630                 635                 640
ttc cgc atc ttc gac gcc ctc aac gac gtg gac cag atg cgc ccg gcc      2268
Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Asp Gln Met Arg Pro Ala
                645                 650                 655
atc gat gcc gtc ctg gag acc ggc acc acc gtc gcc gag gtc gcc atg      2316
Ile Asp Ala Val Leu Glu Thr Gly Thr Thr Val Ala Glu Val Ala Met
            660                 665                 670
gcc tac tcc ggc aac ctg ctg gac ccg aac gag aag ctc tac acg ctc      2364
Ala Tyr Ser Gly Asn Leu Leu Asp Pro Asn Glu Lys Leu Tyr Thr Leu
        675                 680                 685
gac tac tac ctc cgt ctg gcc gag gag atc gtc gag tcc ggt gcc cac      2412
Asp Tyr Tyr Leu Arg Leu Ala Glu Glu Ile Val Glu Ser Gly Ala His
    690                 695                 700
atc ctg gcc atc aag gac atg gcc ggt ctg ctc cgc ccg acc gcg gcc      2460
Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Thr Ala Ala
705                 710                 715                 720

tcc cgc ctg gtg aag gcg ctg cgc agc aac ttc gac ctg ccg gtg cac      2508
Ser Arg Leu Val Lys Ala Leu Arg Ser Asn Phe Asp Leu Pro Val His
                725                 730                 735
gtg cac acc cac gac acc gcc ggc ggt cag ctg gcg acc tac ctg gcc      2556
Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Leu Ala
            740                 745                 750
gcc gcg cag gcg ggt gcc gac gcc gtc gac ggc gcc tcc gcc ccg ctg      2604
Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Ala Pro Leu
        755                 760                 765
gcc ggc acg acc tcg cag ccc tcg ctg tcc gcg atc gtc gcg gcc ttc      2652
Ala Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile Val Ala Ala Phe
    770                 775                 780
gcc gac acc cac cgc gac acc ggc ctg tcc ctg cag gcc gtg tcc gac      2700
Ala Asp Thr His Arg Asp Thr Gly Leu Ser Leu Gln Ala Val Ser Asp
785                 790                 795                 800
ctc gag ccc tac tgg gag gcc gtg cgc cag ctc tac gcc ccc ttc gag      2748
Leu Glu Pro Tyr Trp Glu Ala Val Arg Gln Leu Tyr Ala Pro Phe Glu
                805                 810                 815
gcg ggc gtg ccc ggc ccg acg ggc cgc gtg tac aag cac gag atc ccg      2796
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Ala Gly Val Pro Gly Pro Thr Gly Arg Val Tyr Lys His Glu Ile Pro
            820                 825                 830
ggt ggt cag ctg tcg aac ctg cgc acg cag gcc aag gcc ctg ggt ctg      2844
Gly Gly Gln Leu Ser Asn Leu Arg Thr Gln Ala Lys Ala Leu Gly Leu
        835                 840                 845
gag gac cgc ttc gag ctc atc gag gac tac tac gcc gcc gtc aac gag      2892
Glu Asp Arg Phe Glu Leu Ile Glu Asp Tyr Tyr Ala Ala Val Asn Glu
    850                 855                 860
atg ctg ggc cgc ccc acc aag gtc acc ccg tcc tcc aag gtc gtc ggc      2940
Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
865                 870                 875                 880

gac ctg gcg ctc cac ctc gtc ggc gcg ggc gtc gac ccg cac gac ttc      2988
Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro His Asp Phe
                885                 890                 895
gcc aat gac ccg cag aag tac gac atc ccg gac tcc gtg atc gac ttc      3036
Ala Asn Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Asp Phe
            900                 905                 910
ctc cgc ggt gac ctc ggc aac ccg ccc ggt ggc tgg ccg atg ctg cgg      3084
Leu Arg Gly Asp Leu Gly Asn Pro Pro Gly Gly Trp Pro Met Leu Arg
        915                 920                 925
gag aag gcc ctg gca ggt cgt tcc tcc acg cag tcc aag ctt gtc gac      3132
Glu Lys Ala Leu Ala Gly Arg Ser Ser Thr Gln Ser Lys Leu Val Asp
    930                 935                 940
gtc gcc ccg gag gac gag gag gcc ctg cag agc gcg gac cgc cag acc      3180
Val Ala Pro Glu Asp Glu Glu Ala Leu Gln Ser Ala Asp Arg Gln Thr
945                 950                 955                 960
cgc cgc tcg acc ctg gac agg ctg ctg ttc ccg aag cag gcc gcc gag      3228
Arg Arg Ser Thr Leu Asp Arg Leu Leu Phe Pro Lys Gln Ala Ala Glu
                965                 970                 975
ttc gcg gag cac cgc cgc cag tac ggc aac acc gcc gcc ctc gag gac      3276
Phe Ala Glu His Arg Arg Gln Tyr Gly Asn Thr Ala Ala Leu Glu Asp
            980                 985                 990
cgc gtg ttc ttc tac ggc ctc aag  gag ggc gag gag aac  gtc atc cgc     3324
Arg Val Phe Phe Tyr Gly Leu Lys  Glu Gly Glu Glu Asn  Val Ile Arg
        995                 1000                1005
ctc atc  ggg gag cac ggt cag  ccg ccg atg gtc gtg  cgt ctc gac       3369
Leu Ile  Gly Glu His Gly Gln  Pro Pro Met Val Val  Arg Leu Asp
    1010                1015                1020
gcc gtc  ggt gag ccc gac gag  aag ggc atg cgc cag  gtg gtg acc       3414
Ala Val  Gly Glu Pro Asp Glu  Lys Gly Met Arg Gln  Val Val Thr
    1025                1030                1035
aac gtc  aac ggc cag atc cgt  ccg atg aag gtc cgt  gac cgc tcc       3459
Asn Val  Asn Gly Gln Ile Arg  Pro Met Lys Val Arg  Asp Arg Ser
    1040                1045                1050
gtc gag  tcg gtc acc gcc tcc  gcg gag aag gcc gac  acc acc aac       3504
Val Glu  Ser Val Thr Ala Ser  Ala Glu Lys Ala Asp  Thr Thr Asn
    1055                1060                1065
ccg ggc  cac gtc gcc gcg ccg  ttc gcg ggt gtc gtc  atg gtc acc       3549
Pro Gly  His Val Ala Ala Pro  Phe Ala Gly Val Val  Met Val Thr
    1070                1075                1080
gcg aag  gtg ggc gac gag gtc  aag gcc ggc gac ccg  gta gcc gtg       3594
Ala Lys  Val Gly Asp Glu Val  Lys Ala Gly Asp Pro  Val Ala Val
    1085                1090                1095
atc gag  gcc atg aag atg gag  gcc acc atc acc gcc  tcc aag gac       3639
Ile Glu  Ala Met Lys Met Glu  Ala Thr Ile Thr Ala  Ser Lys Asp
    1100                1105                1110
ggc gtg  gtc gac cgc gtc gcc  ctg gcc cag gcc acg  aag gtg gag       3684
Gly Val  Val Asp Arg Val Ala  Leu Ala Gln Ala Thr  Lys Val Glu
    1115                1120                1125
ggc ggc  gac ctc atc gtc gtc  atc gcc tag ccgcacaacg cgaaagcccc      3734
Gly Gly  Asp Leu Ile Val Val  Ile Ala
    1130                1135
gccactcctt ccgggagtgg cggggcttct ctgtgcgggt gggccgctac ttgatctcga    3794
gcaggacctg gcccttggtc acgccggcac cggcctcgac ggacaggccc tcgaccttgc    3854
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cgccctcggc gacctcctgg ccgtcctcga cgttgacctt gatgacggtg ccctgcatcg    3974
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Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Phe Glu Thr Gly
            20                  25                  30
Ala Ser Thr Val Ala Val Tyr Pro Lys Glu Asp Arg Asn Ser His His
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        35                  40                  45
Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro
    50                  55                  60
Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Arg Ala Ala Lys Lys
65                  70                  75                  80
Thr His Ala Asp Ala Val Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn
                85                  90                  95
Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Leu Thr Phe Ile Gly
            100                 105                 110
Pro Pro Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Ala Ala Val
        115                 120                 125
Glu Ala Ala Arg Lys Ala Gly Leu Pro Val Leu Gln Asp Ser Glu Pro
    130                 135                 140
Ser Thr Asp Ile Asp Glu Leu Val Glu Met Ser Lys Asp Phe Thr Phe
145                 150                 155                 160
Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg
                165                 170                 175
Phe Ile Glu Lys Pro Glu Asp Val Ala Gln Leu Ala Thr Glu Ala Ser
            180                 185                 190
Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly His Val Tyr Leu Glu Arg
        195                 200                 205
Ala Val Leu Asn Pro Gln His Ile Glu Val Gln Ile Leu Ala Asp His
    210                 215                 220
Thr Gly Asp Val Ile His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg
225                 230                 235                 240
Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro
                245                 250                 255
Ala Leu Arg Asp Gln Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser
            260                 265                 270
Ile Gly Tyr Val Cys Ala Gly Thr Val Glu Phe Leu Val Asp Glu Asn
        275                 280                 285
Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His
    290                 295                 300
Thr Ile Thr Glu Glu Val Thr Ser Val Asp Leu Val Lys Ala Gln Met
305                 310                 315                 320
Asn Ile Ala Ala Gly Ala Thr Leu Lys Asp Leu Gly Leu Thr Gln Glu
                325                 330                 335
Ser Ile Lys Leu His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu
            340                 345                 350
Asp Pro Ala Asn Asn Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr
        355                 360                 365
Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Ser Leu
    370                 375                 380
Gly Gly Glu Ile Ser Pro Asn Phe Asp Ser Leu Leu Val Lys Met Thr
385                 390                 395                 400
Cys Arg Gly Ala Asp Phe Ala Thr Ala Val Ala Arg Ala Gln Arg Ala
                405                 410                 415
Leu Asn Glu Phe Thr Ile Ser Gly Val Ala Thr Asn Ile Gly Phe Leu
            420                 425                 430
Arg Ala Leu Leu Arg Glu Glu Asp Phe Gln Thr Arg Arg Ile Ser Thr
        435                 440                 445
Asn Phe Ile Gly Glu His Leu His Leu Leu Ser Ala Pro Pro Ala Asp
    450                 455                 460
Asp Glu Ala Gly Arg Ile Leu Asn Tyr Leu Ala Asp Val Thr Val Asn
465                 470                 475                 480
Arg Pro His Gly Lys Arg Pro Thr Glu Ile Arg Pro Val Thr Lys Leu
                485                 490                 495
Pro Ala Arg Asp Asp Ser Pro Leu Pro Arg Gly Ser Arg Asp Val Leu
            500                 505                 510
Arg Asp Leu Gly Pro Gln Lys Phe Ala Glu Gln Leu Arg Asn Gln Asp
        515                 520                 525
Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His Gln Ser Leu
    530                 535                 540
Leu Ala Thr Arg Ile Arg Ser Ser Ala Leu Val Ala Ala Ala Glu His
545                 550                 555                 560
Val Gly Arg Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly
                565                 570                 575
Ala Thr Tyr Asp Val Ala Met Arg Phe Leu His Glu Asp Pro Trp Glu
            580                 585                 590
Arg Leu Asp Asp Leu Arg Arg Ala Met Pro Asn Val Asn Ile Gln Met
        595                 600                 605
Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Ser Tyr Pro Asp Ser
    610                 615                 620
Val Gly Gln Ala Phe Val Lys Glu Ala Ala Asp Ser Gly Val Asp Ile
625                 630                 635                 640
Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Asp Gln Met Arg Pro Ala
                645                 650                 655
Ile Asp Ala Val Leu Glu Thr Gly Thr Thr Val Ala Glu Val Ala Met
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            660                 665                 670
Ala Tyr Ser Gly Asn Leu Leu Asp Pro Asn Glu Lys Leu Tyr Thr Leu
        675                 680                 685
Asp Tyr Tyr Leu Arg Leu Ala Glu Glu Ile Val Glu Ser Gly Ala His
    690                 695                 700
Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Thr Ala Ala
705                 710                 715                 720
Ser Arg Leu Val Lys Ala Leu Arg Ser Asn Phe Asp Leu Pro Val His
                725                 730                 735
Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Leu Ala
            740                 745                 750
Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Ala Pro Leu
        755                 760                 765
Ala Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile Val Ala Ala Phe
    770                 775                 780
Ala Asp Thr His Arg Asp Thr Gly Leu Ser Leu Gln Ala Val Ser Asp
785                 790                 795                 800
Leu Glu Pro Tyr Trp Glu Ala Val Arg Gln Leu Tyr Ala Pro Phe Glu
                805                 810                 815
Ala Gly Val Pro Gly Pro Thr Gly Arg Val Tyr Lys His Glu Ile Pro
            820                 825                 830
Gly Gly Gln Leu Ser Asn Leu Arg Thr Gln Ala Lys Ala Leu Gly Leu
        835                 840                 845
Glu Asp Arg Phe Glu Leu Ile Glu Asp Tyr Tyr Ala Ala Val Asn Glu
    850                 855                 860
Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
865                 870                 875                 880
Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro His Asp Phe
                885                 890                 895
Ala Asn Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Asp Phe
            900                 905                 910
Leu Arg Gly Asp Leu Gly Asn Pro Pro Gly Gly Trp Pro Met Leu Arg
        915                 920                 925
Glu Lys Ala Leu Ala Gly Arg Ser Ser Thr Gln Ser Lys Leu Val Asp
    930                 935                 940
Val Ala Pro Glu Asp Glu Glu Ala Leu Gln Ser Ala Asp Arg Gln Thr
945                 950                 955                 960
Arg Arg Ser Thr Leu Asp Arg Leu Leu Phe Pro Lys Gln Ala Ala Glu
                965                 970                 975
Phe Ala Glu His Arg Arg Gln Tyr Gly Asn Thr Ala Ala Leu Glu Asp
            980                 985                 990
Arg Val Phe Phe Tyr Gly Leu Lys  Glu Gly Glu Glu Asn  Val Ile Arg
        995                1000                1005
Leu Ile  Gly Glu His Gly Gln  Pro Pro Met Val Val  Arg Leu Asp
    1010                1015                1020
Ala Val  Gly Glu Pro Asp Glu  Lys Gly Met Arg Gln  Val Val Thr
    1025                1030                1035
Asn Val  Asn Gly Gln Ile Arg  Pro Met Lys Val Arg  Asp Arg Ser
    1040                1045                1050
Val Glu  Ser Val Thr Ala Ser  Ala Glu Lys Ala Asp  Thr Thr Asn
    1055                1060                1065
Pro Gly  His Val Ala Ala Pro  Phe Ala Gly Val Val  Met Val Thr
    1070                1075                1080
Ala Lys  Val Gly Asp Glu Val  Lys Ala Gly Asp Pro  Val Ala Val
    1085                1090                1095
Ile Glu  Ala Met Lys Met Glu  Ala Thr Ile Thr Ala  Ser Lys Asp
    1100                1105                1110
Gly Val  Val Asp Arg Val Ala  Leu Ala Gln Ala Thr  Lys Val Glu
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Gly Gly  Asp Leu Ile Val Val  Ile Ala
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cccgaacgcg ttcactgact gaacgggggt gaccggtgga gtggtgtgcc tcatatcggg      180
gcagggtatg ggacaaggcg caaccccaca gactaaagtg ttatccgttc ctcgttcctg      240
gttcggtcgg gtgcgctgac cggccccggg gcctcatttt caaatcagga gatatcacac      300
gtg agc aag ccc gtc gtc ctc atc gcc gac aaa ctg gca cct tcc acc         348
Val Ser Lys Pro Val Val Leu Ile Ala Asp Lys Leu Ala Pro Ser Thr
1               5                  10                  15
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gta gat gcg ctc gga gac gcc gtg gag gtg cgc tgg gtc gac ggc ccg        396
Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro
            20                  25                  30
aac acc ccg gag ctg ctc gcc gcc gtc ccg gag gca gac gca ctg ctg        444
Asn Thr Pro Glu Leu Leu Ala Ala Val Pro Glu Ala Asp Ala Leu Leu
        35                  40                  45
gtc cgt tcc gcg acc acc gtc acc cgt gag gtc ctc gag gcc gca ccg        492
Val Arg Ser Ala Thr Thr Val Thr Arg Glu Val Leu Glu Ala Ala Pro
    50                  55                  60
aac ctg aag atc gtc ggc cgc gcc ggc gtc ggc ctg gac aac gtc gac        540
Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp
65                  70                  75                  80
atc gac gcc gcc acc gag cgt ggc gtc atg gtc gtc aac gcc ccg acc        588
Ile Asp Ala Ala Thr Glu Arg Gly Val Met Val Val Asn Ala Pro Thr
                85                  90                  95
tcc aac atc cac tcc gcc tgc gag cac gcc atc gcc ctg ctc atg gcc        636
Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ala Leu Leu Met Ala
            100                 105                 110
acc gtg cgc cag atc ccg gcc gcc gac gcc acc ctg cgt gag ggc gag        684
Thr Val Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg Glu Gly Glu
        115                 120                 125
tgg aag cgt tcc gcc ttc aag ggc gtg gag atc ttc ggc aag acc atc        732
Trp Lys Arg Ser Ala Phe Lys Gly Val Glu Ile Phe Gly Lys Thr Ile
    130                 135                 140
ggc atc gtc ggc ttc ggc cac atc ggc cag ctc ttc gcc cag cgt ctg        780
Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala Gln Arg Leu
145                 150                 155                 160
tcc gcc ttc gag acc gag atc atc gcc tac gac ccg tac gcg aac ccg        828
Ser Ala Phe Glu Thr Glu Ile Ile Ala Tyr Asp Pro Tyr Ala Asn Pro
                165                 170                 175
acc cgc gcc gcc cag ctc ggc gtc gag ctg gtc gag ctg gag gag ctg        876
Thr Arg Ala Ala Gln Leu Gly Val Glu Leu Val Glu Leu Glu Glu Leu
            180                 185                 190
gtc tcc cgc gcc gac atc gtc acc atc cac ctt ccg aag acc aag gag        924
Val Ser Arg Ala Asp Ile Val Thr Ile His Leu Pro Lys Thr Lys Glu
        195                 200                 205
acg gcc ggc atg ttc aac gcc gag ctg ctc gcc aag tcc aag aag ggc        972
Thr Ala Gly Met Phe Asn Ala Glu Leu Leu Ala Lys Ser Lys Lys Gly
    210                 215                 220
cag atc atc atc aac gcc gcc cgc ggt ggc ctc gtc gat gag cag gca       1020
Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp Glu Gln Ala
225                 230                 235                 240
ctg gct gac gcc atc aag tcc ggc cac atc tgg ggc gcc ggc ttc gac       1068
Leu Ala Asp Ala Ile Lys Ser Gly His Ile Trp Gly Ala Gly Phe Asp
                245                 250                 255
gtc ttc tcc acc gag ccg tgc acc gac tcc ccg ctg ttc ggc ctg ccg       1116
Val Phe Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe Gly Leu Pro
            260                 265                 270
gag gtc gtc gtg acc ccg cac ctg ggt gcc tcc acc gaa gag gcc cag       1164
Glu Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu Glu Ala Gln
        275                 280                 285
gac cgt gcc ggc acc gac gtc gcc gcc tcc gtc ctc aag gcc ctg gcc       1212
Asp Arg Ala Gly Thr Asp Val Ala Ala Ser Val Leu Lys Ala Leu Ala
    290                 295                 300
ggc gag ttc gtc ccg gac gcc gtg aac gtc tcc ggc ggc cgc gtc ggc       1260
Gly Glu Phe Val Pro Asp Ala Val Asn Val Ser Gly Gly Arg Val Gly
305                 310                 315                 320
gag gag gtc gcc ctg tgg ttg gac ctg acc cgc aag ctg ggt ctg ctg       1308
Glu Glu Val Ala Leu Trp Leu Asp Leu Thr Arg Lys Leu Gly Leu Leu
                325                 330                 335
gcc ggt cag ctg ctg gac tcc gcc ccg gtc gac ctc gag gtc gag gcc       1356
Ala Gly Gln Leu Leu Asp Ser Ala Pro Val Asp Leu Glu Val Glu Ala
            340                 345                 350
cgc ggc gag ctc tcc acc gag gac gac ctg tcc gtg ctc ggc ctg tcc       1404
Arg Gly Glu Leu Ser Thr Glu Asp Asp Leu Ser Val Leu Gly Leu Ser
        355                 360                 365
gcc gtc cgt ggc ctg ttc tcc gcc acc acc gac gag ccg gtc acc ttc       1452
Ala Val Arg Gly Leu Phe Ser Ala Thr Thr Asp Glu Pro Val Thr Phe
    370                 375                 380
gtc aac gcc ccg cag atc gcg gag agc cgt ggc ctg gac tac aag gtc       1500
Val Asn Ala Pro Gln Ile Ala Glu Ser Arg Gly Leu Asp Tyr Lys Val
385                 390                 395                 400
gac acc gcg acc gag tcc acc acc cac cgt tcc tcc gtc gag gtc aag       1548
Asp Thr Ala Thr Glu Ser Thr Thr His Arg Ser Ser Val Glu Val Lys
                405                 410                 415
gtc atc ggt gcg gac ggc tcc tcc cgc tcc gtc gtc ggt gcc ctg acc       1596
Val Ile Gly Ala Asp Gly Ser Ser Arg Ser Val Val Gly Ala Leu Thr
            420                 425                 430
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ggc ctg gag cgc gtc gag aag atc gtg cgc atc gac gag cgc ggc ctg       1644
Gly Leu Glu Arg Val Glu Lys Ile Val Arg Ile Asp Glu Arg Gly Leu
        435                 440                 445
gac atg cgc gcc gag ggt cgc aac ctc ttc ctc gag tac acc gac gcc       1692
Asp Met Arg Ala Glu Gly Arg Asn Leu Phe Leu Glu Tyr Thr Asp Ala
    450                 455                 460
ccg ggc gcc ctg ggc aag gtg ggc tcc cag ctg ggc gac gcc ggc atc       1740
Pro Gly Ala Leu Gly Lys Val Gly Ser Gln Leu Gly Asp Ala Gly Ile
465                 470                 475                 480
aac atc gag gcc gcc gcc ctc acc cag gcc acc aag ggt gac ggc gcc       1788
Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Thr Lys Gly Asp Gly Ala
                485                 490                 495
atc ctg atc ctg cgt gtc gac gca gag atc ccg gag gca ctg cag aag       1836
Ile Leu Ile Leu Arg Val Asp Ala Glu Ile Pro Glu Ala Leu Gln Lys
            500                 505                 510
cag atc gcc gag tcc ctg ggt gcc acc aac gat atc cag ctc aac ctg       1884
Gln Ile Ala Glu Ser Leu Gly Ala Thr Asn Asp Ile Gln Leu Asn Leu
        515                 520                 525
gac tag tctccggtcg ccccgtcgac ggcgtgtcgc gtcggtccct cgcggatcgc        1940
Asp

gcggcacgcc gttcgcgttt ctgcgggagg cagtttcatt catgccgcct gaccgggaaa     2000
tgtgcaggta gacagtatgg ttcattccag gcgcgccgtt aatagaccga acggtatgga     2060
ctaactagac ggggaagtgt tgaatgggtc aggcaacgaa ccgactgatc caggagtacc     2120
ccgtgtccga cctcaccccg aaccacaccg ccggcgaacc gctcgagccc atcgacgcgc     2180
agaagctcgc                                                           2190
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<213>  Corynebacterium humireducens
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Val Ser Lys Pro Val Val Leu Ile Ala Asp Lys Leu Ala Pro Ser Thr
1               5                   10                  15
Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro
            20                  25                  30
Asn Thr Pro Glu Leu Leu Ala Ala Val Pro Glu Ala Asp Ala Leu Leu
        35                  40                  45
Val Arg Ser Ala Thr Thr Val Thr Arg Glu Val Leu Glu Ala Ala Pro
    50                  55                  60
Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp
65                  70                  75                  80
Ile Asp Ala Ala Thr Glu Arg Gly Val Met Val Val Asn Ala Pro Thr
                85                  90                  95
Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ala Leu Leu Met Ala
            100                 105                 110
Thr Val Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg Glu Gly Glu
        115                 120                 125
Trp Lys Arg Ser Ala Phe Lys Gly Val Glu Ile Phe Gly Lys Thr Ile
    130                 135                 140
Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala Gln Arg Leu
145                 150                 155                 160
Ser Ala Phe Glu Thr Glu Ile Ile Ala Tyr Asp Pro Tyr Ala Asn Pro
                165                 170                 175
Thr Arg Ala Ala Gln Leu Gly Val Glu Leu Val Glu Leu Glu Glu Leu
            180                 185                 190
Val Ser Arg Ala Asp Ile Val Thr Ile His Leu Pro Lys Thr Lys Glu
        195                 200                 205
Thr Ala Gly Met Phe Asn Ala Glu Leu Leu Ala Lys Ser Lys Lys Gly
    210                 215                 220
Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp Glu Gln Ala
225                 230                 235                 240
Leu Ala Asp Ala Ile Lys Ser Gly His Ile Trp Gly Ala Gly Phe Asp
                245                 250                 255
Val Phe Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe Gly Leu Pro
            260                 265                 270
Glu Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu Glu Ala Gln
        275                 280                 285
Asp Arg Ala Gly Thr Asp Val Ala Ala Ser Val Leu Lys Ala Leu Ala
    290                 295                 300
Gly Glu Phe Val Pro Asp Ala Val Asn Val Ser Gly Gly Arg Val Gly
305                 310                 315                 320
Glu Glu Val Ala Leu Trp Leu Asp Leu Thr Arg Lys Leu Gly Leu Leu
                325                 330                 335
Ala Gly Gln Leu Leu Asp Ser Ala Pro Val Asp Leu Glu Val Glu Ala
            340                 345                 350
Arg Gly Glu Leu Ser Thr Glu Asp Asp Leu Ser Val Leu Gly Leu Ser
        355                 360                 365
Ala Val Arg Gly Leu Phe Ser Ala Thr Thr Asp Glu Pro Val Thr Phe
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    370                 375                 380
Val Asn Ala Pro Gln Ile Ala Glu Ser Arg Gly Leu Asp Tyr Lys Val
385                 390                 395                 400
Asp Thr Ala Thr Glu Ser Thr Thr His Arg Ser Ser Val Glu Val Lys
                405                 410                 415
Val Ile Gly Ala Asp Gly Ser Ser Arg Ser Val Val Gly Ala Leu Thr
            420                 425                 430
Gly Leu Glu Arg Val Glu Lys Ile Val Arg Ile Asp Glu Arg Gly Leu
        435                 440                 445
Asp Met Arg Ala Glu Gly Arg Asn Leu Phe Leu Glu Tyr Thr Asp Ala
    450                 455                 460
Pro Gly Ala Leu Gly Lys Val Gly Ser Gln Leu Gly Asp Ala Gly Ile
465                 470                 475                 480
Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Thr Lys Gly Asp Gly Ala
                485                 490                 495
Ile Leu Ile Leu Arg Val Asp Ala Glu Ile Pro Glu Ala Leu Gln Lys
            500                 505                 510
Gln Ile Ala Glu Ser Leu Gly Ala Thr Asn Asp Ile Gln Leu Asn Leu
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Asp
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ccggccgagg tccgctaaaa gggtttgaca tagacccctc cgactgacac gacccccggt      180
agatccctct accgggggtt gcggcatgtt cgaaacccca tcccatgaaa gaatgatccc      240
gtggcagatc aagctcagaa ccccgatacc gccgacaccg aagcacagca gcagctgcag      300
gtg gcg ctc cag ccc gga ctg gag tcc gca gtc atc acc ctc acc ggc         348
Val Ala Leu Gln Pro Gly Leu Glu Ser Ala Val Ile Thr Leu Thr Gly
1               5                  10                  15
cgt gac cgg ccg ggc gtg acg gcc gcc ttc ttc cgc gtc ctg tcc gct         396
Arg Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala
            20                  25                  30
cac gac gtc cag ctt ctc gac gtc gag cag tcc cag ttc cgt gga tac         444
His Asp Val Gln Leu Leu Asp Val Glu Gln Ser Gln Phe Arg Gly Tyr
        35                  40                  45
ctc tcc ctc gcc gcc tac gtg ggc gtc gac ccg gag cgc gtc gac cgt         492
Leu Ser Leu Ala Ala Tyr Val Gly Val Asp Pro Glu Arg Val Asp Arg
    50                  55                  60
ctc cgc gag ggc ctg acc gag acc ctc aag ggc cac ggg cag ctc gcc         540
Leu Arg Glu Gly Leu Thr Glu Thr Leu Lys Gly His Gly Gln Leu Ala
65                  70                  75                  80
acc gtc gag atg gtc ccg gag ggc cag cac tcc agc ccg cgg tcc acg         588
Thr Val Glu Met Val Pro Glu Gly Gln His Ser Ser Pro Arg Ser Thr
                85                  90                  95
cac gtg gcc gtc gtc ctg ggc aac ccg gtg acc gcc acc gac gtg tcg         636
His Val Ala Val Val Leu Gly Asn Pro Val Thr Ala Thr Asp Val Ser
            100                 105                 110
gcc atc ggt cag acg ctg gcc aac tac ggc gcg aac atc gac cgt atc         684
Ala Ile Gly Gln Thr Leu Ala Asn Tyr Gly Ala Asn Ile Asp Arg Ile
        115                 120                 125
cgc ggc atc gcg gac tac ccg atc acc ggc ctg gag atc atg atc acg         732
Arg Gly Ile Ala Asp Tyr Pro Ile Thr Gly Leu Glu Ile Met Ile Thr
    130                 135                 140
atc gcc aac ccg gag ccg ggc ggc ggc aag gcc atg cgt aag gca ctg         780
Ile Ala Asn Pro Glu Pro Gly Gly Gly Lys Ala Met Arg Lys Ala Leu
145                 150                 155                 160

gcg gag ctg acc acc gag ctg ggc gtc gac atc gcc atc gag cgt gcc         828
Ala Glu Leu Thr Thr Glu Leu Gly Val Asp Ile Ala Ile Glu Arg Ala
                165                 170                 175
ggc ctg ctg cgc cgc tcc aag cgt ctg gtc atc ttc gac tgc gac tcc         876
Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Ile Phe Asp Cys Asp Ser
            180                 185                 190
acc ctc atc acc ggt gag gtc atc gag atg ctg gcg gcc cac gcc ggc         924
Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly
        195                 200                 205
aag gag gcc gag gtc gcc gag gtc acc gag cgg gcc atg cgc ggc gag         972
Lys Glu Ala Glu Val Ala Glu Val Thr Glu Arg Ala Met Arg Gly Glu
    210                 215                 220
ctc gac ttc gag gag tcc ctc cgt gag cgc gtc gcc acc ctc gag ggt        1020
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Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Ala Thr Leu Glu Gly
225                 230                 235                 240
ctc gac gcc tcc gtc atc gac gag gtc gcc cgc gac atc gtc ctg acc      1068
Leu Asp Ala Ser Val Ile Asp Glu Val Ala Arg Asp Ile Val Leu Thr
                245                 250                 255
ccg ggc gcc cgc acg acc atc cgc acc ctg aag aag atg ggc tac cgc      1116
Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Lys Lys Met Gly Tyr Arg
            260                 265                 270
acg gcc gtc gtc tcc ggt ggc ttc atc cag gtc ctc gag gac ctg gcc      1164
Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Asp Leu Ala
        275                 280                 285
gag gac ctc cag ctc gac tac gtc cgc gcg aac acc ctg gag atc gtc      1212
Glu Asp Leu Gln Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val
    290                 295                 300
gac ggc aag ctc acc ggc cgc gtg acc ggt gac atc gtc gac cgt gcc      1260
Asp Gly Lys Leu Thr Gly Arg Val Thr Gly Asp Ile Val Asp Arg Ala
305                 310                 315                 320
cgc aag gcg gag ctg ctg cgc gag ttc gcc gag gac tcc ggc ctg cag      1308
Arg Lys Ala Glu Leu Leu Arg Glu Phe Ala Glu Asp Ser Gly Leu Gln
                325                 330                 335
atg tac cag acc gtg gcc gtg ggt gac ggt gcc aac gac atc gac atg      1356
Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met
            340                 345                 350
ctc tcc gcg gcg ggc ctg ggc atc gcg ttc aac gcc aag ccg gcg ctg      1404
Leu Ser Ala Ala Gly Leu Gly Ile Ala Phe Asn Ala Lys Pro Ala Leu
        355                 360                 365
cgc gag atc gcc gac acc tcc gtc aac cac ccc ttc ctc gac gag gtg      1452
Arg Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val
    370                 375                 380
ctc cac atc ctg ggc gtc ccg cgc gag gag atc gac gag tcc gac ctg      1500
Leu His Ile Leu Gly Val Pro Arg Glu Glu Ile Asp Glu Ser Asp Leu
385                 390                 395                 400
gag gac ggc acc ttc cgc cgg gtc ccg ctc gag gtc tcc gca cgg tag      1548
Glu Asp Gly Thr Phe Arg Arg Val Pro Leu Glu Val Ser Ala Arg
                405                 410                 415
tggaggagac cgatccgctc gccctcgcgc acgccctcct gagcgcgcgg gtgagcgaca     1608
accggcacga ccgctccgag aacccggagc agcaggagac cgtgcaggcg atgcagatcg     1668
ccctgcacgt gccgaagaca caaccgcccc gccgtaccga cctcctcgag gccgcggcgc     1728
gggcggttgt cgccgtctgc ctctccgaca gggtcgcggg ggacccgtcc tggcgggcgg     1788
ggctggaggg ctggtacgac cacctcatcc gcaaggtgac ccgccgggcc cgcaacaagg     1848
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1               5                   10                  15
Arg Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala
            20                  25                  30
His Asp Val Gln Leu Leu Asp Val Glu Gln Ser Gln Phe Arg Gly Tyr
        35                  40                  45
Leu Ser Leu Ala Ala Tyr Val Gly Val Asp Pro Glu Arg Val Asp Arg
    50                  55                  60
Leu Arg Glu Gly Leu Thr Glu Thr Leu Lys Gly His Gly Gln Leu Ala
65                  70                  75                  80
Thr Val Glu Met Val Pro Glu Gly Gln His Ser Ser Pro Arg Ser Thr
                85                  90                  95
His Val Ala Val Val Leu Gly Asn Pro Val Thr Ala Thr Asp Val Ser
            100                 105                 110
Ala Ile Gly Gln Thr Leu Ala Asn Tyr Gly Ala Asn Ile Asp Arg Ile
        115                 120                 125
Arg Gly Ile Ala Asp Tyr Pro Ile Thr Gly Leu Glu Ile Met Ile Thr
    130                 135                 140
Ile Ala Asn Pro Glu Pro Gly Gly Gly Lys Ala Met Arg Lys Ala Leu
145                 150                 155                 160
Ala Glu Leu Thr Thr Glu Leu Gly Val Asp Ile Ala Ile Glu Arg Ala
                165                 170                 175
Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Ile Phe Asp Cys Asp Ser
            180                 185                 190
Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly
        195                 200                 205
Lys Glu Ala Glu Val Ala Glu Val Thr Glu Arg Ala Met Arg Gly Glu
    210                 215                 220
Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Ala Thr Leu Glu Gly
225                 230                 235                 240
Leu Asp Ala Ser Val Ile Asp Glu Val Ala Arg Asp Ile Val Leu Thr
                245                 250                 255
Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Lys Lys Met Gly Tyr Arg
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            260                 265                 270
Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Asp Leu Ala
        275                 280                 285
Glu Asp Leu Gln Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val
    290                 295                 300
Asp Gly Lys Leu Thr Gly Arg Val Thr Gly Asp Ile Val Asp Arg Ala
305                 310                 315                 320
Arg Lys Ala Glu Leu Leu Arg Glu Phe Ala Glu Asp Ser Gly Leu Gln
                325                 330                 335
Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met
            340                 345                 350
Leu Ser Ala Ala Gly Leu Gly Ile Ala Phe Asn Ala Lys Pro Ala Leu
        355                 360                 365
Arg Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val
    370                 375                 380
Leu His Ile Leu Gly Val Pro Arg Glu Glu Ile Asp Glu Ser Asp Leu
385                 390                 395                 400
Glu Asp Gly Thr Phe Arg Arg Val Pro Leu Glu Val Ser Ala Arg
                405                 410                 415
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gaaaagcagg tcacccccat tgaatttgcg aggataagcc cctttgccta ccccagcaac       180
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atactaaggt tgttctcgat tggacagcac ttcaccgacc acgaaaggga cgtcatctcc       300
atg acc gag ttc ccc acc ctc ccc gca gat ctc ctc ccg gca gac ggt         348
Met Thr Glu Phe Pro Thr Leu Pro Ala Asp Leu Leu Pro Ala Asp Gly
1               5                   10                  15
cgt ttc ggc tgc ggc ccc tcc aag gtc cgc ccg gag cag atc cag gcc         396
Arg Phe Gly Cys Gly Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala
            20                  25                  30
atc gtc gac ggc ggc cgc gac atc atc ggc acc tcg cac cgc cag ccg         444
Ile Val Asp Gly Gly Arg Asp Ile Ile Gly Thr Ser His Arg Gln Pro
        35                  40                  45
gcc gtg aag aat gtc gtc ggt tcg gtc cgt gag ggc ctc tcc gac ctg         492
Ala Val Lys Asn Val Val Gly Ser Val Arg Glu Gly Leu Ser Asp Leu
    50                  55                  60
ttc tcc ctg ccg gag ggc tac gag atc atc ctg tcc ctc ggt ggc gcc         540
Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
65                  70                  75                  80
acc gca ttc tgg gac gcc gcc acc ttc ggc ctc atc gag aag aag tcc         588
Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
                85                  90                  95
ggt cac ctg tcc tac ggt gag ttc tcc tcc aag ttc gcc aag gcc tcc         636
Gly His Leu Ser Tyr Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser
            100                 105                 110
cag cag gca ccg tgg ctg gat gag ccg acc atc atc gag gcc ccg gcc         684
Gln Gln Ala Pro Trp Leu Asp Glu Pro Thr Ile Ile Glu Ala Pro Ala
        115                 120                 125
ggc gac gcc ccg gag ccg cag gcc atg gag ggc acc gac gtc atc ggc         732
Gly Asp Ala Pro Glu Pro Gln Ala Met Glu Gly Thr Asp Val Ile Gly
    130                 135                 140
tgg gcc cac aac gag acc tcc acc ggc gcc atg gtg ccg atc gtc cgc         780
Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Ile Val Arg
145                 150                 155                 160
ccg gag ggc tcc gac ggc tcc ctc atc gtc atc gac gcc acc tcc ggc         828
Pro Glu Gly Ser Asp Gly Ser Leu Ile Val Ile Asp Ala Thr Ser Gly
                165                 170                 175

gcc ggc ggc ctc ccg gtg aac atc gcc gac acc gac gtc tac tac ttc         876
Ala Gly Gly Leu Pro Val Asn Ile Ala Asp Thr Asp Val Tyr Tyr Phe
            180                 185                 190
tcc ccg cag aag tgc ttc gcc tcc gac ggt ggc ctg tgg ctc gcc gcc         924
Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala
        195                 200                 205
atg tcc ccg gcc gcc atg gag cgc atc gcg aag atc aag gag tcc ggc         972
Met Ser Pro Ala Ala Met Glu Arg Ile Ala Lys Ile Lys Glu Ser Gly
    210                 215                 220
cgc cac atc ccg gcg ttc ctg gac ctg cag acc gcc gtc gag aac tcc        1020
Arg His Ile Pro Ala Phe Leu Asp Leu Gln Thr Ala Val Glu Asn Ser
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225                 230                 235                 240
ctg aag aac cag acc tac aac acc ccg gcc gtg ggc acc ctg ctc atg      1068
Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Gly Thr Leu Leu Met
                245                 250                 255
ctg gac aac cag gtc aag tgg atg aac gag aac ggt ggc ctg gac ggc      1116
Leu Asp Asn Gln Val Lys Trp Met Asn Glu Asn Gly Gly Leu Asp Gly
            260                 265                 270
atg gtc gcc cgc acc acc gcc tcc tcc gac gcc ctg tac aac tgg gcc      1164
Met Val Ala Arg Thr Thr Ala Ser Ser Asp Ala Leu Tyr Asn Trp Ala
        275                 280                 285
gag gcc cgc gag gag acc acc ccg tac gtc acc gac aag gcg aag cgc      1212
Glu Ala Arg Glu Glu Thr Thr Pro Tyr Val Thr Asp Lys Ala Lys Arg
    290                 295                 300
tcc ctc gtc gtc ggc acc atc gac ttc gac gac tcc gtc gac gcg gcg      1260
Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Val Asp Ala Ala
305                 310                 315                 320
gtc gtc gcc aag gtc ctg cgt gcc aac ggc atc ctc gac gtc gag ccc      1308
Val Val Ala Lys Val Leu Arg Ala Asn Gly Ile Leu Asp Val Glu Pro
                325                 330                 335
tac cgc aag ctg ggc cgc aac cag ctg cgc atc ggc atg ttc ccg gcg      1356
Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala
            340                 345                 350
atc gac tcc cag gac atc gtg acc ctc acc aag gcg atc gac cac gtc      1404
Ile Asp Ser Gln Asp Ile Val Thr Leu Thr Lys Ala Ile Asp His Val
        355                 360                 365
ctc gac tcg ggc gtc gcc gcc aag tag tcgccaggta gtcgcgggca            1451
Leu Asp Ser Gly Val Ala Ala Lys
    370                 375
cccgcacacc acccaacatg cgtcggacct cacacggtcc ggcgcatgtc tgcgttaggg     1511
tggtattcat cacgagagaa ggagaacgca tgcgcgagtt gttcctcgtc cctgaagagt     1571
cctcggccac ttccctggtg ttccggaccg aggacggcgg acagttcttc ctcgacgtca     1631
cttcactgga cgtggcctcc acccgtgcgc tcctgcttgc cgacgtcccg gaggacccct     1691
cccccacgga gtccggcacc gccgccgtca ccgccgtcga                           1731
<210>  70
<211>  376
<212>  PRT
<213>  Corynebacterium humireducens
<400>  70
Met Thr Glu Phe Pro Thr Leu Pro Ala Asp Leu Leu Pro Ala Asp Gly
1               5                   10                  15
Arg Phe Gly Cys Gly Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala
            20                  25                  30
Ile Val Asp Gly Gly Arg Asp Ile Ile Gly Thr Ser His Arg Gln Pro
        35                  40                  45
Ala Val Lys Asn Val Val Gly Ser Val Arg Glu Gly Leu Ser Asp Leu
    50                  55                  60
Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
65                  70                  75                  80
Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
                85                  90                  95
Gly His Leu Ser Tyr Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser
            100                 105                 110
Gln Gln Ala Pro Trp Leu Asp Glu Pro Thr Ile Ile Glu Ala Pro Ala
        115                 120                 125
Gly Asp Ala Pro Glu Pro Gln Ala Met Glu Gly Thr Asp Val Ile Gly
    130                 135                 140
Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Ile Val Arg
145                 150                 155                 160
Pro Glu Gly Ser Asp Gly Ser Leu Ile Val Ile Asp Ala Thr Ser Gly
                165                 170                 175
Ala Gly Gly Leu Pro Val Asn Ile Ala Asp Thr Asp Val Tyr Tyr Phe
            180                 185                 190
Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala
        195                 200                 205
Met Ser Pro Ala Ala Met Glu Arg Ile Ala Lys Ile Lys Glu Ser Gly
    210                 215                 220
Arg His Ile Pro Ala Phe Leu Asp Leu Gln Thr Ala Val Glu Asn Ser
225                 230                 235                 240
Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Gly Thr Leu Leu Met
                245                 250                 255
Leu Asp Asn Gln Val Lys Trp Met Asn Glu Asn Gly Gly Leu Asp Gly
            260                 265                 270
Met Val Ala Arg Thr Thr Ala Ser Ser Asp Ala Leu Tyr Asn Trp Ala
        275                 280                 285
Glu Ala Arg Glu Glu Thr Thr Pro Tyr Val Thr Asp Lys Ala Lys Arg
    290                 295                 300
Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Val Asp Ala Ala
305                 310                 315                 320
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Val Val Ala Lys Val Leu Arg Ala Asn Gly Ile Leu Asp Val Glu Pro
                325                 330                 335
Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala
            340                 345                 350
Ile Asp Ser Gln Asp Ile Val Thr Leu Thr Lys Ala Ile Asp His Val
        355                 360                 365
Leu Asp Ser Gly Val Ala Ala Lys
    370                 375
<210>  71
<211>  1665
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1365)
<223>  gen Alanine-Dehydrogenaza
<400>  71
acctctcgct cagccacctg cgccgcgcga cgaactcctc gcggaagtag ccgaggtggg       60
cggtcggccc gccgaaggcg gtgacgccca gcagcccgaa gctgcggatg acctctcctg      120
tggtgccgtt gttcttgtct gcggattcct tcacgctcgt catggtaggg cggggcgtcg      180
agaagtgcgc gtcgagcgac agtaaccggg attacatcat taaccagccg gttccgacga      240
gcgtccggaa ggcgcctagt agagtcagtg gtcatgcgta tcggaatccc gaaggaaatc      300
atg aac atg gag ggc cgc gtg gcc ctc agc ccg ctc ggg gca ggc acc        348
Met Asn Met Glu Gly Arg Val Ala Leu Ser Pro Leu Gly Ala Gly Thr
1               5                   10                  15
ctc gta gcc gac ggc cat gag gtg att gtt cag gcc ggg gcg ggc gag        396
Leu Val Ala Asp Gly His Glu Val Ile Val Gln Ala Gly Ala Gly Glu
            20                  25                  30
aac tcc tcg ttc acc gat gcc gag tac gag gcg acg ggc gcg cgc gtc        444
Asn Ser Ser Phe Thr Asp Ala Glu Tyr Glu Ala Thr Gly Ala Arg Val
        35                  40                  45
gtc gcc tcc gcg gag gag gcc tgg ggc gcc gag atg gtg ctc aag gtc        492
Val Ala Ser Ala Glu Glu Ala Trp Gly Ala Glu Met Val Leu Lys Val
    50                  55                  60
aag gag ccg ctg ccg gag gag tac ggc ttc ctc cgc ccg gac ctc atc        540
Lys Glu Pro Leu Pro Glu Glu Tyr Gly Phe Leu Arg Pro Asp Leu Ile
65                  70                  75                  80
ctg ttc acc tac ctg cac ctg gcg tcc tcg cgt gag tgc acg aag gcg        588
Leu Phe Thr Tyr Leu His Leu Ala Ser Ser Arg Glu Cys Thr Lys Ala
                85                  90                  95
ctg ctc gac gcc ggc acc ctg tcc ctg gcg tac gag acg gtc ctc gac        636
Leu Leu Asp Ala Gly Thr Leu Ser Leu Ala Tyr Glu Thr Val Leu Asp
            100                 105                 110
gcc cgc ggc ggc ctc ccg ctg ctc acc ccg atg tcc cag gtc gcg ggc        684
Ala Arg Gly Gly Leu Pro Leu Leu Thr Pro Met Ser Gln Val Ala Gly
        115                 120                 125
cgc ctc gcc gtg cag gag ggc gcg cac cac ctc atg agc tcc aag ggg        732
Arg Leu Ala Val Gln Glu Gly Ala His His Leu Met Ser Ser Lys Gly
    130                 135                 140
ggc cgc ggc gtg ctg ctc ggt ggc gtg ccc ggc acc gcc ccg gcg aag        780
Gly Arg Gly Val Leu Leu Gly Gly Val Pro Gly Thr Ala Pro Ala Lys
145                 150                 155                 160
gtc gtc gtc ctc ggc ggc ggt cag gtc ggc gcc tcg gcc gtc gcg atc        828
Val Val Val Leu Gly Gly Gly Gln Val Gly Ala Ser Ala Val Ala Ile
                165                 170                 175
gcg cag ggt ctg cgc gcc agc gtc acg gtc ctc gac ctc gac ccg cag        876
Ala Gln Gly Leu Arg Ala Ser Val Thr Val Leu Asp Leu Asp Pro Gln
            180                 185                 190
gtg ctc gcg cgt ttc gac gac ctc tac cag ggc aac gtc cgc acc ctg        924
Val Leu Ala Arg Phe Asp Asp Leu Tyr Gln Gly Asn Val Arg Thr Leu
        195                 200                 205
ctg tcc gac ccg atg acc atc gag acc gag ctt ctc gac gcc gac ctc        972
Leu Ser Asp Pro Met Thr Ile Glu Thr Glu Leu Leu Asp Ala Asp Leu
    210                 215                 220
gtc atc ggc gcc gtc ctc gtc gcc ggc gcg aag gcc ccg acg ctg gtc       1020
Val Ile Gly Ala Val Leu Val Ala Gly Ala Lys Ala Pro Thr Leu Val
225                 230                 235                 240
agc gac gac ctg gtc gcc cgc atg aag cag ggc gcc gtg ctc gtc gac       1068
Ser Asp Asp Leu Val Ala Arg Met Lys Gln Gly Ala Val Leu Val Asp
                245                 250                 255
gtc gcc atc gac cag ggc ggc tgc ttc gag ccc tcc cgc aag acc tcc       1116
Val Ala Ile Asp Gln Gly Gly Cys Phe Glu Pro Ser Arg Lys Thr Ser
            260                 265                 270
cac gag gac ccg acc tac gag gtc cac ggc acc cgc ttc tac tgc gtg       1164
His Glu Asp Pro Thr Tyr Glu Val His Gly Thr Arg Phe Tyr Cys Val
        275                 280                 285
ccc aac atg ccc ggc gcg gtg gcc aac acc tcg acc cgg gcg ctc acc       1212
Pro Asn Met Pro Gly Ala Val Ala Asn Thr Ser Thr Arg Ala Leu Thr
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    290                 295                 300
tcg gcg acc ctg ccc tac gtc cgc gcg atc gcg gcg ggc ggc gtg gac      1260
Ser Ala Thr Leu Pro Tyr Val Arg Ala Ile Ala Ala Gly Gly Val Asp
305                 310                 315                 320
cgg gcg gtg gac aac cac ccg ggt ctg gag ccg ggc atc atg acc tgc      1308
Arg Ala Val Asp Asn His Pro Gly Leu Glu Pro Gly Ile Met Thr Cys
                325                 330                 335
gac ggc cgc ctg atc agt gag cca gtg aag gag gcg ttc ccg gat ctt      1356
Asp Gly Arg Leu Ile Ser Glu Pro Val Lys Glu Ala Phe Pro Asp Leu
            340                 345                 350
ctc ggt tga tgagcatcgc cgccacccgc tccatgtgat cccagatctg              1405
Leu Gly

gtggcggtac ccggcgggga tggtctcctc gtcgatgctg tcgagtgaca ccttcatcag    1465
ctccagccag cggatcgcag ccgcgcggtc cacggggaac tcgtggtggc ggcggcgcag    1525
catcggggcg ccgcgcttct cgttgaaggt ggccggtccg ccccagtact gggcgaggaa    1585
ccacttgagg cggttctcgg cgccctccca gtcgtcctcg gggtacatgg gccccaggat    1645
gtcgtccgtc ttcacctgcg                                               1665
<210>  72
<211>  354
<212>  PRT
<213>  Corynebacterium humireducens
<400>  72
Met Asn Met Glu Gly Arg Val Ala Leu Ser Pro Leu Gly Ala Gly Thr
1               5                  10                  15
Leu Val Ala Asp Gly His Glu Val Ile Val Gln Ala Gly Ala Gly Glu
            20                  25                  30
Asn Ser Ser Phe Thr Asp Ala Glu Tyr Glu Ala Thr Gly Ala Arg Val
        35                  40                  45
Val Ala Ser Ala Glu Glu Ala Trp Gly Ala Glu Met Val Leu Lys Val
    50                  55                  60
Lys Glu Pro Leu Pro Glu Glu Tyr Gly Phe Leu Arg Pro Asp Leu Ile
65                  70                  75                  80
Leu Phe Thr Tyr Leu His Leu Ala Ser Ser Arg Glu Cys Thr Lys Ala
                85                  90                  95
Leu Leu Asp Ala Gly Thr Leu Ser Leu Ala Tyr Glu Thr Val Leu Asp
            100                 105                 110
Ala Arg Gly Gly Leu Pro Leu Leu Thr Pro Met Ser Gln Val Ala Gly
        115                 120                 125
Arg Leu Ala Val Gln Glu Gly Ala His His Leu Met Ser Ser Lys Gly
    130                 135                 140
Gly Arg Gly Val Leu Leu Gly Gly Val Pro Gly Thr Ala Pro Ala Lys
145                 150                 155                 160
Val Val Val Leu Gly Gly Gly Gln Val Gly Ala Ser Ala Val Ala Ile
                165                 170                 175
Ala Gln Gly Leu Arg Ala Ser Val Thr Val Leu Asp Leu Asp Pro Gln
            180                 185                 190
Val Leu Ala Arg Phe Asp Asp Leu Tyr Gln Gly Asn Val Arg Thr Leu
        195                 200                 205
Leu Ser Asp Pro Met Thr Ile Glu Thr Glu Leu Leu Asp Ala Asp Leu
    210                 215                 220
Val Ile Gly Ala Val Leu Val Ala Gly Ala Lys Ala Pro Thr Leu Val
225                 230                 235                 240
Ser Asp Asp Leu Val Ala Arg Met Lys Gln Gly Ala Val Leu Val Asp
                245                 250                 255
Val Ala Ile Asp Gln Gly Gly Cys Phe Glu Pro Ser Arg Lys Thr Ser
            260                 265                 270
His Glu Asp Pro Thr Tyr Glu Val His Gly Thr Arg Phe Tyr Cys Val
        275                 280                 285
Pro Asn Met Pro Gly Ala Val Ala Asn Thr Ser Thr Arg Ala Leu Thr
    290                 295                 300
Ser Ala Thr Leu Pro Tyr Val Arg Ala Ile Ala Ala Gly Gly Val Asp
305                 310                 315                 320
Arg Ala Val Asp Asn His Pro Gly Leu Glu Pro Gly Ile Met Thr Cys
                325                 330                 335
Asp Gly Arg Leu Ile Ser Glu Pro Val Lys Glu Ala Phe Pro Asp Leu
            340                 345                 350
Leu Gly


<210>  73
<211>  1515
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1215)
<223>  gen cysD
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<400> 73
cctgaccccg tacgcggggt gggtcaccgg cctgcgccgc gctgacggac cgacccgggc 60
gcacgccccg gcgctcagcc ttgacgcgac ggggcggctg aagatctcgc cgctggtcac 120
gtggtccctc gtggacacgg aggcgttcat cgcggaccac gacctcatcc gacacccgct 180
gaccacgcag ggctacccgt ccatcgggtg cgccacctgc accctccccg tcgccgacgg 240
ggaggatccc cgggccggcc gctgggccgg acagaacaag acagaatgcg ggctccactc 300
atg acc acc acc acc ctc acc aga ctc tcc ccc cat ctg cag gac ctc 348
Met Thr Thr Thr Thr Leu Thr Arg Leu Ser Pro His Leu Gln Asp Leu
1 5 10 15
gag aac gag tcc atc cac atc ctc cgg gag gtg gcc ggg cag ttc gac 396
Glu Asn Glu Ser Ile His Ile Leu Arg Glu Val Ala Gly Gln Phe Asp
20 25 30
cgg gtc ggg ctg ctg ttc tcc ggc ggc aag gac tcc gtc gtc gtg ctc 444
Arg Val Gly Leu Leu Phe Ser Gly Gly Lys Asp Ser Val Val Val Leu
35 40 45
gag ctg gcg cgc cgg gcc ttc gct ccg gcg gcc gtg ccc ttc gag ctg 492
Glu Leu Ala Arg Arg Ala Phe Ala Pro Ala Ala Val Pro Phe Glu Leu
50 55 60
ctc cac gtg gac acc ggc cac aac ttc ccc gag gtc atc gag ttc cgt 540
Leu His Val Asp Thr Gly His Asn Phe Pro Glu Val Ile Glu Phe Arg
65 70 75 80
gac cga gtc gtc gcc gag acc ggc gtg cgg ctg cgc gtc gcg cac gtg 588
Asp Arg Val Val Ala Glu Thr Gly Val Arg Leu Arg Val Ala His Val
85 90 95
cag gac tgg atc gac cgc ggt gac ctc gtc gaa cgt ccc gac ggc acc 636
Gln Asp Trp Ile Asp Arg Gly Asp Leu Val Glu Arg Pro Asp Gly Thr
100 105 110
cgc aat ccc ctg cag acc gtc ccc ctc gtg gag acc atc gcc gag cag 684
Arg Asn Pro Leu Gln Thr Val Pro Leu Val Glu Thr Ile Ala Glu Gln
115 120 125
ggc tac gac gcc gtc ctc ggt ggc gcc cgc cgc gac gag gag cgg gcg 732
Gly Tyr Asp Ala Val Leu Gly Gly Ala Arg Arg Asp Glu Glu Arg Ala
130 135 140
cgc gcc aag gag cgt gtc ttc tcc gtg cgc gac tcc ttc ggc ggc tgg 780
Arg Ala Lys Glu Arg Val Phe Ser Val Arg Asp Ser Phe Gly Gly Trp
145 150 155 160

gat ccg cgc cgc cag cgc ccg gag ctg tgg cac ctc tac aac ggc ggc 828
Asp Pro Arg Arg Gln Arg Pro Glu Leu Trp His Leu Tyr Asn Gly Gly
165 170 175
cac ctg ccg ggc gag aac gtc cgc gtc ttc ccc atc tcc aac tgg acc 876
His Leu Pro Gly Glu Asn Val Arg Val Phe Pro Ile Ser Asn Trp Thr
180 185 190
gag gcc gac atc tgg gag tac atc ggc gcc cgc ggc atc gcg ctg ccg 924
Glu Ala Asp Ile Trp Glu Tyr Ile Gly Ala Arg Gly Ile Ala Leu Pro
195 200 205
gag atc tac ttc gcg cat gag cgg gcc gtc ttc gag cgg gac ggc atg 972
Glu Ile Tyr Phe Ala His Glu Arg Ala Val Phe Glu Arg Asp Gly Met
210 215 220
tgg ctg acc gcc ggc gag tgg ggt ggg ccc cgc gag ggc gag acc ctc 1020
Trp Leu Thr Ala Gly Glu Trp Gly Gly Pro Arg Glu Gly Glu Thr Leu
225 230 235 240
gag gtc cgc cgc gtg cgc tac cgc acc gtc ggc gac atg tcc tgc acc 1068
Glu Val Arg Arg Val Arg Tyr Arg Thr Val Gly Asp Met Ser Cys Thr
245 250 255
ggt gcg gtg ctc tcc gac gcc acc acg gtc gac gac gtc atc gcc gag 1116
Gly Ala Val Leu Ser Asp Ala Thr Thr Val Asp Asp Val Ile Ala Glu
260 265 270
atc gcc acc tcc acc ctc acc gag cgc ggg gcc acc cgc gcc gac gac 1164
Ile Ala Thr Ser Thr Leu Thr Glu Arg Gly Ala Thr Arg Ala Asp Asp
275 280 285
cgc ctc agt gaa tcc gcc atg gaa gac cgc aag aag gaa ggc tac ttc 1212
Arg Leu Ser Glu Ser Ala Met Glu Asp Arg Lys Lys Glu Gly Tyr Phe
290 295 300
tga tgaccaccac gctcctgcgc acccgcgaga cgctgcgcct gtgcaccgcc 1265
ggctccgtcg acgacggcaa gtccaccctc gtgggccgcc tgctccacga cacccgctcc 1325
gtcctcgccg accagctcgc cgccgtcgag cgcacctccg ccgaccgcgg tttccacggc 1385
ggcctggacc tctcactgct cgtcgacggc ctccgcgccg aacgcgagca gggcatcacc 1445
atcgacgtgg cctaccgcta cttcgccacc gaccgccgca ccttcatcct cgccgacacc 1505
cccggccacg 1515

<210> 74
<211> 304
<212> PRT
<213> Corynebacterium humireducens
<400> 74
Met Thr Thr Thr Thr Leu Thr Arg Leu Ser Pro His Leu Gln Asp Leu
1 5 10 15

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Glu Asn Glu Ser Ile His Ile Leu Arg Glu Val Ala Gly Gln Phe Asp
            20                  25                  30
Arg Val Gly Leu Leu Phe Ser Gly Gly Lys Asp Ser Val Val Val Leu
        35                  40                  45
Glu Leu Ala Arg Arg Ala Phe Ala Pro Ala Ala Val Pro Phe Glu Leu
    50                  55                  60
Leu His Val Asp Thr Gly His Asn Phe Pro Glu Val Ile Glu Phe Arg
65                  70                  75                  80
Asp Arg Val Val Ala Glu Thr Gly Val Arg Leu Arg Val Ala His Val
                85                  90                  95
Gln Asp Trp Ile Asp Arg Gly Asp Leu Val Glu Arg Pro Asp Gly Thr
            100                 105                 110
Arg Asn Pro Leu Gln Thr Val Pro Leu Val Glu Thr Ile Ala Glu Gln
        115                 120                 125
Gly Tyr Asp Ala Val Leu Gly Gly Ala Arg Arg Asp Glu Glu Arg Ala
    130                 135                 140
Arg Ala Lys Glu Arg Val Phe Ser Val Arg Asp Ser Phe Gly Gly Trp
145                 150                 155                 160
Asp Pro Arg Arg Gln Arg Pro Glu Leu Trp His Leu Tyr Asn Gly Gly
                165                 170                 175
His Leu Pro Gly Glu Asn Val Arg Val Phe Pro Ile Ser Asn Trp Thr
            180                 185                 190
Glu Ala Asp Ile Trp Glu Tyr Ile Gly Ala Arg Gly Ile Ala Leu Pro
        195                 200                 205
Glu Ile Tyr Phe Ala His Glu Arg Ala Val Phe Glu Arg Asp Gly Met
    210                 215                 220
Trp Leu Thr Ala Gly Glu Trp Gly Gly Pro Arg Glu Gly Glu Thr Leu
225                 230                 235                 240
Glu Val Arg Arg Val Arg Tyr Arg Thr Val Gly Asp Met Ser Cys Thr
                245                 250                 255
Gly Ala Val Leu Ser Asp Ala Thr Thr Val Asp Asp Val Ile Ala Glu
            260                 265                 270
Ile Ala Thr Ser Thr Leu Thr Glu Arg Gly Ala Thr Arg Ala Asp Asp
        275                 280                 285
Arg Leu Ser Glu Ser Ala Met Glu Asp Arg Lys Lys Glu Gly Tyr Phe
    290                 295                 300
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<210> 75
<211> 1575
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1275)
<223> gen cysH
<400> 75

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cgtgcgcatc gccgtcaacg gctgccccaa ctcgtgtgcc cgcacgcagg tcgcggacat       60
cggcttcaag ggccagaccg tcaccgacgc cgacggcaac cgggtcgagg gcttccaggt      120
gcacctcggc gggtcgatga gcctcaacgc caacttcggc cgcaagctcc gcggccacaa      180
ggtgctcgcc gacgacatcg gggactacgt cacccgcgtg gtcacccact tccgggacca      240
gcgccgaccg gaggagacct tccaggagtg ggtccagcgc gccgccgagg aggacctcca      300
gtg agt ttc cgt cgc gcc ccc aac ccg aac cgc aac cat ccg ctg cac         348
Val Ser Phe Arg Arg Ala Pro Asn Pro Asn Arg Asn His Pro Leu His
1               5                  10                  15
tgc ccg tgg tgc gcc ggc gag gat ctg ctg ccc aac acg gag gac gac       396
Cys Pro Trp Cys Ala Gly Glu Asp Leu Leu Pro Asn Thr Glu Asp Asp
            20                  25                  30
ttc gcc tgg ctg tgc cgc gac tgc acc cgg gtg ttc tcc gtc cgc tac       444
Phe Ala Trp Leu Cys Arg Asp Cys Thr Arg Val Phe Ser Val Arg Tyr
        35                  40                  45
cac ggg cag gac gcc ccg gcg cgc cga ccg gcc ccg gca ctc tcc acg       492
His Gly Gln Asp Ala Pro Ala Arg Arg Pro Ala Pro Ala Leu Ser Thr
    50                  55                  60
agt gcg gcg atc cag ctc tcc ctg tcc cgt cgc ggc cac ctc aac gac       540
Ser Ala Ala Ile Gln Leu Ser Leu Ser Arg Arg Gly His Leu Asn Asp
65                  70                  75                  80
ccc gcc gtc agc ccg gca ggc ccc acc gcc acc ggg gac ctg ccg ggg       588
Pro Ala Val Ser Pro Ala Gly Pro Thr Ala Thr Gly Asp Leu Pro Gly
                85                  90                  95
gcg gtg cgg gag gag aac gcg cgg ctc gtc gag aag cac gcg gat gag       636
Ala Val Arg Glu Glu Asn Ala Arg Leu Val Glu Lys His Ala Asp Glu
            100                 105                 110

ctg tac gac gcc ccc gcc gac gtc atc ctg gcg tgg gcc cgg gag cac       684
Leu Tyr Asp Ala Pro Ala Asp Val Ile Leu Ala Trp Ala Arg Glu His
        115                 120                 125
gtg ccg ggt cgc ctc gcg gtg acg ctc tcg atg gag aac acc gtc ctc       732
Val Pro Gly Arg Leu Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu
    130                 135                 140
```

```
gcg gag ctg gcc gcc cgg cac acg ccc gac gcc gac ctg ctc ttc ctc        780
Ala Glu Leu Ala Ala Arg His Thr Pro Asp Ala Asp Leu Leu Phe Leu
145                 150                 155                 160
gac acc ggc tac cac ttc gag gag acg ctg gcg gtg gcg cgg gac gtc        828
Asp Thr Gly Tyr His Phe Glu Glu Thr Leu Ala Val Ala Arg Asp Val
                165                 170                 175
gac agg cgg tac ccg cag acg ctg gtg acc gcg acg ccg acg ctc acc        876
Asp Arg Arg Tyr Pro Gln Thr Leu Val Thr Ala Thr Pro Thr Leu Thr
            180                 185                 190
cgg gcg gag cag gac gcc gcc tac ggg ccc ggc ctg tac cgg cgc gac        924
Arg Ala Glu Gln Asp Ala Ala Tyr Gly Pro Gly Leu Tyr Arg Arg Asp
        195                 200                 205
ccg gcc gcg tgc tgc cgc atg cgc aag gtc gag ccg ctg gcc gtg cac        972
Pro Ala Ala Cys Cys Arg Met Arg Lys Val Glu Pro Leu Ala Val His
    210                 215                 220
ctg acc ccg tac gcg ggg tgg gtc acc ggc ctg cgc cgc gct gac gga       1020
Leu Thr Pro Tyr Ala Gly Trp Val Thr Gly Leu Arg Arg Ala Asp Gly
225                 230                 235                 240
ccg acc cgg gcg cac gcc ccg gcg ctc agc ctt gac gcg acg ggg cgg       1068
Pro Thr Arg Ala His Ala Pro Ala Leu Ser Leu Asp Ala Thr Gly Arg
                245                 250                 255
ctg aag atc tcg ccg ctg gtc acg tgg tcc ctc gtg gac acg gag gcg       1116
Leu Lys Ile Ser Pro Leu Val Thr Trp Ser Leu Val Asp Thr Glu Ala
            260                 265                 270
ttc atc gcg gac cac gac ctc atc cga cac ccc ctg acc acg cag ggc       1164
Phe Ile Ala Asp His Asp Leu Ile Arg His Pro Leu Thr Thr Gln Gly
        275                 280                 285
tac ccg tcc atc ggg tgc gcc acc tgc acc ctc ccc gtc gcc gac ggg       1212
Tyr Pro Ser Ile Gly Cys Ala Thr Cys Thr Leu Pro Val Ala Asp Gly
    290                 295                 300
gag gat ccc cgg gcc ggc cgc tgg gcc gga cag aac aag aca gaa tgc       1260
Glu Asp Pro Arg Ala Gly Arg Trp Ala Gly Gln Asn Lys Thr Glu Cys
305                 310                 315                 320
ggg ctc cac tca tga ccaccaccac cctcaccaga ctctcccccc atctgcagga       1315
Gly Leu His Ser

cctcgagaac gagtccatcc acatcctccg ggaggtggcc gggcagttcg accgggtcgg      1375
gctgctgttc tccggcggca aggactccgt cgtcgtgctc gagctggcgc gccgggcctt      1435
cgctccggcg gccgtgccct tcgagctgct ccacgtggac accggccaca acttccccga      1495
ggtcatcgag ttccgtgacc gagtcgtcgc cgagaccggc gtgcggctgc gcgtcgcgca      1555
cgtgcaggac tggatcgacc                                                 1575
<210>  76
<211>  324
<212>  PRT
<213>  Corynebacterium humireducens
<400>  76
Val Ser Phe Arg Arg Ala Pro Asn Pro Asn Arg Asn His Pro Leu His
1                 5                  10                  15
Cys Pro Trp Cys Ala Gly Glu Asp Leu Leu Pro Asn Thr Glu Asp Asp
            20                  25                  30
Phe Ala Trp Leu Cys Arg Asp Cys Thr Arg Val Phe Ser Val Arg Tyr
        35                  40                  45
His Gly Gln Asp Ala Pro Ala Arg Arg Pro Ala Pro Ala Leu Ser Thr
    50                  55                  60
Ser Ala Ala Ile Gln Leu Ser Leu Ser Arg Arg Gly His Leu Asn Asp
65                  70                  75                  80
Pro Ala Val Ser Pro Ala Gly Pro Thr Ala Thr Gly Asp Leu Pro Gly
                85                  90                  95
Ala Val Arg Glu Glu Asn Ala Arg Leu Val Glu Lys His Ala Asp Glu
            100                 105                 110
Leu Tyr Asp Ala Pro Ala Asp Val Ile Leu Ala Trp Ala Arg Glu His
        115                 120                 125
Val Pro Gly Arg Leu Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu
    130                 135                 140
Ala Glu Leu Ala Ala Arg His Thr Pro Asp Ala Asp Leu Leu Phe Leu
145                 150                 155                 160
Asp Thr Gly Tyr His Phe Glu Glu Thr Leu Ala Val Ala Arg Asp Val
                165                 170                 175
Asp Arg Arg Tyr Pro Gln Thr Leu Val Thr Ala Thr Pro Thr Leu Thr
            180                 185                 190
Arg Ala Glu Gln Asp Ala Ala Tyr Gly Pro Gly Leu Tyr Arg Arg Asp
        195                 200                 205
Pro Ala Ala Cys Cys Arg Met Arg Lys Val Glu Pro Leu Ala Val His
    210                 215                 220
Leu Thr Pro Tyr Ala Gly Trp Val Thr Gly Leu Arg Arg Ala Asp Gly
225                 230                 235                 240
Pro Thr Arg Ala His Ala Pro Ala Leu Ser Leu Asp Ala Thr Gly Arg
                245                 250                 255
```

```
Leu Lys Ile Ser Pro Leu Val Thr Trp Ser Leu Val Asp Thr Glu Ala
            260                 265                 270
Phe Ile Ala Asp His Asp Leu Ile Arg His Pro Leu Thr Thr Gln Gly
        275                 280                 285
Tyr Pro Ser Ile Gly Cys Ala Thr Cys Thr Leu Pro Val Ala Asp Gly
    290                 295                 300
Glu Asp Pro Arg Ala Gly Arg Trp Ala Gly Gln Asn Lys Thr Glu Cys
305                 310                 315                 320
Gly Leu His Ser
<210>  77
<211>  2295
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<213>  Corynebacterium humireducens
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tacagccatg atcgggaaag ttgcccaaaa tcatgacgta tctacatctc tccaccattg      180
ccatgaactg atctgtctgc tctaatccac tgcagacgcc ccggcagggg ctccgtggcg      240
gcgcccggcg ccgaatccac gtgaatgaaa tagacagaac agttcagtag ggagatggtc      300
atg gac acg acc acc acg atc gag aag gca ccc cgc cgc gag cgc ccc         348
Met Asp Thr Thr Thr Thr Ile Glu Lys Ala Pro Arg Arg Glu Arg Pro
1               5                   10                  15
aga cgc gcc cgc aag ccg gag ggc cag tgg cgg atc gac ggc acc acg         396
Arg Arg Ala Arg Lys Pro Glu Gly Gln Trp Arg Ile Asp Gly Thr Thr
            20                  25                  30
ccg ctc aac cac gtg gag gag gtg aag cag gac ggc gac atc ctc gcc         444
Pro Leu Asn His Val Glu Glu Val Lys Gln Asp Gly Asp Ile Leu Ala
        35                  40                  45
gtc tac gac cgg gtg gtc aac atc tac tcg aag cag ggt ttc gac tcc         492
Val Tyr Asp Arg Val Val Asn Ile Tyr Ser Lys Gln Gly Phe Asp Ser
    50                  55                  60
atc ccc gcc gac gac ctc gcc ccg cgc ttc aag tgg ctg ggc ctg tac         540
Ile Pro Ala Asp Asp Leu Ala Pro Arg Phe Lys Trp Leu Gly Leu Tyr
65                  70                  75                  80
acg cag cgc cgc cag gat ctc ggc ggt gag ctc acc ggc cag ctg ccc         588
Thr Gln Arg Arg Gln Asp Leu Gly Gly Glu Leu Thr Gly Gln Leu Pro
                85                  90                  95
gac gcc gag ctg cag gac cgc tac ttc atg atg cgc gtg cgt ttc gag         636
Asp Ala Glu Leu Gln Asp Arg Tyr Phe Met Met Arg Val Arg Phe Glu
            100                 105                 110
ggc ggc cag gta acc ccg gcc cgc ctc cgc gcg gtg ggg gag atc tcc         684
Gly Gly Gln Val Thr Pro Ala Arg Leu Arg Ala Val Gly Glu Ile Ser
        115                 120                 125
cgc gac tac gcc cgc agc acc gcg gac ttc acc gat cgg cag aac atc         732
Arg Asp Tyr Ala Arg Ser Thr Ala Asp Phe Thr Asp Arg Gln Asn Ile
    130                 135                 140
cag ctg cac tgg ctg cgc atc gag gac atc ccg gcg atc tgg gag aag         780
Gln Leu His Trp Leu Arg Ile Glu Asp Ile Pro Ala Ile Trp Glu Lys
145                 150                 155                 160
ctc gac tcc gtg ggg ctc agc ccc ctg ctg ggc tgc ggt gac gtg ccg         828
Leu Asp Ser Val Gly Leu Ser Pro Leu Leu Gly Cys Gly Asp Val Pro
                165                 170                 175
cgc atc atc ctc ggc tcc ccg gtc gcg ggg gtc gcc gcc gag gag atc         876
Arg Ile Ile Leu Gly Ser Pro Val Ala Gly Val Ala Ala Glu Glu Ile
            180                 185                 190
atc gac gcc acc ccg gcg atc gag cgg atc cag cgc gag cac ctg ccg         924
Ile Asp Ala Thr Pro Ala Ile Glu Arg Ile Gln Arg Glu His Leu Pro
        195                 200                 205
aac ccg gag ttc cac aac ctg ccg cgc aag ttc aag tcc gcg atc tcc         972
Asn Pro Glu Phe His Asn Leu Pro Arg Lys Phe Lys Ser Ala Ile Ser
    210                 215                 220
ggc cac tcg cgc cag gac gtc acc cac gag atc cag gac gtc gcc ttc        1020
Gly His Ser Arg Gln Asp Val Thr His Glu Ile Gln Asp Val Ala Phe
225                 230                 235                 240
atc ggt tcc gtc cac ccc gag cac ggc ccg ggt ttc gag tgc ttc gtc        1068
Ile Gly Ser Val His Pro Glu His Gly Pro Gly Phe Glu Cys Phe Val
                245                 250                 255
ggc ggt ggc ctg tcc acc aac ccg atg ctc gcg cag tcg ctc ggc gcg        1116
Gly Gly Gly Leu Ser Thr Asn Pro Met Leu Ala Gln Ser Leu Gly Ala
            260                 265                 270
tgg atc ccg ctg gag gac gtg ccg gac gtg tgg gcc ggc gtc gcc cgg        1164
Trp Ile Pro Leu Glu Asp Val Pro Asp Val Trp Ala Gly Val Ala Arg
        275                 280                 285
atc ttc cgc gac tac ggt tac cgc cgc ctg cgg aat cgt gcc cgt ctc        1212
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Ile Phe Arg Asp Tyr Gly Tyr Arg Arg Leu Arg Asn Arg Ala Arg Leu
    290                 295                 300
aag ttc ctc gtg gcg gaa tgg ggg atc gag aag ttc cgg gac gtc ctc      1260
Lys Phe Leu Val Ala Glu Trp Gly Ile Glu Lys Phe Arg Asp Val Leu
305                 310                 315                 320
gag acg gag tac ctc gga cgc ccg ctc atc gac gga ccc cgc cag ccc      1308
Glu Thr Glu Tyr Leu Gly Arg Pro Leu Ile Asp Gly Pro Arg Gln Pro
                325                 330                 335
acc aac ccc ggc tac cgc gac cac atc ggc atc cac ccg cag aag gac      1356
Thr Asn Pro Gly Tyr Arg Asp His Ile Gly Ile His Pro Gln Lys Asp
            340                 345                 350
ggc cgc ttc tac ctg ggc gtg aag ccg acc gtc ggg cac acc acc ggt      1404
Gly Arg Phe Tyr Leu Gly Val Lys Pro Thr Val Gly His Thr Thr Gly
        355                 360                 365
gag cag ctc atc gcc atc gcc gag gtg gcg gag cgt ttc ggc atc gag      1452
Glu Gln Leu Ile Ala Ile Ala Glu Val Ala Glu Arg Phe Gly Ile Glu
    370                 375                 380
cgc atc cgc acc acc tcg gag aag gag ctg ctc ttc ctc gac gtc gag      1500
Arg Ile Arg Thr Thr Ser Glu Lys Glu Leu Leu Phe Leu Asp Val Glu
385                 390                 395                 400
cgc acc gac ctc acc gcc ctg gcc gcc gcc ctc gac gag acc ggc ctg      1548
Arg Thr Asp Leu Thr Ala Leu Ala Ala Ala Leu Asp Glu Thr Gly Leu
                405                 410                 415
tac tcg aag ccg agc gag tgg cgc cgc aac atc atc tcg tgc acc ggc      1596
Tyr Ser Lys Pro Ser Glu Trp Arg Arg Asn Ile Ile Ser Cys Thr Gly
            420                 425                 430
ctg gag ttc tgc aaa ctg gcg cac gcg acg acc aag tcg cgt gcc gtg      1644
Leu Glu Phe Cys Lys Leu Ala His Ala Thr Thr Lys Ser Arg Ala Val
        435                 440                 445
gcc ctg gtc gac gag ctg gag gaa cgc gtc ggc gac atc gac gtg ccc      1692
Ala Leu Val Asp Glu Leu Glu Glu Arg Val Gly Asp Ile Asp Val Pro
    450                 455                 460
gtg cgc atc gcc gtc aac ggc tgc ccc aac tcg tgt gcc cgc acg cag      1740
Val Arg Ile Ala Val Asn Gly Cys Pro Asn Ser Cys Ala Arg Thr Gln
465                 470                 475                 480
gtc gcg gac atc ggc ttc aag ggc cag acc gtc acc gac gcc gac ggc      1788
Val Ala Asp Ile Gly Phe Lys Gly Gln Thr Val Thr Asp Ala Asp Gly
                485                 490                 495
aac cgg gtc gag ggc ttc cag gtg cac ctc ggc ggg tcg atg agc ctc      1836
Asn Arg Val Glu Gly Phe Gln Val His Leu Gly Gly Ser Met Ser Leu
            500                 505                 510
aac gcc aac ttc ggc cgc aag ctc cgc ggc cac aag gtg ctc gcc gac      1884
Asn Ala Asn Phe Gly Arg Lys Leu Arg Gly His Lys Val Leu Ala Asp
        515                 520                 525
gac atc ggg gac tac gtc acc cgc gtg gtc acc cac ttc cgg gac cag      1932
Asp Ile Gly Asp Tyr Val Thr Arg Val Val Thr His Phe Arg Asp Gln
    530                 535                 540
cgc cga ccg gag gag acc ttc cag gag tgg gtc cag cgc gcc gcc gag      1980
Arg Arg Pro Glu Glu Thr Phe Gln Glu Trp Val Gln Arg Ala Ala Glu
545                 550                 555                 560
gag gac ctc cag tga gtttccgtcg cgcccccaac ccgaaccgca accatccgct      2035
Glu Asp Leu Gln

gcactgcccg tggtgcgccg gcgaggatct gctgcccaac acggaggacg acttcgcctg     2095
gctgtgccgc gactgcaccc gggtgttctc cgtccgctac cacgggcagg acgccccggc     2155
gcgccgaccg gccccggcac tctccacgag tgcggcgatc cagctctccc tgtcccgtcg     2215
cggccacctc aacgaccccg ccgtcagccc ggcaggcccc accgccaccg gggacctgcc     2275
gggggcggtg cgggaggaga                                                2295
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<213>  Corynebacterium humireducens
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1               5                   10                  15
Arg Arg Ala Arg Lys Pro Glu Gly Gln Trp Arg Ile Asp Gly Thr Thr
            20                  25                  30
Pro Leu Asn His Val Glu Glu Val Lys Gln Asp Gly Asp Ile Leu Ala
        35                  40                  45
Val Tyr Asp Arg Val Val Asn Ile Tyr Ser Lys Gln Gly Phe Asp Ser
    50                  55                  60
Ile Pro Ala Asp Asp Leu Ala Pro Arg Phe Lys Trp Leu Gly Leu Tyr
65                  70                  75                  80
Thr Gln Arg Arg Gln Asp Leu Gly Gly Glu Leu Thr Gly Gln Leu Pro
                85                  90                  95
Asp Ala Glu Leu Gln Asp Arg Tyr Phe Met Met Arg Val Arg Phe Glu
            100                 105                 110
Gly Gly Gln Val Thr Pro Ala Arg Leu Arg Ala Val Gly Glu Ile Ser
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        115                 120                 125
Arg Asp Tyr Ala Arg Ser Thr Ala Asp Phe Thr Asp Arg Gln Asn Ile
    130                 135                 140
Gln Leu His Trp Leu Arg Ile Glu Asp Ile Pro Ala Ile Trp Glu Lys
145                 150                 155                 160
Leu Asp Ser Val Gly Leu Ser Pro Leu Leu Gly Cys Gly Asp Val Pro
                165                 170                 175
Arg Ile Ile Leu Gly Ser Pro Val Ala Gly Val Ala Ala Glu Glu Ile
            180                 185                 190
Ile Asp Ala Thr Pro Ala Ile Glu Arg Ile Gln Arg Glu His Leu Pro
        195                 200                 205
Asn Pro Glu Phe His Asn Leu Pro Arg Lys Phe Lys Ser Ala Ile Ser
    210                 215                 220
Gly His Ser Arg Gln Asp Val Thr His Glu Ile Gln Asp Val Ala Phe
225                 230                 235                 240
Ile Gly Ser Val His Pro Glu His Gly Pro Gly Phe Glu Cys Phe Val
                245                 250                 255
Gly Gly Gly Leu Ser Thr Asn Pro Met Leu Ala Gln Ser Leu Gly Ala
            260                 265                 270
Trp Ile Pro Leu Glu Asp Val Pro Asp Val Trp Ala Gly Val Ala Arg
        275                 280                 285
Ile Phe Arg Asp Tyr Gly Tyr Arg Arg Leu Arg Asn Arg Ala Arg Leu
    290                 295                 300
Lys Phe Leu Val Ala Glu Trp Gly Ile Glu Lys Phe Arg Asp Val Leu
305                 310                 315                 320
Glu Thr Glu Tyr Leu Gly Arg Pro Leu Ile Asp Gly Pro Arg Gln Pro
                325                 330                 335
Thr Asn Pro Gly Tyr Arg Asp His Ile Gly Ile His Pro Gln Lys Asp
            340                 345                 350
Gly Arg Phe Tyr Leu Gly Val Lys Pro Thr Val Gly His Thr Thr Gly
        355                 360                 365
Glu Gln Leu Ile Ala Ile Ala Glu Val Ala Glu Arg Phe Gly Ile Glu
    370                 375                 380
Arg Ile Arg Thr Thr Ser Glu Lys Glu Leu Leu Phe Leu Asp Val Glu
385                 390                 395                 400
Arg Thr Asp Leu Thr Ala Leu Ala Ala Ala Leu Asp Glu Thr Gly Leu
                405                 410                 415
Tyr Ser Lys Pro Ser Glu Trp Arg Arg Asn Ile Ile Ser Cys Thr Gly
            420                 425                 430
Leu Glu Phe Cys Lys Leu Ala His Ala Thr Thr Lys Ser Arg Ala Val
        435                 440                 445
Ala Leu Val Asp Glu Leu Glu Glu Arg Val Gly Asp Ile Asp Val Pro
    450                 455                 460
Val Arg Ile Ala Val Asn Gly Cys Pro Asn Ser Cys Ala Arg Thr Gln
465                 470                 475                 480
Val Ala Asp Ile Gly Phe Lys Gly Gln Thr Val Thr Asp Ala Asp Gly
                485                 490                 495
Asn Arg Val Glu Gly Phe Gln Val His Leu Gly Gly Ser Met Ser Leu
            500                 505                 510
Asn Ala Asn Phe Gly Arg Lys Leu Arg Gly His Lys Val Leu Ala Asp
        515                 520                 525
Asp Ile Gly Asp Tyr Val Thr Arg Val Val Thr His Phe Arg Asp Gln
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Arg Arg Pro Glu Glu Thr Phe Gln Glu Trp Val Gln Arg Ala Ala Glu
545                 550                 555                 560
Glu Asp Leu Gln
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<223>  gen cysJ
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aactttcccg atcatggctg tacgtagtgt ttatatccga catacattca ctgaattgaa      180
ttgggggcgt cgaagagcga tgcccggacc ctgaattgaa gtcgcctttt cgcttgcatt      240
accgcccagg ggtgctactt tcacagacca gtcagtctag tgatttcccg aaaggaaccc      300
atg agc cag ccc acc ctc cgc atc gcc gtc atc ggc gcc ggc ccc gcc        348
Met Ser Gln Pro Thr Leu Arg Ile Ala Val Ile Gly Ala Gly Pro Ala
1               5                   10                  15
ggc atc tac gcc tcc gac ctc ctg gtg aag aac gcc gcc tcc atc ggc        396
Gly Ile Tyr Ala Ser Asp Leu Leu Val Lys Asn Ala Ala Ser Ile Gly
            20                  25                  30
cgt gag gtc cac gtc gac ctc atc gag aag ctg ccc gcc ccc ttc ggg        444
Arg Glu Val His Val Asp Leu Ile Glu Lys Leu Pro Ala Pro Phe Gly
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        35                  40                  45
ctc atc cgc tac ggc gtc gcc ccc gac cac ccg cgc atc aag ggc atc        492
Leu Ile Arg Tyr Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile
    50                  55                  60
atc acc tcc ctg cac cgc gtc ctc gac cgc ccc gag atc cgc ctg ctc        540
Ile Thr Ser Leu His Arg Val Leu Asp Arg Pro Glu Ile Arg Leu Leu
65                  70                  75                  80
ggc aac atc gag atc ggc cgc gac gtc acc gtc gag gag ctg cgc gaa        588
Gly Asn Ile Glu Ile Gly Arg Asp Val Thr Val Glu Glu Leu Arg Glu
                85                  90                  95
cac tac gac gcc gtc atc ttc gcc acc ggc gcc atc gcc gac cgc gac        636
His Tyr Asp Ala Val Ile Phe Ala Thr Gly Ala Ile Ala Asp Arg Asp
            100                 105                 110
ctg gac atc ccg ggc gtc gac gcg cag ggc tcc ttc ggc gcc gcc gac        684
Leu Asp Ile Pro Gly Val Asp Ala Gln Gly Ser Phe Gly Ala Ala Asp
        115                 120                 125
ttc gtc ggc ttc tac gac ggc aac ccc gag ttc ccc cgc acc tgg gac        732
Phe Val Gly Phe Tyr Asp Gly Asn Pro Glu Phe Pro Arg Thr Trp Asp
    130                 135                 140
ctg tcc gcg cag tcc gtc gcc gtc atc ggc gtg ggc aac gtg ggc ctc        780
Leu Ser Ala Gln Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu
145                 150                 155                 160
gac gtc gcg cgc gtc ctg tcc aag acc gcc gac gaa ctc aac gtc acc        828
Asp Val Ala Arg Val Leu Ser Lys Thr Ala Asp Glu Leu Asn Val Thr
                165                 170                 175
gag atc ccc gac aac gtc tac gag acc ctc cgc acc aac cag gcc acc        876
Glu Ile Pro Asp Asn Val Tyr Glu Thr Leu Arg Thr Asn Gln Ala Thr
            180                 185                 190
gag gtc cac gtc ttc ggc cgc cgc ggc ccc gcg cag gcc aag ttc acc        924
Glu Val His Val Phe Gly Arg Arg Gly Pro Ala Gln Ala Lys Phe Thr
        195                 200                 205
ccg cag gaa ctc aag gaa ctc gac cac tcc ccc acc gtc aac gtc gtc        972
Pro Gln Glu Leu Lys Glu Leu Asp His Ser Pro Thr Val Asn Val Val
    210                 215                 220
gtc gac ccc gag gac atc gac tac gac gac gcc agc atc gag gcc cgc       1020
Val Asp Pro Glu Asp Ile Asp Tyr Asp Asp Ala Ser Ile Glu Ala Arg
225                 230                 235                 240
agc agc tcc aag tcg cag gac ctc gtg tgc cag acc ctc gag ggc tac       1068
Ser Ser Ser Lys Ser Gln Asp Leu Val Cys Gln Thr Leu Glu Gly Tyr
                245                 250                 255
gcc atc cgc gaa ccc aag gac gcc ccg cac acc ctg cag atc cac ctc       1116
Ala Ile Arg Glu Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu
            260                 265                 270
ttc gag tct ccc acc gag atc ctc acc cgc gac ggc cgt gtc gtc ggc       1164
Phe Glu Ser Pro Thr Glu Ile Leu Thr Arg Asp Gly Arg Val Val Gly
        275                 280                 285
ctg cgc acc gaa cgc acc gaa ctc gac ggc acc ggc cac gtc cgc ggc       1212
Leu Arg Thr Glu Arg Thr Glu Leu Asp Gly Thr Gly His Val Arg Gly
    290                 295                 300
acc ggc acc ttc acc gac tgg ccc gtc cag gcc gtc tac cgc gcc gtc       1260
Thr Gly Thr Phe Thr Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val
305                 310                 315                 320
ggc tac cgc tcc gag ccg gtg ccg ggc gtg ccc ttc aac cat gtc gag       1308
Gly Tyr Arg Ser Glu Pro Val Pro Gly Val Pro Phe Asn His Val Glu
                325                 330                 335
cat gtg atc ccg aac gac ggc ggc cac gtc ctc gac ccc gcc ggc acc       1356
His Val Ile Pro Asn Asp Gly Gly His Val Leu Asp Pro Ala Gly Thr
            340                 345                 350
ccc gtc ccc ggc ctc tac gcc acc ggc tgg atc aag cgc ggc ccc gtc       1404
Pro Val Pro Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Val
        355                 360                 365
gga ctc atc ggc aac acc aag tcc gac gcc aag gag acc acc gac ctc       1452
Gly Leu Ile Gly Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Asp Leu
    370                 375                 380
ctg ctc gcc gac gcc gcc gcc gga ctt ctc gac gcc ccc ctc cac ccc       1500
Leu Leu Ala Asp Ala Ala Ala Gly Leu Leu Asp Ala Pro Leu His Pro
385                 390                 395                 400
gcc gac gcc ttc ctc cag ctt ctc gac gcc cgc ggc atc ccc gtc acc       1548
Ala Asp Ala Phe Leu Gln Leu Leu Asp Ala Arg Gly Ile Pro Val Thr
                405                 410                 415
acc tgg gag ggc tgg tac cgg ctc gac gcc gcc gag cgc gcc ctc ggc       1596
Thr Trp Glu Gly Trp Tyr Arg Leu Asp Ala Ala Glu Arg Ala Leu Gly
            420                 425                 430
gag gcc tcc ggc gtg gag ggc aag gag cgc cgg aag atc gtc gaa tgg       1644
Glu Ala Ser Gly Val Glu Gly Lys Glu Arg Arg Lys Ile Val Glu Trp
        435                 440                 445

gag gag atg gtc agc cac gca cac atc acc ccg gcc tat gtg tga           1689
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Glu Glu Met Val Ser His Ala His Ile Thr Pro Ala Tyr Val
    450                 455                 460
tttctcaggc tcagggccgg cagctgagac tgggcagcgc tatgccacgg gccatgacac     1749
gccgggccgg ataaaaattc ctgaccctga gtcgatctaa ctgcggtaac ggtccggtag     1809
gcgaattgtt accgatcagc aaccgtccaa attcataccc actaatgtga tcactgttac     1869
tctcaagagt ggaaagtaca actgacaatt cttaaggaga aacatcatgc gcggtagcgg     1929
actcatctgg accatcgtcg gcatcctggc catcatcgcc ctagtcatct ggatcatgtc     1989
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Gly Ile Tyr Ala Ser Asp Leu Leu Val Lys Asn Ala Ala Ser Ile Gly
            20                  25                  30
Arg Glu Val His Val Asp Leu Ile Glu Lys Leu Pro Ala Pro Phe Gly
        35                  40                  45
Leu Ile Arg Tyr Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile
    50                  55                  60
Ile Thr Ser Leu His Arg Val Leu Asp Arg Pro Glu Ile Arg Leu Leu
65                  70                  75                  80
Gly Asn Ile Glu Ile Gly Arg Asp Val Thr Val Glu Glu Leu Arg Glu
                85                  90                  95
His Tyr Asp Ala Val Ile Phe Ala Thr Gly Ala Ile Ala Asp Arg Asp
            100                 105                 110
Leu Asp Ile Pro Gly Val Asp Ala Gln Gly Ser Phe Gly Ala Ala Asp
        115                 120                 125
Phe Val Gly Phe Tyr Asp Gly Asn Pro Glu Phe Pro Arg Thr Trp Asp
    130                 135                 140
Leu Ser Ala Gln Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu
145                 150                 155                 160
Asp Val Ala Arg Val Leu Ser Lys Thr Ala Asp Glu Leu Asn Val Thr
                165                 170                 175
Glu Ile Pro Asp Asn Val Tyr Glu Thr Leu Arg Thr Asn Gln Ala Thr
            180                 185                 190
Glu Val His Val Phe Gly Arg Arg Gly Pro Ala Gln Ala Lys Phe Thr
        195                 200                 205
Pro Gln Glu Leu Lys Glu Leu Asp His Ser Pro Thr Val Asn Val Val
    210                 215                 220
Val Asp Pro Glu Asp Ile Asp Tyr Asp Asp Ala Ser Ile Glu Ala Arg
225                 230                 235                 240
Ser Ser Ser Lys Ser Gln Asp Leu Val Cys Gln Thr Leu Glu Gly Tyr
                245                 250                 255
Ala Ile Arg Glu Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu
            260                 265                 270
Phe Glu Ser Pro Thr Glu Ile Leu Thr Arg Asp Gly Arg Val Val Gly
        275                 280                 285
Leu Arg Thr Glu Arg Thr Glu Leu Asp Gly Thr Gly His Val Arg Gly
    290                 295                 300
Thr Gly Thr Phe Thr Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val
305                 310                 315                 320
Gly Tyr Arg Ser Glu Pro Val Pro Gly Val Pro Phe Asn His Val Glu
                325                 330                 335
His Val Ile Pro Asn Asp Gly Gly His Val Leu Asp Pro Ala Gly Thr
            340                 345                 350
Pro Val Pro Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Val
        355                 360                 365
Gly Leu Ile Gly Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Asp Leu
    370                 375                 380
Leu Leu Ala Asp Ala Ala Ala Gly Leu Leu Asp Ala Pro Leu His Pro
385                 390                 395                 400
Ala Asp Ala Phe Leu Gln Leu Leu Asp Ala Arg Gly Ile Pro Val Thr
                405                 410                 415
Thr Trp Glu Gly Trp Tyr Arg Leu Asp Ala Ala Glu Arg Ala Leu Gly
            420                 425                 430
Glu Ala Ser Gly Val Glu Gly Lys Glu Arg Arg Lys Ile Val Glu Trp
        435                 440                 445
Glu Glu Met Val Ser His Ala His Ile Thr Pro Ala Tyr Val
    450                 455                 460
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<222>  (301)..(1569)
<223>  gen cysN
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gcgctaccgc accgtcggcg acatgtcctg caccggtgcg gtgctctccg acgccaccac     180
ggtcgacgac gtcatcgccg agatcgccac ctccaccctc accgagcgcg gggccacccg     240
cgccgacgac cgcctcagtg aatccgccat ggaagaccgc aagaaggaag gctacttctg     300
atg acc acc acg ctc ctg cgc acc cgc gag acg ctg cgc ctg tgc acc       348
Met Thr Thr Thr Leu Leu Arg Thr Arg Glu Thr Leu Arg Leu Cys Thr
1               5                  10                  15
gcc ggc tcc gtc gac gac ggc aag tcc acc ctc gtg ggc cgc ctg ctc       396
Ala Gly Ser Val Asp Asp Gly Lys Ser Thr Leu Val Gly Arg Leu Leu
            20                  25                  30
cac gac acc cgc tcc gtc ctc gcc gac cag ctc gcc gcc gtc gag cgc       444
His Asp Thr Arg Ser Val Leu Ala Asp Gln Leu Ala Ala Val Glu Arg
        35                  40                  45
acc tcc gcc gac cgc ggt ttc cac ggc ggc ctg gac ctc tca ctg ctc       492
Thr Ser Ala Asp Arg Gly Phe His Gly Gly Leu Asp Leu Ser Leu Leu
    50                  55                  60
gtc gac ggc ctc cgc gcc gaa cgc gag cag ggc atc acc atc gac gtg       540
Val Asp Gly Leu Arg Ala Glu Arg Glu Gln Gly Ile Thr Ile Asp Val
65                  70                  75                  80
gcc tac cgc tac ttc gcc acc gac cgc cgc acc ttc atc ctc gcc gac       588
Ala Tyr Arg Tyr Phe Ala Thr Asp Arg Arg Thr Phe Ile Leu Ala Asp
                85                  90                  95
acc ccc ggc cac gtg cag tac acg cgc aac acc gtc acc ggc gtg tcc       636
Thr Pro Gly His Val Gln Tyr Thr Arg Asn Thr Val Thr Gly Val Ser
            100                 105                 110
acg tcg cag gtg gtc gtc ctg ctt gtc gac gcc cgc cac ggc gtc gtc       684
Thr Ser Gln Val Val Val Leu Leu Val Asp Ala Arg His Gly Val Val
        115                 120                 125
gag cag acc cgc cgc cac ctc acc gtc gcg gcg ctc ctc ggg gtg cgc       732
Glu Gln Thr Arg Arg His Leu Thr Val Ala Ala Leu Leu Gly Val Arg
    130                 135                 140
aca gtg ctc ctc gcg gtg aat aag atc gac ctc gtt gac tgg tcc gag       780
Thr Val Leu Leu Ala Val Asn Lys Ile Asp Leu Val Asp Trp Ser Glu
145                 150                 155                 160
gcc gtc ttc cgg gac atc gag gcg gag ttc acg tcg ctg gcc acc gac       828
Ala Val Phe Arg Asp Ile Glu Ala Glu Phe Thr Ser Leu Ala Thr Asp
                165                 170                 175
gtc ggc gtc gac gac gcg cac gtc atc ccc gtc tcc gcg ctg ctg ggc       876
Val Gly Val Asp Asp Ala His Val Ile Pro Val Ser Ala Leu Leu Gly
            180                 185                 190
gac aac gtc gtc gaa ccc tcg gcg aac ctc ccc tgg tac gag ggg ccg       924
Asp Asn Val Val Glu Pro Ser Ala Asn Leu Pro Trp Tyr Glu Gly Pro
        195                 200                 205
acg gtg ctg gaa ctg ctc gag agc gtc gag gtc cac cgc ggc cgc gcc       972
Thr Val Leu Glu Leu Leu Glu Ser Val Glu Val His Arg Gly Arg Ala
    210                 215                 220
cac gcc ctc ggc ttc cgc ctg ccg atc cag tac gtc atc cgc gag cac      1020
His Ala Leu Gly Phe Arg Leu Pro Ile Gln Tyr Val Ile Arg Glu His
225                 230                 235                 240
tcc tcc gac tac cgc ggc tac gcc ggg cgt gtc gac gcc ggc gtg ctc      1068
Ser Ser Asp Tyr Arg Gly Tyr Ala Gly Arg Val Asp Ala Gly Val Leu
                245                 250                 255
acc gtc ggc gac acc gtc cac ctc ccc gag ggg cgc acc agc acc gtc      1116
Thr Val Gly Asp Thr Val His Leu Pro Glu Gly Arg Thr Ser Thr Val
            260                 265                 270
acc cac atc gac acc gcc gac ggc gag gtc cgc tcc gcc cac gcc ggt      1164
Thr His Ile Asp Thr Ala Asp Gly Glu Val Arg Ser Ala His Ala Gly
        275                 280                 285
gac tcc gtg gtc ctg cgc ctg gcc gac gac atc gac ctc atc cgc ggc      1212
Asp Ser Val Val Leu Arg Leu Ala Asp Asp Ile Asp Leu Ile Arg Gly
    290                 295                 300
gac ctc atc gcc ggt gag gac cgc ccg gag ccg acc cgc tcc ttc gcc      1260
Asp Leu Ile Ala Gly Glu Asp Arg Pro Glu Pro Thr Arg Ser Phe Ala
305                 310                 315                 320
gcc aca ctc gtc gga ctc ggc gac cgc acc ctg cgc ccc ggc tcc ccc      1308
Ala Thr Leu Val Gly Leu Gly Asp Arg Thr Leu Arg Pro Gly Ser Pro
                325                 330                 335
gtg aag gtc cgc tac ggc acc tca ctc gtg cgg gga cgc gtc gcg gcg      1356
Val Lys Val Arg Tyr Gly Thr Ser Leu Val Arg Gly Arg Val Ala Ala
            340                 345                 350
atc gag cgg ctg ctc gac atc gac ggc cgc acc gac cac ctc tcc ccg      1404
Ile Glu Arg Leu Leu Asp Ile Asp Gly Arg Thr Asp His Leu Ser Pro
        355                 360                 365
gac gac ctc ggc ctc aac gac atc gcc cac gtg cgt atc gac gtc gcc      1452
Asp Asp Leu Gly Leu Asn Asp Ile Ala His Val Arg Ile Asp Val Ala
    370                 375                 380
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acc gag ctc ccc gtc gag ccc tac gcc gcc cgc ggc gcc gtc ggc tcc      1500
Thr Glu Leu Pro Val Glu Pro Tyr Ala Ala Arg Gly Ala Val Gly Ser
385                 390                 395                 400
ttc ctg ctc atc gac cag gcc agc ggc gac acc ctc gcc gcc ggg ctc      1548
Phe Leu Leu Ile Asp Gln Ala Ser Gly Asp Thr Leu Ala Ala Gly Leu
                405                 410                 415
gtc ggc cac cgg ctc cgc tga cccgtgaccg ccctgctcac cctctcccac          1599
Val Gly His Arg Leu Arg
            420
gggtcccgcc acccgcgcgc cgccgccggc gtcgaccgcc tcacccgggc ggccggggag     1659
gtgctgggcg tcaccgcccg cgccgcccac ctcgagttcg acacccccctc cctcatcgac    1719
gccgcccgcg acctcgtcgc ccgcggccac gaccacgccg tggtcgtccc cctgctgttc     1779
accgacgcct tccacgcgcg tcacgacgtc cccgccgccc tcgacgcggc ccgccgcgcc     1839
accggcctgc ggctcacgcc cgcccggggc                                      1869
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<213>  Corynebacterium humireducens
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1               5                  10                  15
Ala Gly Ser Val Asp Asp Gly Lys Ser Thr Leu Val Gly Arg Leu Leu
            20                  25                  30
His Asp Thr Arg Ser Val Leu Ala Asp Gln Leu Ala Ala Val Glu Arg
        35                  40                  45
Thr Ser Ala Asp Arg Gly Phe His Gly Gly Leu Asp Leu Ser Leu Leu
    50                  55                  60
Val Asp Gly Leu Arg Ala Glu Arg Glu Gln Gly Ile Thr Ile Asp Val
65                  70                  75                  80
Ala Tyr Arg Tyr Phe Ala Thr Asp Arg Arg Thr Phe Ile Leu Ala Asp
                85                  90                  95
Thr Pro Gly His Val Gln Tyr Thr Arg Asn Thr Val Thr Gly Val Ser
            100                 105                 110
Thr Ser Gln Val Val Val Leu Leu Val Asp Ala Arg His Gly Val Val
        115                 120                 125
Glu Gln Thr Arg Arg His Leu Thr Val Ala Ala Leu Leu Gly Val Arg
    130                 135                 140
Thr Val Leu Leu Ala Val Asn Lys Ile Asp Leu Val Asp Trp Ser Glu
145                 150                 155                 160
Ala Val Phe Arg Asp Ile Glu Ala Glu Phe Thr Ser Leu Ala Thr Asp
                165                 170                 175
Val Gly Val Asp Asp Ala His Val Ile Pro Val Ser Ala Leu Leu Gly
            180                 185                 190
Asp Asn Val Val Glu Pro Ser Ala Asn Leu Pro Trp Tyr Glu Gly Pro
        195                 200                 205
Thr Val Leu Glu Leu Leu Glu Ser Val Glu Val His Arg Gly Arg Ala
    210                 215                 220
His Ala Leu Gly Phe Arg Leu Pro Ile Gln Tyr Val Ile Arg Glu His
225                 230                 235                 240
Ser Ser Asp Tyr Arg Gly Tyr Ala Gly Arg Val Asp Ala Gly Val Leu
                245                 250                 255
Thr Val Gly Asp Thr Val His Leu Pro Glu Gly Arg Thr Ser Thr Val
            260                 265                 270
Thr His Ile Asp Thr Ala Asp Gly Glu Val Arg Ser Ala His Ala Gly
        275                 280                 285
Asp Ser Val Val Leu Arg Leu Ala Asp Asp Ile Asp Leu Ile Arg Gly
    290                 295                 300
Asp Leu Ile Ala Gly Glu Asp Arg Pro Glu Pro Thr Arg Ser Phe Ala
305                 310                 315                 320
Ala Thr Leu Val Gly Leu Gly Asp Arg Thr Leu Arg Pro Gly Ser Pro
                325                 330                 335
Val Lys Val Arg Tyr Gly Thr Ser Leu Val Arg Gly Arg Val Ala Ala
            340                 345                 350
Ile Glu Arg Leu Leu Asp Ile Asp Gly Arg Thr Asp His Leu Ser Pro
        355                 360                 365
Asp Asp Leu Gly Leu Asn Asp Ile Ala His Val Arg Ile Asp Val Ala
    370                 375                 380
Thr Glu Leu Pro Val Glu Pro Tyr Ala Ala Arg Gly Ala Val Gly Ser
385                 390                 395                 400
Phe Leu Leu Ile Asp Gln Ala Ser Gly Asp Thr Leu Ala Ala Gly Leu
                405                 410                 415
Val Gly His Arg Leu Arg
            420
<210>  83
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<213>  Corynebacterium humireducens
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<222> (301)..(948)
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cacctctccc cggacgacct cggcctcaac gacatcgccc acgtgcgtat cgacgtcgcc 180
accgagctcc ccgtcgagcc ctacgccgcc cgcggcgccg tcggctcctt cctgctcatc 240
gaccaggcca gcggcgacac cctcgccgcc gggctcgtcg gccaccggct ccgctgaccc 300
gtg acc gcc ctg ctc acc ctc tcc cac ggg tcc cgc cac ccg cgc gcc 348
Val Thr Ala Leu Leu Thr Leu Ser His Gly Ser Arg His Pro Arg Ala
1 5 10 15
gcc gcc ggc gtc gac cgc ctc acc cgg gcg gcc ggg gag gtg ctg ggc 396
Ala Ala Gly Val Asp Arg Leu Thr Arg Ala Ala Gly Glu Val Leu Gly
20 25 30
gtc acc gcc cgc gcc gcc cac ctc gag ttc gac acc ccc tcc ctc atc 444
Val Thr Ala Arg Ala Ala His Leu Glu Phe Asp Thr Pro Ser Leu Ile
35 40 45
gac gcc gcc cgc gac ctc gtc gcc cgc ggc cac gac cac gcc gtg gtc 492
Asp Ala Ala Arg Asp Leu Val Ala Arg Gly His Asp His Ala Val Val
50 55 60
gtc ccc ctg ctg ttc acc gac gcc ttc cac gcg cgt cac gac gtc ccc 540
Val Pro Leu Leu Phe Thr Asp Ala Phe His Ala Arg His Asp Val Pro
65 70 75 80
gcc gcc ctc gac gcg gcc cgc cgc gcc acc ggc ctg cgg ctc acg ccc 588
Ala Ala Leu Asp Ala Ala Arg Arg Ala Thr Gly Leu Arg Leu Thr Pro
85 90 95
gcc cgg ggc ctc ggc acc ggc ccc gac atc gcc gac gtc ctt gcc cgc 636
Ala Arg Gly Leu Gly Thr Gly Pro Asp Ile Ala Asp Val Leu Ala Arg
100 105 110
cac acc cgc ccc cgc aac ccg gac ctc gtc ctc ggg cac gtc gga tcc 684
His Thr Arg Pro Arg Asn Pro Asp Leu Val Leu Gly His Val Gly Ser
115 120 125
tcc tcc gtc gca gcc gag gcc gcc gtc cgg tcg ctg gcc gac ctc ctc 732
Ser Ser Val Ala Ala Glu Ala Ala Val Arg Ser Leu Ala Asp Leu Leu
130 135 140
gcc gcc cgc ctc ggg cgg gac gtc gcg gtg gtg cgg gcg acg ggg gag 780
Ala Ala Arg Leu Gly Arg Asp Val Ala Val Val Arg Ala Thr Gly Glu
145 150 155 160
aag gcg gcg tcg ata agc agc ggt gcc cac ctc gtc ccc ctc ttc gtc 828
Lys Ala Ala Ser Ile Ser Ser Gly Ala His Leu Val Pro Leu Phe Val
165 170 175
acc gac gcc ctg ctg ctc gac cgc ctg cgc gcc gcc caa ccc cac gcg 876
Thr Asp Ala Leu Leu Leu Asp Arg Leu Arg Ala Ala Gln Pro His Ala
180 185 190
acc tcc gac cgc ccg ctc acc gac gcc ctc cgc gac gtc gtg gcg gcg 924
Thr Ser Asp Arg Pro Leu Thr Asp Ala Leu Arg Asp Val Val Ala Ala
195 200 205
cgg tac cgg gcc gcc ctc acc tag gaacccacca tgaacacact cctgctcatc 978
Arg Tyr Arg Ala Ala Leu Thr
210 215
gccctcgcgg ggctcgccgc ccagctcgtc gacggcggcc tcggcatggg cttcggcgcc 1038
acctccacca cgatcctcat cgtgctcgcc ggactcggcc ccgccacagc cagcgccgtc 1098
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<400> 84
Val Thr Ala Leu Leu Thr Leu Ser His Gly Ser Arg His Pro Arg Ala
1 5 10 15
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20 25 30
Val Thr Ala Arg Ala Ala His Leu Glu Phe Asp Thr Pro Ser Leu Ile
35 40 45
Asp Ala Ala Arg Asp Leu Val Ala Arg Gly His Asp His Ala Val Val
50 55 60
Val Pro Leu Leu Phe Thr Asp Ala Phe His Ala Arg His Asp Val Pro
65 70 75 80
Ala Ala Leu Asp Ala Ala Arg Arg Ala Thr Gly Leu Arg Leu Thr Pro
85 90 95
Ala Arg Gly Leu Gly Thr Gly Pro Asp Ile Ala Asp Val Leu Ala Arg
100 105 110
His Thr Arg Pro Arg Asn Pro Asp Leu Val Leu Gly His Val Gly Ser

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        115                 120                 125
Ser Ser Val Ala Ala Glu Ala Ala Val Arg Ser Leu Ala Asp Leu Leu
    130                 135                 140
Ala Ala Arg Leu Gly Arg Asp Val Ala Val Val Arg Ala Thr Gly Glu
145                 150                 155                 160
Lys Ala Ala Ser Ile Ser Ser Gly Ala His Leu Val Pro Leu Phe Val
                165                 170                 175
Thr Asp Ala Leu Leu Leu Asp Arg Leu Arg Ala Ala Gln Pro His Ala
            180                 185                 190
Thr Ser Asp Arg Pro Leu Thr Asp Ala Leu Arg Asp Val Val Ala Ala
        195                 200                 205
Arg Tyr Arg Ala Ala Leu Thr
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gagaaggcgg cgtcgataag cagcggtgcc cacctcgtcc ccctcttcgt caccgacgcc      180
ctgctgctcg accgcctgcg cgccgcccaa ccccacgcga cctccgaccg cccgctcacc      240
gacgccctcc gcgacgtcgt ggcggcgcgg taccgggccg ccctcaccta ggaacccacc      300
atg aac aca ctc ctg ctc atc gcc ctc gcg ggg ctc gcc gcc cag ctc         348
Met Asn Thr Leu Leu Leu Ile Ala Leu Ala Gly Leu Ala Ala Gln Leu
1               5                  10                  15
gtc gac ggc ggc ctc ggc atg ggc ttc ggc gcc acc tcc acc acg atc         396
Val Asp Gly Gly Leu Gly Met Gly Phe Gly Ala Thr Ser Thr Thr Ile
            20                  25                  30
ctc atc gtg ctc gcc gga ctc ggc ccc gcc aca gcc agc gcc gtc gtc         444
Leu Ile Val Leu Ala Gly Leu Gly Pro Ala Thr Ala Ser Ala Val Val
        35                  40                  45
cac acc gcg gaa ctg ggc acc acc ctc gtc tcc ggc gtc tcg cac tgg         492
His Thr Ala Glu Leu Gly Thr Thr Leu Val Ser Gly Val Ser His Trp
    50                  55                  60
cgt ttc gga aac gtc gac tgg cag gtc gtc cgc cgc ctc gcc atc ccc         540
Arg Phe Gly Asn Val Asp Trp Gln Val Val Arg Arg Leu Ala Ile Pro
65                  70                  75                  80
ggt gcc gtg ggc gcc ttc gcc ggg gca acc gtg ctc tcc cac tta tcg         588
Gly Ala Val Gly Ala Phe Ala Gly Ala Thr Val Leu Ser His Leu Ser
                85                  90                  95
acg cag gcc gcc gcc ccc gtc acc gcc acg atc ctc acc ctc atc ggc         636
Thr Gln Ala Ala Ala Pro Val Thr Ala Thr Ile Leu Thr Leu Ile Gly
            100                 105                 110
gcc aac ctc gtg tgg cgc ttc tcc cgc gga cgc atc cac ccg cgc cgc         684
Ala Asn Leu Val Trp Arg Phe Ser Arg Gly Arg Ile His Pro Arg Arg
        115                 120                 125
gcc ggg aag ggg cac tcg cgc ggc ttc ctc ggc ggg ctc ggc ctg ttc         732
Ala Gly Lys Gly His Ser Arg Gly Phe Leu Gly Gly Leu Gly Leu Phe
    130                 135                 140
ggc ggc ttc atc gac gcc tcc gga ggc ggc ggc tgg ggc ccg gtg acc         780
Gly Gly Phe Ile Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
145                 150                 155                 160
acc tcg acc ctg atg acg ctg ggg cgg gcg gaa ccg cgc cgc atc gtc         828
Thr Ser Thr Leu Met Thr Leu Gly Arg Ala Glu Pro Arg Arg Ile Val
                165                 170                 175
ggc acg gtc aac acc gcc gag ttc ctg gtc acc gcc gcg gcg acc gcc         876
Gly Thr Val Asn Thr Ala Glu Phe Leu Val Thr Ala Ala Ala Thr Ala
            180                 185                 190
ggc ttc gtc atc ggc ctg tgg gac gac ctg gtg gcc aac ctc gcg gcc         924
Gly Phe Val Ile Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ala Ala
        195                 200                 205
gtg ctc gcg ctg ctc atc ggc ggt gtc atc gcc gcg ccg gtc gcc gcg         972
Val Leu Ala Leu Leu Ile Gly Gly Val Ile Ala Ala Pro Val Ala Ala
    210                 215                 220
tgg ctg gtc acc cgc ctc aac ccg gcc gcc ctc ggc ggc gtc gtg ggc        1020
Trp Leu Val Thr Arg Leu Asn Pro Ala Ala Leu Gly Gly Val Val Gly
225                 230                 235                 240

acc ctg ctg gtc gcg ctg aac ctc ccc aag gtg ctg ccc ttc gcc gga        1068
Thr Leu Leu Val Ala Leu Asn Leu Pro Lys Val Leu Pro Phe Ala Gly
                245                 250                 255
gga ccg gtg ctg ctg gcc gtc atc gtc gtc ggc ctg ggc ttc tcg tgg        1116
Gly Pro Val Leu Leu Ala Val Ile Val Val Gly Leu Gly Phe Ser Trp
```

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            260                 265                 270
gtc ggc tgg cga cgc tcc ctc cgt gcc cgc gcc gcc gcc ggg cag ccc      1164
Val Gly Trp Arg Arg Ser Leu Arg Ala Arg Ala Ala Ala Gly Gln Pro
        275                 280                 285
gtc acc gga acg acg agc acc ccc acc gga cag tcg gtg ggg gtg cgg      1212
Val Thr Gly Thr Thr Ser Thr Pro Thr Gly Gln Ser Val Gly Val Arg
    290                 295                 300
tag ggcgggggct acagggcggc gacgtcgccg atgacgtaca cggccgggga          1265
cccgatgcgg ttcccggcca tcgtcgtggc cagggttccc aacgtgcacc ggaaggaacg    1325
ctgcccagtg gtggtgccct cctggatgac ggcggccggg gtgtgggggt cgaggccggc    1385
gtcgacaagc gtggcggtga tggcggcgac gttgcgcaca cccatgatca ccgagatcgt    1445
gccgcccgcc cgcgccagcg cggcccagtc gacgagcgag tccgggtgcc ccggcggcag    1505
atgcccggag                                                          1515
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<213>  Corynebacterium humireducens
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Met Asn Thr Leu Leu Leu Ile Ala Leu Ala Gly Leu Ala Ala Gln Leu
1               5                  10                  15
Val Asp Gly Gly Leu Gly Met Gly Phe Gly Ala Thr Ser Thr Thr Ile
            20                  25                  30
Leu Ile Val Leu Ala Gly Leu Gly Pro Ala Thr Ala Ser Ala Val Val
        35                  40                  45
His Thr Ala Glu Leu Gly Thr Thr Leu Val Ser Gly Val Ser His Trp
    50                  55                  60
Arg Phe Gly Asn Val Asp Trp Gln Val Val Arg Arg Leu Ala Ile Pro
65                  70                  75                  80
Gly Ala Val Gly Ala Phe Ala Gly Ala Thr Val Leu Ser His Leu Ser
                85                  90                  95
Thr Gln Ala Ala Ala Pro Val Thr Ala Thr Ile Leu Thr Leu Ile Gly
            100                 105                 110
Ala Asn Leu Val Trp Arg Phe Ser Arg Gly Arg Ile His Pro Arg Arg
        115                 120                 125
Ala Gly Lys Gly His Ser Arg Gly Phe Leu Gly Gly Leu Gly Leu Phe
    130                 135                 140
Gly Gly Phe Ile Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
145                 150                 155                 160
Thr Ser Thr Leu Met Thr Leu Gly Arg Ala Glu Pro Arg Arg Ile Val
                165                 170                 175
Gly Thr Val Asn Thr Ala Glu Phe Leu Val Thr Ala Ala Ala Thr Ala
            180                 185                 190
Gly Phe Val Ile Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ala Ala
        195                 200                 205
Val Leu Ala Leu Leu Ile Gly Gly Val Ile Ala Ala Pro Val Ala Ala
    210                 215                 220
Trp Leu Val Thr Arg Leu Asn Pro Ala Ala Leu Gly Gly Val Val Gly
225                 230                 235                 240
Thr Leu Leu Val Ala Leu Asn Leu Pro Lys Val Leu Pro Phe Ala Gly
                245                 250                 255
Gly Pro Val Leu Leu Ala Val Ile Val Val Gly Leu Gly Phe Ser Trp
            260                 265                 270
Val Gly Trp Arg Arg Ser Leu Arg Ala Arg Ala Ala Ala Gly Gln Pro
        275                 280                 285
Val Thr Gly Thr Thr Ser Thr Pro Thr Gly Gln Ser Val Gly Val Arg
    290                 295                 300
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<222>  (301)..(2616)
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cggacaccac caccgaactg ctggaccgca tcggcatcac ccccgaccct cgggttaggg     180
agtgaggcgg gagaccgccg ccgctgcatc tcatgttgat agcgacctgc tgcacgcacc     240
gggagccccc gaagcagacc aggttgtaca cccaagattt tccgaaaggc ctccctttc      300
atg tct tcc acc gct ttc ccc acc ttc acc atc gag ggc tac ccg cgc       348
Met Ser Ser Thr Ala Phe Pro Thr Phe Thr Ile Glu Gly Tyr Pro Arg
1               5                  10                  15
gtc ggc gcc aac cgc gag ctc aag aag gcc ctc gag tcc ttc tgg gcc       396
Val Gly Ala Asn Arg Glu Leu Lys Lys Ala Leu Glu Ser Phe Trp Ala
            20                  25                  30
ggc cgc atc gac gag gag acc ttc atc tcc tcc gcg cac tcc atc cgc       444
Gly Arg Ile Asp Glu Glu Thr Phe Ile Ser Ser Ala His Ser Ile Arg
```

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        35                  40                  45
ctg gag aac tac gcc cgt ctg cgt gac ctc ggc ctg gac cag gac tac       492
Leu Glu Asn Tyr Ala Arg Leu Arg Asp Leu Gly Leu Asp Gln Asp Tyr
    50                  55                  60

gcc atc ccg gcc gac gtc gcc ctc tac gac cag gtg ctc gag acc ggc       540
Ala Ile Pro Ala Asp Val Ala Leu Tyr Asp Gln Val Leu Glu Thr Gly
65                  70                  75                  80
gtc acc gtc ggc ctg atc ggt ggc gac gcc gcc gag gtc gac ctc acc       588
Val Thr Val Gly Leu Ile Gly Gly Asp Ala Ala Glu Val Asp Leu Thr
                85                  90                  95
gag tac ttc gcc ctg gcc cgc ggc acc gcc gag cgt tcc ccg ctc gag       636
Glu Tyr Phe Ala Leu Ala Arg Gly Thr Ala Glu Arg Ser Pro Leu Glu
            100                 105                 110
atg acc aag tgg ttc gac acc aac tac cac tac ctc gtc ccg gag gtc       684
Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Val
        115                 120                 125
gcc gag gac acc gtc atc acc ccg cgc ccg cag cgc atc ctc gac atc       732
Ala Glu Asp Thr Val Ile Thr Pro Arg Pro Gln Arg Ile Leu Asp Ile
    130                 135                 140
gtc gcc gag gcc aag gag gcc ggc cac acc gtc cgt ccg ttc ctg gtc       780
Val Ala Glu Ala Lys Glu Ala Gly His Thr Val Arg Pro Phe Leu Val
145                 150                 155                 160
ggc ccg gtc acc ctg ctg gcc aag tcc aag gcc gcc gag aac gcc ggc       828
Gly Pro Val Thr Leu Leu Ala Lys Ser Lys Ala Ala Glu Asn Ala Gly
                165                 170                 175
gag ggc ttc aac ccg ctg tcc cgc ctc gag gac ctc acc gcc gcc tac       876
Glu Gly Phe Asn Pro Leu Ser Arg Leu Glu Asp Leu Thr Ala Ala Tyr
            180                 185                 190
gcc cag gtc ctc gcc gcc ctc aag gag gcc ggc gtg gag tgg gtc cag       924
Ala Gln Val Leu Ala Ala Leu Lys Glu Ala Gly Val Glu Trp Val Gln
        195                 200                 205
ctc gcc gag ccg gcc ctg gtc gcc gac ctg acc atc cgt tcc gac gcc       972
Leu Ala Glu Pro Ala Leu Val Ala Asp Leu Thr Ile Arg Ser Asp Ala
    210                 215                 220
gac ctg gcc gcc gac gcg aag gcc acc tac gag gcg ctc ctc ggc tcc      1020
Asp Leu Ala Ala Asp Ala Lys Ala Thr Tyr Glu Ala Leu Leu Gly Ser
225                 230                 235                 240
gag gac cgc ccg cag gtc ctc atc acc acc ccc tac ggt gcc ctg cgc      1068
Glu Asp Arg Pro Gln Val Leu Ile Thr Thr Pro Tyr Gly Ala Leu Arg
                245                 250                 255
aac ggc ctc gac gcc ctc gtc gcc gcc aag ccg gag gcc ctg cag gtc      1116
Asn Gly Leu Asp Ala Leu Val Ala Ala Lys Pro Glu Ala Leu Gln Val
            260                 265                 270
gac ctc gca ccg gtc acc ctc gcc aac gag gag ggc tac gtc gag cgc      1164
Asp Leu Ala Pro Val Thr Leu Ala Asn Glu Glu Gly Tyr Val Glu Arg
        275                 280                 285
gtc gcc aag gca gtc gcc ggc acc ggc atc acc ctg gcc gcc ggc gtc      1212
Val Ala Lys Ala Val Ala Gly Thr Gly Ile Thr Leu Ala Ala Gly Val
    290                 295                 300
atc gac ggc cgc aac atc tgg gcc gcc gac ctg cgc gag cgc ctc tcc      1260
Ile Asp Gly Arg Asn Ile Trp Ala Ala Asp Leu Arg Glu Arg Leu Ser
305                 310                 315                 320
gtc ctg gag gag ctg aag aag ggc ggc gtc gag aag atc gcc gtc acc      1308
Val Leu Glu Glu Leu Lys Lys Gly Gly Val Glu Lys Ile Ala Val Thr
                325                 330                 335
tcc tcc gtc tcc ctg cag cac gtc ccg cac acc gtc tcc gtg gag aag      1356
Ser Ser Val Ser Leu Gln His Val Pro His Thr Val Ser Val Glu Lys
            340                 345                 350
aac ctc ccg gtc gac gtc gcc ggc tgg ctc tcc ttc gcc gac gag aag      1404
Asn Leu Pro Val Asp Val Ala Gly Trp Leu Ser Phe Ala Asp Glu Lys
        355                 360                 365
atc ggc gag gca cag gcc ctg gcc acc gca ctc gag ggc ggc tcc gtc      1452
Ile Gly Glu Ala Gln Ala Leu Ala Thr Ala Leu Glu Gly Gly Ser Val
    370                 375                 380
gcc gcc gca gac gcc ttc gcc cgc tcc gac cgc gcc gtg cgc acc cgt      1500
Ala Ala Ala Asp Ala Phe Ala Arg Ser Asp Arg Ala Val Arg Thr Arg
385                 390                 395                 400
cgt gag tcc gcc cgc acc cac aac cag gcc gtc cag gac cgc gtc gcc      1548
Arg Glu Ser Ala Arg Thr His Asn Gln Ala Val Gln Asp Arg Val Ala
                405                 410                 415
gct ctg ccg gac ggc cag gtc gca cgc gag ccg gag ttc gag ggc cgc      1596
Ala Leu Pro Asp Gly Gln Val Ala Arg Glu Pro Glu Phe Glu Gly Arg
            420                 425                 430
gtc gag gca cag aag gtg ctc aac ctg ccg aag ctg ccg acc acc acg      1644
Val Glu Ala Gln Lys Val Leu Asn Leu Pro Lys Leu Pro Thr Thr Thr
        435                 440                 445
atc ggc tcc ttc ccg cag acc acc gag atc cgc aag gca cgc gcc gac      1692
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Ile Gly Ser Phe Pro Gln Thr Thr Glu Ile Arg Lys Ala Arg Ala Asp
    450                 455                 460
cac cgc tcc ggc gcc ctc acc gac gag cag tac acc gac gcc ctc aag      1740
His Arg Ser Gly Ala Leu Thr Asp Glu Gln Tyr Thr Asp Ala Leu Lys
465                 470                 475                 480

gac gag gtc aag tcc gtc atc gag ctg cag gag cgc ctc ggc atc gac      1788
Asp Glu Val Lys Ser Val Ile Glu Leu Gln Glu Arg Leu Gly Ile Asp
                485                 490                 495
gtc ctc gtc cac ggc gag ccc gag cgc aac gac atg gtc cag tac ttc      1836
Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe
            500                 505                 510
gcc gag ctt ctc gac ggc ttc gtg acc acc gag cac ggc tgg gtc cag      1884
Ala Glu Leu Leu Asp Gly Phe Val Thr Thr Glu His Gly Trp Val Gln
        515                 520                 525
tcc tac ggc tcc cgc tgc acc cgc ccg tcc atc gtc gtc ggc gac gtc      1932
Ser Tyr Gly Ser Arg Cys Thr Arg Pro Ser Ile Val Val Gly Asp Val
    530                 535                 540
tcc cgc ccg aag gcc atg acc gtc gag tgg gcc aag tac gcc cag tcc      1980
Ser Arg Pro Lys Ala Met Thr Val Glu Trp Ala Lys Tyr Ala Gln Ser
545                 550                 555                 560
ctc tcc gac aag cac gtc aag ggc atg ctg acc ggc ccg gtc acc atc      2028
Leu Ser Asp Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile
                565                 570                 575
ctc gcg tgg tcc ttc acc cgt gac gac gtt ccg aag tcc gtc tcc gcc      2076
Leu Ala Trp Ser Phe Thr Arg Asp Asp Val Pro Lys Ser Val Ser Ala
            580                 585                 590
gac cag atc ggc gtc gcc ctc gcc gac gag gtc gcc gac ctc gag gcc      2124
Asp Gln Ile Gly Val Ala Leu Ala Asp Glu Val Ala Asp Leu Glu Ala
        595                 600                 605
gcc ggc atc aac gtc atc cag atc gac gag ccg gcc ctg cgc gag ctg      2172
Ala Gly Ile Asn Val Ile Gln Ile Asp Glu Pro Ala Leu Arg Glu Leu
    610                 615                 620
ctg ccg ctg cgt gag gag gac cgc ccg gca tac ctg gac tgg gcc gtc      2220
Leu Pro Leu Arg Glu Glu Asp Arg Pro Ala Tyr Leu Asp Trp Ala Val
625                 630                 635                 640
cgc tcc ttc cgc ctc gtc tcc ctg gac gcg aag ccg acc acc cag atc      2268
Arg Ser Phe Arg Leu Val Ser Leu Asp Ala Lys Pro Thr Thr Gln Ile
                645                 650                 655
cac acc cac ctc tgc tac tcg gag ttc ggg cag atc atc gac gcc gtc      2316
His Thr His Leu Cys Tyr Ser Glu Phe Gly Gln Ile Ile Asp Ala Val
            660                 665                 670
gcc gcc ctc gac gcc gac gtc acc tcc atc gag gcc gcc cgc tcc cgc      2364
Ala Ala Leu Asp Ala Asp Val Thr Ser Ile Glu Ala Ala Arg Ser Arg
        675                 680                 685
atg gag ctg ctg ggt gac ctg gac gag tcc ttc cac tcc gag atc ggc      2412
Met Glu Leu Leu Gly Asp Leu Asp Glu Ser Phe His Ser Glu Ile Gly
    690                 695                 700
ccg ggc atc tgg gac atc cac tcc ccg cgc gtc ccg gac gtc gcc gag      2460
Pro Gly Ile Trp Asp Ile His Ser Pro Arg Val Pro Asp Val Ala Glu
705                 710                 715                 720
ctc acc gag ctg atc aag gcc gcc ctg gtc aac gtc ccg acc gag cgc      2508
Leu Thr Glu Leu Ile Lys Ala Ala Leu Val Asn Val Pro Thr Glu Arg
                725                 730                 735
ctc tgg gtc aac ccg gac tgc ggt ctg aag acc cgc ggc tac gcc gag      2556
Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Tyr Ala Glu
            740                 745                 750
acc gag gcg tcc ctg cgc aac atg gtc ctc gcc cgc gac ctc gtg gtc      2604
Thr Glu Ala Ser Leu Arg Asn Met Val Leu Ala Arg Asp Leu Val Val
        755                 760                 765
gag tcc ctg taa cacctgcgta gcaactacgt tgcgggcccg gttccacttc           2656
Glu Ser Leu
    770
ggtggggccg ggcccctcgt gattccgggg gcggctagcg ctcgtcgatg acctccgcga     2716
aggcggccac cttccggcgg agatcctcga tgagggcgtc cccgtccctc cgggacttct     2776
cctccgacgc cgggtcatcc cagcctgtct cccagtggtg gtgggaccgc cagtggtcgc     2836
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gataggtgtc cgtgccgttc                                                2916
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1               5                  10                  15
Val Gly Ala Asn Arg Glu Leu Lys Lys Ala Leu Glu Ser Phe Trp Ala
            20                  25                  30
Gly Arg Ile Asp Glu Glu Thr Phe Ile Ser Ser Ala His Ser Ile Arg
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        35                  40                  45
Leu Glu Asn Tyr Ala Arg Leu Arg Asp Leu Gly Leu Asp Gln Asp Tyr
    50                  55                  60
Ala Ile Pro Ala Asp Val Ala Leu Tyr Asp Gln Val Leu Glu Thr Gly
65                  70                  75                  80
Val Thr Val Gly Leu Ile Gly Gly Asp Ala Ala Glu Val Asp Leu Thr
                85                  90                  95
Glu Tyr Phe Ala Leu Ala Arg Gly Thr Ala Glu Arg Ser Pro Leu Glu
            100                 105                 110
Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Val
        115                 120                 125
Ala Glu Asp Thr Val Ile Thr Pro Arg Pro Gln Arg Ile Leu Asp Ile
    130                 135                 140
Val Ala Glu Ala Lys Glu Ala Gly His Thr Val Arg Pro Phe Leu Val
145                 150                 155                 160
Gly Pro Val Thr Leu Leu Ala Lys Ser Lys Ala Ala Glu Asn Ala Gly
                165                 170                 175
Glu Gly Phe Asn Pro Leu Ser Arg Leu Glu Asp Leu Thr Ala Ala Tyr
            180                 185                 190
Ala Gln Val Leu Ala Ala Leu Lys Glu Ala Gly Val Glu Trp Val Gln
        195                 200                 205
Leu Ala Glu Pro Ala Leu Val Ala Asp Leu Thr Ile Arg Ser Asp Ala
    210                 215                 220
Asp Leu Ala Ala Asp Ala Lys Ala Thr Tyr Glu Ala Leu Leu Gly Ser
225                 230                 235                 240
Glu Asp Arg Pro Gln Val Leu Ile Thr Thr Pro Tyr Gly Ala Leu Arg
                245                 250                 255
Asn Gly Leu Asp Ala Leu Val Ala Ala Lys Pro Glu Ala Leu Gln Val
            260                 265                 270
Asp Leu Ala Pro Val Thr Leu Ala Asn Glu Glu Gly Tyr Val Glu Arg
        275                 280                 285
Val Ala Lys Ala Val Ala Gly Thr Gly Ile Thr Leu Ala Ala Gly Val
    290                 295                 300
Ile Asp Gly Arg Asn Ile Trp Ala Ala Asp Leu Arg Glu Arg Leu Ser
305                 310                 315                 320
Val Leu Glu Glu Leu Lys Lys Gly Gly Val Glu Lys Ile Ala Val Thr
                325                 330                 335
Ser Ser Val Ser Leu Gln His Val Pro His Thr Val Ser Val Glu Lys
            340                 345                 350
Asn Leu Pro Val Asp Val Ala Gly Trp Leu Ser Phe Ala Asp Glu Lys
        355                 360                 365
Ile Gly Glu Ala Gln Ala Leu Ala Thr Ala Leu Glu Gly Gly Ser Val
    370                 375                 380
Ala Ala Ala Asp Ala Phe Ala Arg Ser Asp Arg Ala Val Arg Thr Arg
385                 390                 395                 400
Arg Glu Ser Ala Arg Thr His Asn Gln Ala Val Gln Asp Arg Val Ala
                405                 410                 415
Ala Leu Pro Asp Gly Gln Val Ala Arg Glu Pro Glu Phe Glu Gly Arg
            420                 425                 430
Val Glu Ala Gln Lys Val Leu Asn Leu Pro Lys Leu Pro Thr Thr Thr
        435                 440                 445
Ile Gly Ser Phe Pro Gln Thr Thr Glu Ile Arg Lys Ala Arg Ala Asp
    450                 455                 460
His Arg Ser Gly Ala Leu Thr Asp Glu Gln Tyr Thr Asp Ala Leu Lys
465                 470                 475                 480
Asp Glu Val Lys Ser Val Ile Glu Leu Gln Glu Arg Leu Gly Ile Asp
                485                 490                 495
Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe
            500                 505                 510
Ala Glu Leu Leu Asp Gly Phe Val Thr Thr Glu His Gly Trp Val Gln
        515                 520                 525
Ser Tyr Gly Ser Arg Cys Thr Arg Pro Ser Ile Val Val Gly Asp Val
    530                 535                 540
Ser Arg Pro Lys Ala Met Thr Val Glu Trp Ala Lys Tyr Ala Gln Ser
545                 550                 555                 560
Leu Ser Asp Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile
                565                 570                 575
Leu Ala Trp Ser Phe Thr Arg Asp Asp Val Pro Lys Ser Val Ser Ala
            580                 585                 590
Asp Gln Ile Gly Val Ala Leu Ala Asp Glu Val Ala Asp Leu Glu Ala
        595                 600                 605
Ala Gly Ile Asn Val Ile Gln Ile Asp Glu Pro Ala Leu Arg Glu Leu
    610                 615                 620
Leu Pro Leu Arg Glu Glu Asp Arg Pro Ala Tyr Leu Asp Trp Ala Val
625                 630                 635                 640
Arg Ser Phe Arg Leu Val Ser Leu Asp Ala Lys Pro Thr Thr Gln Ile
                645                 650                 655
His Thr His Leu Cys Tyr Ser Glu Phe Gly Gln Ile Ile Asp Ala Val
```

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            660                 665                 670
Ala Ala Leu Asp Ala Asp Val Thr Ser Ile Glu Ala Ala Arg Ser Arg
        675                 680                 685
Met Glu Leu Leu Gly Asp Leu Asp Glu Ser Phe His Ser Glu Ile Gly
    690                 695                 700
Pro Gly Ile Trp Asp Ile His Ser Pro Arg Val Pro Asp Val Ala Glu
705                 710                 715                 720
Leu Thr Glu Leu Ile Lys Ala Ala Leu Val Asn Val Pro Thr Glu Arg
                725                 730                 735
Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Tyr Ala Glu
            740                 745                 750
Thr Glu Ala Ser Leu Arg Asn Met Val Leu Ala Arg Asp Leu Val Val
        755                 760                 765
Glu Ser Leu
    770
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acacggcgga cgtcggcaag cgactcgaag ggcgcctgcc gcgtgaacag attgacggcg      120
tagggccccg tgacctgcgc cagctgctcc tccaggagcg cggcgggcgc gccgcccggc      180
gcgaggaaac cgagggaacc ggcggctgcg gcggcgtcga caagcgcggg cgacgagggg      240
ccgccggcca tgggcgcgac gatgatctgc gggatgtcca tgtgtgagag actatcgggc      300
gtg ttc aag atc ttc gac ctc ttc cgc cgc aag cag acg acc ccg gcg        348
Val Phe Lys Ile Phe Asp Leu Phe Arg Arg Lys Gln Thr Thr Pro Ala
1               5                   10                  15
ctc agc gcc gac tgg atc atc ctc ggc ctg ggc aac ccg ggg ccg aaa        396
Leu Ser Ala Asp Trp Ile Ile Leu Gly Leu Gly Asn Pro Gly Pro Lys
            20                  25                  30
tac gcc gcc acg cgc cac aac gtg ggc tac atg gcc gtc gac gag ctt        444
Tyr Ala Ala Thr Arg His Asn Val Gly Tyr Met Ala Val Asp Glu Leu
        35                  40                  45
ctc gac gcc acc ccg ctc cag ccc ctc ccc ggt acg aag gca ctg cac        492
Leu Asp Ala Thr Pro Leu Gln Pro Leu Pro Gly Thr Lys Ala Leu His
    50                  55                  60
gcg aag acg atg atc gcg ggg cag gac gtg ctc gtg ctg cgt tcg acg        540
Ala Lys Thr Met Ile Ala Gly Gln Asp Val Leu Val Leu Arg Ser Thr
65                  70                  75                  80
acc tac atg aac ctc tcc ggc gag gct gtc gcc cca ctc gcg gag cag        588
Thr Tyr Met Asn Leu Ser Gly Glu Ala Val Ala Pro Leu Ala Glu Gln
                85                  90                  95
ctc ggg gtg ccg gcg gag cgg atc atc gcc atc cac gac gag ctc gac        636
Leu Gly Val Pro Ala Glu Arg Ile Ile Ala Ile His Asp Glu Leu Asp
            100                 105                 110
ctg ccg gtg ggc acc gtg cgg gtg aag aag ggc ggc aac gag aac ggc        684
Leu Pro Val Gly Thr Val Arg Val Lys Lys Gly Gly Asn Glu Asn Gly
        115                 120                 125
cac aac ggc ctg aag tcc atg acc gag cac ctg ggc acc cgc gac tac        732
His Asn Gly Leu Lys Ser Met Thr Glu His Leu Gly Thr Arg Asp Tyr
    130                 135                 140
ctg cgg gtg cgc atc ggc atc gcc cgc ccg ccg cag ggc gtg tcg gtg        780
Leu Arg Val Arg Ile Gly Ile Ala Arg Pro Pro Gln Gly Val Ser Val
145                 150                 155                 160
acc gac cat gtc ctc ggc ccc atc gac ggc ggc gag aac atc cgc ctg        828
Thr Asp His Val Leu Gly Pro Ile Asp Gly Gly Glu Asn Ile Arg Leu
                165                 170                 175
gcc gcc gag gcg gcg cgg ctc atc gtc gag cag ggg ctg ggc agg gcg        876
Ala Ala Glu Ala Ala Arg Leu Ile Val Glu Gln Gly Leu Gly Arg Ala
            180                 185                 190
cag aac gtc atc cac gcg cgg tga tcgcccccgg gcgctgctgc accaaagggg       930
Gln Asn Val Ile His Ala Arg
        195
gtattcgagt cggggcattg atcgggtgac gcccacgcgc tacccgatca atgcctcagt      990
tcgaataccc cctcggcccc ggcggccccg caggatctac ttcgccatct gcgcgacgag     1050
cttctccagg tcgccgagca tcgtctccag ctcgccgagg cgacgctcct gcggggagaa     1110
cacgccctcc tccgcgtcgt tgaaggtcga caggtacacc tggttgcgca cgtcgtactg     1170
ctggaagttg ccgacgatct gccgccagct                                     1200
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1               5                  10                  15
Leu Ser Ala Asp Trp Ile Ile Leu Gly Leu Gly Asn Pro Gly Pro Lys
            20                  25                  30
Tyr Ala Ala Thr Arg His Asn Val Gly Tyr Met Ala Val Asp Glu Leu
        35                  40                  45
Leu Asp Ala Thr Pro Leu Gln Pro Leu Pro Gly Thr Lys Ala Leu His
    50                  55                  60
Ala Lys Thr Met Ile Ala Gly Gln Asp Val Leu Val Leu Arg Ser Thr
65                  70                  75                  80
Thr Tyr Met Asn Leu Ser Gly Glu Ala Val Ala Pro Leu Ala Glu Gln
                85                  90                  95
Leu Gly Val Pro Ala Glu Arg Ile Ile Ala Ile His Asp Glu Leu Asp
            100                 105                 110
Leu Pro Val Gly Thr Val Arg Val Lys Lys Gly Gly Asn Glu Asn Gly
        115                 120                 125
His Asn Gly Leu Lys Ser Met Thr Glu His Leu Gly Thr Arg Asp Tyr
    130                 135                 140
Leu Arg Val Arg Ile Gly Ile Ala Arg Pro Pro Gln Gly Val Ser Val
145                 150                 155                 160

Thr Asp His Val Leu Gly Pro Ile Asp Gly Gly Glu Asn Ile Arg Leu
                165                 170                 175
Ala Ala Glu Ala Ala Arg Leu Ile Val Glu Gln Gly Leu Gly Arg Ala
            180                 185                 190
Gln Asn Val Ile His Ala Arg
        195
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tcaccctgcc ggaggacgtc accctggtcg acgacgccga gctgctcgtc ttcaacatca      120
ccttcgagga ggtcgccgac gttccggagg agggcgagga ggccaccgaa gacgctgtcg      180
gcgaggccgg caaggacgag gctgccgagg gcgaggagta gtcactcccc ttccgccacg      240
tgtgacgccc ctgaccggcc ggtcaggggc gtctcccctt ttctgtgcca gactgatcgg      300
gtg act gat tct cca ctt ctc atc gtc ggc ctg ggt aac ccg ggc gcg        348
Val Thr Asp Ser Pro Leu Leu Ile Val Gly Leu Gly Asn Pro Gly Ala
1               5                  10                  15
aag tac gcc gac acc cgc cac aac atc ggc gtc atg ctt ctc gac gag        396
Lys Tyr Ala Asp Thr Arg His Asn Ile Gly Val Met Leu Leu Asp Glu
            20                  25                  30
ctc gcc tcc cgc atc acc ccc gtc ccc gcc agc ttc gcc gtg cac aag        444
Leu Ala Ser Arg Ile Thr Pro Val Pro Ala Ser Phe Ala Val His Lys
        35                  40                  45
cgc acg aac acc gag gtc gcc gag gtc cgt cat cgc ggc cgt cgc ctc        492
Arg Thr Asn Thr Glu Val Ala Glu Val Arg His Arg Gly Arg Arg Leu
    50                  55                  60
gtg ctg gcc cgg acc cgc ggc tac atg aac gtc tcc ggt gga ccg gtg        540
Val Leu Ala Arg Thr Arg Gly Tyr Met Asn Val Ser Gly Gly Pro Val
65                  70                  75                  80
aag gca ctg gcg acc ttc ttc agg atc gcc ccc ggc gac atc atc gtc        588
Lys Ala Leu Ala Thr Phe Phe Arg Ile Ala Pro Gly Asp Ile Ile Val
                85                  90                  95
gcc cac gac gaa ctc gag ctg gac ttc ggc gag cac cgc ctc cgc acc        636
Ala His Asp Glu Leu Glu Leu Asp Phe Gly Glu His Arg Leu Arg Thr
            100                 105                 110
ggc ggc ggc gac cac ggc cac aac ggc ctg aag tcc gtg acc aag tcg        684
Gly Gly Gly Asp His Gly His Asn Gly Leu Lys Ser Val Thr Lys Ser
        115                 120                 125
ctg gga acg aag gag tac cag cgc ctg gcg ctc ggc atc ggc cgt ccg        732
Leu Gly Thr Lys Glu Tyr Gln Arg Leu Ala Leu Gly Ile Gly Arg Pro
    130                 135                 140
ccc ggg cgt atg gac ccc gcc gcc ttc gtg ctc aag ccc ttc acc cgc        780
Pro Gly Arg Met Asp Pro Ala Ala Phe Val Leu Lys Pro Phe Thr Arg
145                 150                 155                 160
cag gag gcc ggg gag ctg ccc ttc ctg ctc tcc gac gcc gcc gac gaa        828
Gln Glu Ala Gly Glu Leu Pro Phe Leu Leu Ser Asp Ala Ala Asp Glu
                165                 170                 175
ctc gaa cgc gcc ctc tga cctcccaggg tggaacctgg tcccggaagg                876
Leu Glu Arg Ala Leu
            180
ttccggacgc tgcccgggtg tctagatggt gagctcctcc ggggccgcct ccccctcgcg      936
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ccgggcgatg atcttgtgga tctggtactc ccactcctgc agctcctccg gcagctcccc      996
cttcgagggg tcacggagat actcgcgacg cccggcgtcg tagccccaca gccagtcgac     1056
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gacgccgtcg acgtgccaca gctccccca                                       1146
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1               5                  10                  15
Lys Tyr Ala Asp Thr Arg His Asn Ile Gly Val Met Leu Leu Asp Glu
            20                  25                  30
Leu Ala Ser Arg Ile Thr Pro Val Pro Ala Ser Phe Ala Val His Lys
        35                  40                  45
Arg Thr Asn Thr Glu Val Ala Glu Val Arg His Arg Gly Arg Arg Leu
    50                  55                  60
Val Leu Ala Arg Thr Arg Gly Tyr Met Asn Val Ser Gly Gly Pro Val
65                  70                  75                  80
Lys Ala Leu Ala Thr Phe Phe Arg Ile Ala Pro Gly Asp Ile Ile Val
                85                  90                  95
Ala His Asp Glu Leu Glu Leu Asp Phe Gly Glu His Arg Leu Arg Thr
            100                 105                 110
Gly Gly Gly Asp His Gly His Asn Gly Leu Lys Ser Val Thr Lys Ser
        115                 120                 125
Leu Gly Thr Lys Glu Tyr Gln Arg Leu Ala Leu Gly Ile Gly Arg Pro
    130                 135                 140
Pro Gly Arg Met Asp Pro Ala Ala Phe Val Leu Lys Pro Phe Thr Arg
145                 150                 155                 160
Gln Glu Ala Gly Glu Leu Pro Phe Leu Leu Ser Asp Ala Ala Asp Glu
                165                 170                 175
Leu Glu Arg Ala Leu
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gtcggtctcc gacctctacg cgccggtcac gggcaccgtc accgaggtca acgacgcggt      180
ccacgacgac tacgccgtga tcaacgacga ccccttcggc gcgggctggc tcttcgccgt      240
cgaggtcgac gaggtcggac cgctcatgac cgccgccgag tacgcggagg ccaacggcgt      300
gtg acc gcc cgg gac cgg tac cct ggt ccc atc atg act gca ccc cgt         348
Val Thr Ala Arg Asp Arg Tyr Pro Gly Pro Ile Met Thr Ala Pro Arg
1               5                  10                  15
gag ccc ttc ttc cct gcg gac cgt tcc atc cgt gcc tcc ggc gag ccc        396
Glu Pro Phe Phe Pro Ala Asp Arg Ser Ile Arg Ala Ser Gly Glu Pro
            20                  25                  30
ccg gag atc cgt tat ctc ggc gtc gtc gac tac cag gag gcc tgg aat        444
Pro Glu Ile Arg Tyr Leu Gly Val Val Asp Tyr Gln Glu Ala Trp Asn
        35                  40                  45
ctg cag gcc gag ctg gcg tcg caa cgc gcg gcc ggg gag atc ggt gac        492
Leu Gln Ala Glu Leu Ala Ser Gln Arg Ala Ala Gly Glu Ile Gly Asp
    50                  55                  60
cag ctc ctc atc ctc gag cac ccg agc gtg tac acc gcc ggc aag cgc        540
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
65                  70                  75                  80
acg cag ccg gag gac cgc ccc acc aac ggc ctg ccg gtc atc gac gtc        588
Thr Gln Pro Glu Asp Arg Pro Thr Asn Gly Leu Pro Val Ile Asp Val
                85                  90                  95
gac cgg ggt ggc cgc atc acc tgg cac ggc gag gga cag ctg gtg gtc        636
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Glu Gly Gln Leu Val Val
            100                 105                 110
tac ccg atc atc aaa ctg gcc gac ccg gtg gac gtc gtg gac tat gtc        684
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Val Asp Val Val Asp Tyr Val
        115                 120                 125
cgc cgc ctc gag gag gcg gtg atc gcg acg gtg cgg gag gtg ggc gtc        732
Arg Arg Leu Glu Glu Ala Val Ile Ala Thr Val Arg Glu Val Gly Val
    130                 135                 140
ggc aat gcg ggt cgc atc gac ggc cgc tcc gga gtc tgg gtc ccc gcc        780
Gly Asn Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala
145                 150                 155                 160
gac ggg acc cga cgc gac cgg aag gtg gcg gcg ctc ggc atc cgt gtc        828
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Asp Gly Thr Arg Arg Asp Arg Lys Val Ala Ala Leu Gly Ile Arg Val
                165                 170                 175
acc cgc ggg gtg acc atg cac ggg ctg agc ctg aac tgc tcg aac acg      876
Thr Arg Gly Val Thr Met His Gly Leu Ser Leu Asn Cys Ser Asn Thr
            180                 185                 190
ctc gag cac tac ggg cac atc gtg gcg tgc ggc atc gac gac gcc gac      924
Leu Glu His Tyr Gly His Ile Val Ala Cys Gly Ile Asp Asp Ala Asp
        195                 200                 205
gtc acc acc ctc agc atg gaa ctg ggg cgc gac gtc agc gtc ggg gag      972
Val Thr Thr Leu Ser Met Glu Leu Gly Arg Asp Val Ser Val Gly Glu
    210                 215                 220
gtc acg gca ccg ctt gtc gac gcc ctc ctg gcc gcc ctc gcc ggt gaa     1020
Val Thr Ala Pro Leu Val Asp Ala Leu Leu Ala Ala Leu Ala Gly Glu
225                 230                 235                 240
ctc gcc gtc gcg gac cac acc ttc gga tcg gcg ccc gat ccg acg aag     1068
Leu Ala Val Ala Asp His Thr Phe Gly Ser Ala Pro Asp Pro Thr Lys
                245                 250                 255
att ccc gcg aaa acg cgc tga cctctaagtt tatccctatc agtagaaaga        1119
Ile Pro Ala Lys Thr Arg
            260
gtatggtggc gttgtgacta tcgcacctga aggacgcaag ctgctccggg tggagaagcg    1179
caatgcgcag acccccatcg agacgaagcc ccgttggatc cgcaacgcgg tgaagaccgg    1239
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Glu Pro Phe Phe Pro Ala Asp Arg Ser Ile Arg Ala Ser Gly Glu Pro
            20                  25                  30
Pro Glu Ile Arg Tyr Leu Gly Val Val Asp Tyr Gln Glu Ala Trp Asn
        35                  40                  45
Leu Gln Ala Glu Leu Ala Ser Gln Arg Ala Ala Gly Glu Ile Gly Asp
    50                  55                  60
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg
65                  70                  75                  80
Thr Gln Pro Glu Asp Arg Pro Thr Asn Gly Leu Pro Val Ile Asp Val
                85                  90                  95
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Glu Gly Gln Leu Val Val
            100                 105                 110
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Val Asp Val Val Asp Tyr Val
        115                 120                 125
Arg Arg Leu Glu Glu Ala Val Ile Ala Thr Val Arg Glu Val Gly Val
    130                 135                 140
Gly Asn Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala
145                 150                 155                 160
Asp Gly Thr Arg Arg Asp Arg Lys Val Ala Ala Leu Gly Ile Arg Val
                165                 170                 175
Thr Arg Gly Val Thr Met His Gly Leu Ser Leu Asn Cys Ser Asn Thr
            180                 185                 190
Leu Glu His Tyr Gly His Ile Val Ala Cys Gly Ile Asp Asp Ala Asp
        195                 200                 205
Val Thr Thr Leu Ser Met Glu Leu Gly Arg Asp Val Ser Val Gly Glu
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Val Thr Ala Pro Leu Val Asp Ala Leu Leu Ala Ala Leu Ala Gly Glu
225                 230                 235                 240
Leu Ala Val Ala Asp His Thr Phe Gly Ser Ala Pro Asp Pro Thr Lys
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Ile Pro Ala Lys Thr Arg
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ggccatcggc ctcttctagg tcgaccccgg aagcatctgc ttatcgacgc cccggccccc     180
ggtcggggcg ttcgtcgttg cggcaccaca gtcccgccac cgtcccaccg cccccacggg     240
ggcgggatcc ttttgtgggg ggcggtgaca cgggggaaac ggtcacctat ccttggtggc     300
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gtg act gaa cat tat gac gtt gtt gta ctc ggt gcg ggc ccc ggt ggc        348
Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
1               5                  10                  15
tac gtc gcc gcc atc cgc gca gcc cag ctc ggc aag aag gtt gct gtc        396
Tyr Val Ala Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
            20                  25                  30
gtc gag aag cag tac tgg ggc gga gtc tgc ctc aac gtg ggc tgc atc        444
Val Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
        35                  40                  45
ccc tcg aag gcg ctg atc aag aac gcc gag atc gcc cac atc ttc acg        492
Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Thr
    50                  55                  60
cac gag aag aag acg ttc ggc atc aac ggc gac gtc tcc ttc aac tac        540
His Glu Lys Lys Thr Phe Gly Ile Asn Gly Asp Val Ser Phe Asn Tyr
65                  70                  75                  80
gag gac gcc cac aag cgc tcc cgt cag gtg tcg gag aag atc gtc ggc        588
Glu Asp Ala His Lys Arg Ser Arg Gln Val Ser Glu Lys Ile Val Gly
                85                  90                  95
ggc gtc cac tac ctg atg aag aag aac aag atc acc gag atc gac ggc        636
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
            100                 105                 110
ttc gga acc ttc agg gac gcc aag acc atc gag gtc agc gag ggc aag        684
Phe Gly Thr Phe Arg Asp Ala Lys Thr Ile Glu Val Ser Glu Gly Lys
        115                 120                 125
gac gcc ggc aag gtc gtc acc ttc gac gac tgc atc atc gcc acc ggc        732
Asp Ala Gly Lys Val Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    130                 135                 140
tcc gtg gtc aac agc ctc cgt ggc gtc gag ttc tcc gag aac gtc gtc        780
Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
145                 150                 155                 160
tcc tac gag gag cag atc ctc aac ccg gtc gcc ccg gag aag atg gtc        828
Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Glu Lys Met Val
                165                 170                 175
atc gtc ggt gcc ggc gcc atc ggc atg gag ttc gcc tac gtg ctc tcc        876
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Ser
            180                 185                 190
aac tac ggc gtc gac gtc acc gtc atc gag tac atg gac cgt gtc ctg        924
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Tyr Met Asp Arg Val Leu
        195                 200                 205
ccg aac gag gac gag gac gtc tcc aag gtc atc gcc aag gcc tac aag        972
Pro Asn Glu Asp Glu Asp Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
    210                 215                 220
aag atg ggc gtc acg ctc ctc ccg ggc cac gcc acc acc gcc gtg cgc       1020
Lys Met Gly Val Thr Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
225                 230                 235                 240
gac aac ggc gac tcc gtc gag gtc gac tac cag aag aag ggc tcg gac       1068
Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                245                 250                 255
aag acc gag acc atc gtc gcc gac cgc gtc ctc gtc tcc gtc ggc ttc       1116
Lys Thr Glu Thr Ile Val Ala Asp Arg Val Leu Val Ser Val Gly Phe
            260                 265                 270
cgc ccg cgt gtc gag ggc ttc ggc ctg gag aac acc ggc gtc gag ctc       1164
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Glu Leu
        275                 280                 285
acc gag cgc ggt gcc atc gcc atc gac gac ttc atg cgc acc aac gtc       1212
Thr Glu Arg Gly Ala Ile Ala Ile Asp Asp Phe Met Arg Thr Asn Val
    290                 295                 300
gag cac atc tac gcc atc ggt gac gtc acc gcc aag ctg cag ctg gcc       1260
Glu His Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
305                 310                 315                 320
cac gtc gcc gag gcg cag ggc atc gtc gcc gcc gag acc atc gcc ggc       1308
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                325                 330                 335
gcc gag acc cac gag ctg ggc gac tac atg atg atg ccg cgc gcc acc       1356
Ala Glu Thr His Glu Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            340                 345                 350
ttc tgt aac ccg cag gtc gcg tcc ttc ggc tac acc gag gcg cag gcc       1404
Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Ala Gln Ala
        355                 360                 365
aag gag aag tgg ccg gac cgc gag atc aag gtc gcg tcc ttc ccg ttc       1452
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    370                 375                 380
tcc gcg aac ggc aag gcc gtc ggc ctg gcc gag acc gag ggc ttc gcc       1500
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Glu Gly Phe Ala
385                 390                 395                 400
aag atc gtc gcc gac gcc gag tac ggc gag ctg ctg ggc ggc cac ctg       1548
Lys Ile Val Ala Asp Ala Glu Tyr Gly Glu Leu Leu Gly Gly His Leu
                405                 410                 415
```

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gtc ggc gcc aac gcg tcc gag ctg ctc aac gag ctg gtc ctc gcg cag      1596
Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
            420                 425                 430
aac tac gat ctc acc acc gag gag atc agc cgc gcg gtc cac atc cac      1644
Asn Tyr Asp Leu Thr Thr Glu Glu Ile Ser Arg Ala Val His Ile His
        435                 440                 445
ccg acc ctg tcg gag gcc gtc aag gag gcc gca cac ggc atc gac ggc      1692
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Asp Gly
    450                 455                 460
cac atg atc aac ttc tag tccccccggaa aaaggggcct cccggctggg            1740
His Met Ile Asn Phe
465
aggccccttt tctcatgctt tccgacgccc ccggggcgtc gccaagcgcc tagttgtagg    1800
gcgcgaccga cgaccggtgg gcgtcgatgg tgatctcctc gtggatcggc gggaacgcgc    1860
gctgcgcgca gttctcccgc gggcacacgc ggcagccggc gccgatcggg gtggcgctgg    1920
acaggtcggc gaggttgagt ccctgcgcgt agaccgtgcg gtcggcgtgg cgggcctcgc    1980
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            20                  25                  30
Val Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
        35                  40                  45
Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Thr
    50                  55                  60
His Glu Lys Lys Thr Phe Gly Ile Asn Gly Asp Val Ser Phe Asn Tyr
65                  70                  75                  80
Glu Asp Ala His Lys Arg Ser Arg Gln Val Ser Glu Lys Ile Val Gly
                85                  90                  95
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
            100                 105                 110
Phe Gly Thr Phe Arg Asp Ala Lys Thr Ile Glu Val Ser Glu Gly Lys
        115                 120                 125
Asp Ala Gly Lys Val Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    130                 135                 140
Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
145                 150                 155                 160
Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Glu Lys Met Val
                165                 170                 175
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Ser
            180                 185                 190
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Tyr Met Asp Arg Val Leu
        195                 200                 205
Pro Asn Glu Asp Glu Asp Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
    210                 215                 220
Lys Met Gly Val Thr Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
225                 230                 235                 240
Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                245                 250                 255
Lys Thr Glu Thr Ile Val Ala Asp Arg Val Leu Val Ser Val Gly Phe
            260                 265                 270
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Glu Leu
        275                 280                 285
Thr Glu Arg Gly Ala Ile Ala Ile Asp Asp Phe Met Arg Thr Asn Val
    290                 295                 300
Glu His Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
305                 310                 315                 320
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                325                 330                 335
Ala Glu Thr His Glu Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            340                 345                 350
Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Ala Gln Ala
        355                 360                 365
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    370                 375                 380
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Glu Gly Phe Ala
385                 390                 395                 400
Lys Ile Val Ala Asp Ala Glu Tyr Gly Glu Leu Leu Gly Gly His Leu
                405                 410                 415
Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
            420                 425                 430
Asn Tyr Asp Leu Thr Thr Glu Glu Ile Ser Arg Ala Val His Ile His
        435                 440                 445
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His Met Ile Asn Phe
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cttgtgccga cgacagccac caggccgacc ccttccgcac caagggaaga gtcaccaggt      180
agcgtttcaa ttgcattgtc cttgtgaaat taggagcttg ataacgtggc agcttcgcaa      240
acgcccaccc cggccacggt cgccaagaag tccccgggag ccgagaacgc acccgagcgg      300
atg acc ggc gcc cag gcg atc gtc cgg tcc ctc gag gag ctc ggc acc        348
Met Thr Gly Ala Gln Ala Ile Val Arg Ser Leu Glu Glu Leu Gly Thr
1               5                  10                  15
gac atc gtc ttc ggc ctg ccc ggc ggt gcc atc ctc ccc ctg tac gac       396
Asp Ile Val Phe Gly Leu Pro Gly Gly Ala Ile Leu Pro Leu Tyr Asp
            20                  25                  30
ccc ctc ttc tcc tcg aag aag ctg cgt cac gtg ctg gtg cgc cac gag        444
Pro Leu Phe Ser Ser Lys Lys Leu Arg His Val Leu Val Arg His Glu
        35                  40                  45
cag ggc tcg ggc cac gct gcc acc ggt tac gca cag gtc acc ggc aag        492
Gln Gly Ser Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Lys
    50                  55                  60
gtc ggc gtc tgc atc gcc acc tcc ggc ccg ggt gcc acc aac ctg gtc        540
Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
65                  70                  75                  80
acc ccg ctg gcc gac gcc aac ctg gac tcc gtc ccg atg gtc gcc att        588
Thr Pro Leu Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
                85                  90                  95
acc ggc cag gtc ggc cgt tcc ctg ctg ggc acc gac gcc ttc cag gag        636
Thr Gly Gln Val Gly Arg Ser Leu Leu Gly Thr Asp Ala Phe Gln Glu
            100                 105                 110
gcc gac atc cgg ggt gtg acc atg ccg atc acg aag cac aac ttc atg        684
Ala Asp Ile Arg Gly Val Thr Met Pro Ile Thr Lys His Asn Phe Met
        115                 120                 125
gtc acc gac ccc aac gac atc gcc cgc acc ctg atg gag gcc ttc cac        732
Val Thr Asp Pro Asn Asp Ile Ala Arg Thr Leu Met Glu Ala Phe His
    130                 135                 140

ctc gct ctg acc ggt cgc ccg ggc ccc gtc ctg gtc gac atc ccg aag        780
Leu Ala Leu Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
145                 150                 155                 160
gac atc cag aac gcg gag ttc gac ttc gtc tgg ccg ccg aag atg gat        828
Asp Ile Gln Asn Ala Glu Phe Asp Phe Val Trp Pro Pro Lys Met Asp
                165                 170                 175
ctg ccg ggc tac aag ccg gtc acc acg ccg cac tcc cgc cag atc acc        876
Leu Pro Gly Tyr Lys Pro Val Thr Thr Pro His Ser Arg Gln Ile Thr
            180                 185                 190
cag gcc gtc cag atg atc gcc gag gcc gag cgt ccc tgc ctc tac gtc        924
Gln Ala Val Gln Met Ile Ala Glu Ala Glu Arg Pro Cys Leu Tyr Val
        195                 200                 205
ggc ggc ggc gtc atc aag gcc gac gcc aac aag gag ctg ctg gag ttc        972
Gly Gly Gly Val Ile Lys Ala Asp Ala Asn Lys Glu Leu Leu Glu Phe
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gcc gag tac acc ggc gtc ccg gtc gtc acc acc ctc atg gcc ctg ggc       1020
Ala Glu Tyr Thr Gly Val Pro Val Val Thr Thr Leu Met Ala Leu Gly
225                 230                 235                 240
gcg ttc ccg gag tcc cac ccg ctg cac atg ggc atg ccg ggc atg cac       1068
Ala Phe Pro Glu Ser His Pro Leu His Met Gly Met Pro Gly Met His
                245                 250                 255
ggc gcc gtc ccg gcc gtc ggt gcc atg cag ggc gct gac ctg ctc atc       1116
Gly Ala Val Pro Ala Val Gly Ala Met Gln Gly Ala Asp Leu Leu Ile
            260                 265                 270
acc atc ggc gcg cgt ttc gac gac cgc gtc acc ggc aac ctc gac gag       1164
Thr Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Asp Glu
        275                 280                 285
ttc gcc ccg gac gcc cag gtc atc cac gcc gac atc gac ccg gcc gag       1212
Phe Ala Pro Asp Ala Gln Val Ile His Ala Asp Ile Asp Pro Ala Glu
    290                 295                 300
atc ggc aag atc cgc gag gcc gcc gtc ccg atc gtc ggc gac gcc cgc       1260
Ile Gly Lys Ile Arg Glu Ala Ala Val Pro Ile Val Gly Asp Ala Arg
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305                 310                 315                 320
gag gtc ctc tcc gca ctc ctg cgc acc tac aag tcc tcc aag aac ctc      1308
Glu Val Leu Ser Ala Leu Leu Arg Thr Tyr Lys Ser Ser Lys Asn Leu
                325                 330                 335
acc ccg ccg aag atc acc gag tgg gtc gag tac ctg acg gac ctc aag      1356
Thr Pro Pro Lys Ile Thr Glu Trp Val Glu Tyr Leu Thr Asp Leu Lys
            340                 345                 350
gag cgc ttc ccg cgc ggc tac gac gag cag tcg gac ggc atg atg agc      1404
Glu Arg Phe Pro Arg Gly Tyr Asp Glu Gln Ser Asp Gly Met Met Ser
        355                 360                 365
ccg cag ttc gtc atc gag acc ctg tcc aag gag gtc ggc ccg gac gcg      1452
Pro Gln Phe Val Ile Glu Thr Leu Ser Lys Glu Val Gly Pro Asp Ala
    370                 375                 380
atc tac gtc gcc ggc gtc ggc cag cac cag atg tgg gcc gcg cag ttc      1500
Ile Tyr Val Ala Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe
385                 390                 395                 400
atc gac ttc gag aag ccg cgc acc tgg ctc aac tcc ggt ggt ctg ggc      1548
Ile Asp Phe Glu Lys Pro Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly
                405                 410                 415
acg atg ggc tac tcc atc ccc gcc gcc atg ggc gcc aag gcc ggt ctg      1596
Thr Met Gly Tyr Ser Ile Pro Ala Ala Met Gly Ala Lys Ala Gly Leu
            420                 425                 430
ccg gac gcc gag gtc tgg gcc atc gac ggt gac ggc tgc ttc cag atg      1644
Pro Asp Ala Glu Val Trp Ala Ile Asp Gly Asp Gly Cys Phe Gln Met
        435                 440                 445
acc aac cag gag ctc acc acc gcc gcg gtc gag ggc ttc ccg atc aag      1692
Thr Asn Gln Glu Leu Thr Thr Ala Ala Val Glu Gly Phe Pro Ile Lys
    450                 455                 460
gtc gcc ctg atc aac aac ggc aac ctg ggc atg gtc cgc cag tgg cag      1740
Val Ala Leu Ile Asn Asn Gly Asn Leu Gly Met Val Arg Gln Trp Gln
465                 470                 475                 480
acc ctg ttc tac ggt ggc cgc tac tcg aac acg aag ctg cgt gag cag      1788
Thr Leu Phe Tyr Gly Gly Arg Tyr Ser Asn Thr Lys Leu Arg Glu Gln
                485                 490                 495
gac gag tac gtg ccg gac ttc gtc acg ctg tcc gag gcg ctc ggc tgc      1836
Asp Glu Tyr Val Pro Asp Phe Val Thr Leu Ser Glu Ala Leu Gly Cys
            500                 505                 510
gtc gcc ttc cgc gtc acc cgc gag gag gac gtc ctg ccg acg atc cag      1884
Val Ala Phe Arg Val Thr Arg Glu Glu Asp Val Leu Pro Thr Ile Gln
        515                 520                 525
aag gca cgc gag atc aac gac cgc ccg gtc gtc atc gac ttc atc gtc      1932
Lys Ala Arg Glu Ile Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val
    530                 535                 540
ggt gag gac gcc cag gtc tgg ccg atg gtc gcc gcc ggc gcc tcc aac      1980
Gly Glu Asp Ala Gln Val Trp Pro Met Val Ala Ala Gly Ala Ser Asn
545                 550                 555                 560
tcg gac atc gag tac gca cgt ggt ctg cgc ccc ttc ttc gag ggt gac      2028
Ser Asp Ile Glu Tyr Ala Arg Gly Leu Arg Pro Phe Phe Glu Gly Asp
                565                 570                 575
gag tcc gcg ggt gag tcc ccg gcc gac atc cac ggt gtc atg gag aac      2076
Glu Ser Ala Gly Glu Ser Pro Ala Asp Ile His Gly Val Met Glu Asn
            580                 585                 590
gcc cag gag gag acc gtc gag gaa gtc ctc gag gag cgc gcg aac gac      2124
Ala Gln Glu Glu Thr Val Glu Glu Val Leu Glu Glu Arg Ala Asn Asp
        595                 600                 605
agc gag aag gag aac tag gacaatggcg aacaccgaca tcatccgcaa             2172
Ser Glu Lys Glu Asn
    610
caccctcagc gtcctggtcc aggacgtcga cggcatcatc tcccgcgtcg caggcatgtt     2232
cacccgccgt ggctacaacc tggtgtccat cgtctcggcg cacaccgaca ccccgggcat     2292
cagccgcatc accatcgtgg tcgacgccaa cgagctggtc atcgagcagg tcaccaagca     2352
gctcaacaag atcatcccgg tgctcaaggt cgtccgcctc gaggaggaca ccaccatcgc     2412
ccgcgccatc atgctggtga aggtcaacgc                                      2442
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Asp Ile Val Phe Gly Leu Pro Gly Gly Ala Ile Leu Pro Leu Tyr Asp
            20                  25                  30
Pro Leu Phe Ser Ser Lys Lys Leu Arg His Val Leu Val Arg His Glu
        35                  40                  45
Gln Gly Ser Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Lys
    50                  55                  60
Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
65                  70                  75                  80
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Thr Pro Leu Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
                85                  90                  95
Thr Gly Gln Val Gly Arg Ser Leu Leu Gly Thr Asp Ala Phe Gln Glu
            100                 105                 110
Ala Asp Ile Arg Gly Val Thr Met Pro Ile Thr Lys His Asn Phe Met
        115                 120                 125
Val Thr Asp Pro Asn Asp Ile Ala Arg Thr Leu Met Glu Ala Phe His
    130                 135                 140
Leu Ala Leu Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
145                 150                 155                 160
Asp Ile Gln Asn Ala Glu Phe Asp Phe Val Trp Pro Pro Lys Met Asp
                165                 170                 175
Leu Pro Gly Tyr Lys Pro Val Thr Thr Pro His Ser Arg Gln Ile Thr
            180                 185                 190
Gln Ala Val Gln Met Ile Ala Glu Ala Glu Arg Pro Cys Leu Tyr Val
        195                 200                 205
Gly Gly Gly Val Ile Lys Ala Asp Ala Asn Lys Glu Leu Leu Glu Phe
    210                 215                 220
Ala Glu Tyr Thr Gly Val Pro Val Val Thr Thr Leu Met Ala Leu Gly
225                 230                 235                 240
Ala Phe Pro Glu Ser His Pro Leu His Met Gly Met Pro Gly Met His
                245                 250                 255
Gly Ala Val Pro Ala Val Gly Ala Met Gln Gly Ala Asp Leu Leu Ile
            260                 265                 270
Thr Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Asp Glu
        275                 280                 285
Phe Ala Pro Asp Ala Gln Val Ile His Ala Asp Ile Asp Pro Ala Glu
    290                 295                 300
Ile Gly Lys Ile Arg Glu Ala Ala Val Pro Ile Val Gly Asp Ala Arg
305                 310                 315                 320
Glu Val Leu Ser Ala Leu Leu Arg Thr Tyr Lys Ser Ser Lys Asn Leu
                325                 330                 335
Thr Pro Pro Lys Ile Thr Glu Trp Val Glu Tyr Leu Thr Asp Leu Lys
            340                 345                 350
Glu Arg Phe Pro Arg Gly Tyr Asp Glu Gln Ser Asp Gly Met Met Ser
        355                 360                 365
Pro Gln Phe Val Ile Glu Thr Leu Ser Lys Glu Val Gly Pro Asp Ala
    370                 375                 380
Ile Tyr Val Ala Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe
385                 390                 395                 400
Ile Asp Phe Glu Lys Pro Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly
                405                 410                 415
Thr Met Gly Tyr Ser Ile Pro Ala Ala Met Gly Ala Lys Ala Gly Leu
            420                 425                 430
Pro Asp Ala Glu Val Trp Ala Ile Asp Gly Asp Gly Cys Phe Gln Met
        435                 440                 445
Thr Asn Gln Glu Leu Thr Thr Ala Ala Val Glu Gly Phe Pro Ile Lys
    450                 455                 460
Val Ala Leu Ile Asn Asn Gly Asn Leu Gly Met Val Arg Gln Trp Gln
465                 470                 475                 480
Thr Leu Phe Tyr Gly Gly Arg Tyr Ser Asn Thr Lys Leu Arg Glu Gln
                485                 490                 495
Asp Glu Tyr Val Pro Asp Phe Val Thr Leu Ser Glu Ala Leu Gly Cys
            500                 505                 510
Val Ala Phe Arg Val Thr Arg Glu Glu Asp Val Leu Pro Thr Ile Gln
        515                 520                 525
Lys Ala Arg Glu Ile Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val
    530                 535                 540
Gly Glu Asp Ala Gln Val Trp Pro Met Val Ala Ala Gly Ala Ser Asn
545                 550                 555                 560
Ser Asp Ile Glu Tyr Ala Arg Gly Leu Arg Pro Phe Phe Glu Gly Asp
                565                 570                 575
Glu Ser Ala Gly Glu Ser Pro Ala Asp Ile His Gly Val Met Glu Asn
            580                 585                 590
Ala Gln Glu Glu Thr Val Glu Glu Val Leu Glu Glu Arg Ala Asn Asp
        595                 600                 605
Ser Glu Lys Glu Asn
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cctcatccca cctggtgaga caacacgcat gaaagtccca ccaggtgggg taccctgtc       240
tcatgttgtg gtacaaacaa caacagcact tgtataagac gaaaggcgag tttttctccc      300
atg gct att gaa ctg ctt tac gac gcc gac gct gac ctc tcc ctc atc         348
Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1               5                  10                  15
cag ggc cgc aag gtc gcc atc atc ggc tac ggc tcc cag ggc cac gcc        396
Gln Gly Arg Lys Val Ala Ile Ile Gly Tyr Gly Ser Gln Gly His Ala
            20                  25                  30
cac gcc cag aac ctg cgt gac tcc ggc gtc gag gtc tgc atc ggc ctg        444
His Ala Gln Asn Leu Arg Asp Ser Gly Val Glu Val Cys Ile Gly Leu
        35                  40                  45
cgc gac ggc tcc aag tcc gcg gag aag gcc aag gag gcc ggc ttc gag        492
Arg Asp Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
    50                  55                  60
gtc aag tcc aac gcc gac gcc gcc gcc tgg gca gac gtc atc atg ctg        540
Val Lys Ser Asn Ala Asp Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65                  70                  75                  80
ctc gcc ccg gac acc tcc cag aag tcc atc tac gag aac gac atc gag        588
Leu Ala Pro Asp Thr Ser Gln Lys Ser Ile Tyr Glu Asn Asp Ile Glu
                85                  90                  95
ccg aac ctc aac gac ggt gac gcc ctg ctg ttc ggc cac ggc ctg aac        636
Pro Asn Leu Asn Asp Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
            100                 105                 110
gtc cac ttc ggc ctg atc aag ccg gcc gag aac atc gtc gtc ggc atg        684
Val His Phe Gly Leu Ile Lys Pro Ala Glu Asn Ile Val Val Gly Met
        115                 120                 125
gtc gcc ccg aag ggc ccg ggc cac ctc gtc cgt cgt cag ttc gtc gac        732
Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
    130                 135                 140
ggc aag ggc gtc ccc tgc ctc atc gcc gtc gac cag gac ccg aag ggc        780
Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Lys Gly
145                 150                 155                 160
aac ggc aag gac ctg ctg ctg tcc tac gcc gcc gcc atc ggt ggt gcc        828
Asn Gly Lys Asp Leu Leu Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
                165                 170                 175
cgt gca ggc gtc atc ccg acc acc ttc gag gct gag acc gtc acc gac        876
Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
            180                 185                 190
ctg ttc ggt gag cag gcc gtc ctc tgc ggt ggc acc gag gag ctc gtc        924
Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
        195                 200                 205
aag acc ggc ttc gag gtt ctg gtc gag gct ggc tac gag ccg gag atg        972
Lys Thr Gly Phe Glu Val Leu Val Glu Ala Gly Tyr Glu Pro Glu Met
    210                 215                 220
gcc tac ttc gag tgc ctc cac gag ctc aag ctg atc gtt gac ctc atg       1020
Ala Tyr Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
225                 230                 235                 240
ttc gag ggc ggc atc gcc aac atg aac tac tcc gtc tcc gac acc gcc       1068
Phe Glu Gly Gly Ile Ala Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
                245                 250                 255
gag ttc ggt ggc tac ctc tcc ggc ccg cgc gtc atc gac gcc ggc acc       1116
Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Gly Thr
            260                 265                 270
aag gag cgc atg aag gac atc ctg acc gac atc cag gac ggc acc ttc       1164
Lys Glu Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
        275                 280                 285
acc aag cgc ctc atc gcc aac gtc gag aac ggc aac aag gag ctc gag       1212
Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Lys Glu Leu Glu
    290                 295                 300
ggt ctg cgc gag gag tac gcc aag cac cag atc gag gag acc ggc gcc       1260
Gly Leu Arg Glu Glu Tyr Ala Lys His Gln Ile Glu Glu Thr Gly Ala
305                 310                 315                 320
aag ctg cgt gac ctc atg agc tgg gtc aag gtc gag atc acc gag acc       1308
Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Glu Ile Thr Glu Thr
                325                 330                 335
gcc taa gcccccacgc ttgtcgacgc cccaccggtt cgccggtggg gcgttcgtct       1364
Ala

ttgccgggcc agctgagggg cctgcctcag gggtggagca ggtcgagcag gtgccgccgg     1424
agggcggggt cggggtcggc gtcgcgacgc gggcgggga ggtccacggt gatgtcggcg      1484
atgaccgtgg cgtcgggga gggggacatg acgaggatgc ggtcggagag caggatcgcc      1544
tcgtcgacgt cgtgggtgac catgacgacg gtgcggcggt cggactccca cagggagagc     1604
agctccagct                                                           1614
<210>  100
<211>  337
<212>  PRT
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<213> Corynebacterium humireducens
<400> 100

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Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1               5                  10                  15
Gln Gly Arg Lys Val Ala Ile Ile Gly Tyr Gly Ser Gln Gly His Ala
            20                  25                  30
His Ala Gln Asn Leu Arg Asp Ser Gly Val Glu Val Cys Ile Gly Leu
        35                  40                  45
Arg Asp Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
    50                  55                  60
Val Lys Ser Asn Ala Asp Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65                  70                  75                  80
Leu Ala Pro Asp Thr Ser Gln Lys Ser Ile Tyr Glu Asn Asp Ile Glu
                85                  90                  95
Pro Asn Leu Asn Asp Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
            100                 105                 110
Val His Phe Gly Leu Ile Lys Pro Ala Glu Asn Ile Val Val Gly Met
        115                 120                 125
Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
    130                 135                 140
Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Lys Gly
145                 150                 155                 160
Asn Gly Lys Asp Leu Leu Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
                165                 170                 175
Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
            180                 185                 190
Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
        195                 200                 205
Lys Thr Gly Phe Glu Val Leu Val Glu Ala Gly Tyr Glu Pro Glu Met
    210                 215                 220
Ala Tyr Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
225                 230                 235                 240
Phe Glu Gly Gly Ile Ala Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
                245                 250                 255
Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Gly Thr
            260                 265                 270
Lys Glu Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
        275                 280                 285
Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Lys Glu Leu Glu
    290                 295                 300
Gly Leu Arg Glu Glu Tyr Ala Lys His Gln Ile Glu Glu Thr Gly Ala
305                 310                 315                 320
Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Glu Ile Thr Glu Thr
                325                 330                 335
Ala
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<210> 101
<211> 2439
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(2139)
<223> gen ilvD
<400> 101

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gaggacgtct ccggcatcgg cttcaagggc tcccgcgccc tgctgaccac ccgcgacggc        60
accgagcacg ccatgcccgg cgtgaccttc aactccctgc cgcagctggc ggaggcctcc       120
cagggccgga tccccgatgt cctcacctcc gcccaggagg cggccgacga caaggtcacc       180
atcatccacc gcgacgggca gcagatcctc atctccaagg aggagtacgc tgctcgacag       240
gccgcgcagc aggccaaccg ctcgtcctct gacaaccctg aaaacctgaa ggagcagtaa       300
gtg ttc ccg ctt cga tcc aaa gtc acc acc gtc gga cgc aac gcc gcc          348
Val Phe Pro Leu Arg Ser Lys Val Thr Thr Val Gly Arg Asn Ala Ala
1               5                  10                  15
gga gcc cgc gcc ctg tgg cgc gcc acg ggc acc aag gag cac gag ttc        396
Gly Ala Arg Ala Leu Trp Arg Ala Thr Gly Thr Lys Glu His Glu Phe
            20                  25                  30
ggt aag ccg atc gtc gcg atc gtg aac tcc tac acc cag ttc gtc ccg        444
Gly Lys Pro Ile Val Ala Ile Val Asn Ser Tyr Thr Gln Phe Val Pro
        35                  40                  45
ggc cac gtc cac ctg aag aac gtg ggc gac atc gtc gcg gac gcc gtc        492
Gly His Val His Leu Lys Asn Val Gly Asp Ile Val Ala Asp Ala Val
    50                  55                  60
cgt gcc gcc ggt ggc gtg ccg aag gag ttc cac acc atc gcc gtc gac        540
Arg Ala Ala Gly Gly Val Pro Lys Glu Phe His Thr Ile Ala Val Asp
65                  70                  75                  80
gac ggc atc gcc atg gga cac ggc ggc atg ctc tac tcg ctg ccc agc        588
Asp Gly Ile Ala Met Gly His Gly Gly Met Leu Tyr Ser Leu Pro Ser
                85                  90                  95
cgt gag atc atc gcc gac tct gtc gag tac atg gtc aac gcc cac acc        636
```

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Arg Glu Ile Ile Ala Asp Ser Val Glu Tyr Met Val Asn Ala His Thr
            100                 105                 110
gcc gac gcg atg gtc tgc atc tcc aac tgc gac aag atc acc ccg ggc      684
Ala Asp Ala Met Val Cys Ile Ser Asn Cys Asp Lys Ile Thr Pro Gly
        115                 120                 125
atg ctc aac gcc gcg ctg cgt ctc aac atc ccg gcc gtg ttc gtc tcc      732
Met Leu Asn Ala Ala Leu Arg Leu Asn Ile Pro Ala Val Phe Val Ser
    130                 135                 140
ggc ggt ccg atg gag gcc ggc aag gcc gtc gtc gtc gac ggc gtc gcc      780
Gly Gly Pro Met Glu Ala Gly Lys Ala Val Val Val Asp Gly Val Ala
145                 150                 155                 160
cag acc ccg acc gac ctc atc acc gcc atc gcc gcc tcc gcc gac gac      828
Gln Thr Pro Thr Asp Leu Ile Thr Ala Ile Ala Ala Ser Ala Asp Asp
                165                 170                 175
aac gtc tcc gat gag ggc ctg gcc acc atc gag gag tcg gcc tgc ccg      876
Asn Val Ser Asp Glu Gly Leu Ala Thr Ile Glu Glu Ser Ala Cys Pro
            180                 185                 190
acc tgt ggc tcc tgc tcc ggc atg ttc acc gcc aac tcg atg aac tgc      924
Thr Cys Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys
        195                 200                 205
ctc acc gag gcc ctg ggc ctg tcc ctg ccg ggc aac ggc acg acg ctg      972
Leu Thr Glu Ala Leu Gly Leu Ser Leu Pro Gly Asn Gly Thr Thr Leu
    210                 215                 220
gcc acc cac tcc gcc cgc cgt cgt ctc ttc gag cag gcc ggc gag acc     1020
Ala Thr His Ser Ala Arg Arg Arg Leu Phe Glu Gln Ala Gly Glu Thr
225                 230                 235                 240

atc gtc gag ctg tgc agg cgc tac tac ggc gag gag gac gag tcc gtc     1068
Ile Val Glu Leu Cys Arg Arg Tyr Tyr Gly Glu Glu Asp Glu Ser Val
                245                 250                 255
ctg ccg cgc aac atc gcc acc aag gac gcc ttc cgc aac gcg atg gcc     1116
Leu Pro Arg Asn Ile Ala Thr Lys Asp Ala Phe Arg Asn Ala Met Ala
            260                 265                 270
ctc gac atg gcc atg ggc ggc tcc acc aac acg atc ctc cac acg ctg     1164
Leu Asp Met Ala Met Gly Gly Ser Thr Asn Thr Ile Leu His Thr Leu
        275                 280                 285
gcc gcc gcc cag gag ggt gag gtc gac ttc acc ctg gcg gac atc gag     1212
Ala Ala Ala Gln Glu Gly Glu Val Asp Phe Thr Leu Ala Asp Ile Glu
    290                 295                 300
gag atc tcc cac cag gtg ccg tgc atc tcc aag gtc gcc ccg aac ggc     1260
Glu Ile Ser His Gln Val Pro Cys Ile Ser Lys Val Ala Pro Asn Gly
305                 310                 315                 320
atc tac cac atc gag gac gtc cac cgc gcc ggc ggc atc ccg gcc atc     1308
Ile Tyr His Ile Glu Asp Val His Arg Ala Gly Gly Ile Pro Ala Ile
                325                 330                 335
ctc ggc gag ctg cgt cgc gcg aac ctg ctc aac gag gac gtc cac tcc     1356
Leu Gly Glu Leu Arg Arg Ala Asn Leu Leu Asn Glu Asp Val His Ser
            340                 345                 350
atc acc tac gac tcc ctc gac gag tgg ctg ggt gac tgg gac atc cgt     1404
Ile Thr Tyr Asp Ser Leu Asp Glu Trp Leu Gly Asp Trp Asp Ile Arg
        355                 360                 365
ggc ggc cgg gcc atc gac gcc gcg acc gag ctc ttc cac gcc gcc ccg     1452
Gly Gly Arg Ala Ile Asp Ala Ala Thr Glu Leu Phe His Ala Ala Pro
    370                 375                 380
ggt ggc gtg cgc acc acg gag ccc ttc tcc acc gac aac cgc tgg gac     1500
Gly Gly Val Arg Thr Thr Glu Pro Phe Ser Thr Asp Asn Arg Trp Asp
385                 390                 395                 400
agc ctg gac acc gac ccg gtc aac ggc tgc atc cac gac gtc gag cac     1548
Ser Leu Asp Thr Asp Pro Val Asn Gly Cys Ile His Asp Val Glu His
                405                 410                 415
gcc cac tcc gcg gac ggc ggc ctg gtg gtc ctg cgc ggc aac ctg gcg     1596
Ala His Ser Ala Asp Gly Gly Leu Val Val Leu Arg Gly Asn Leu Ala
            420                 425                 430
ccg gac ggc tcc gtc ctc aag acc gcc ggc gtc gag gag gag ctg tgg     1644
Pro Asp Gly Ser Val Leu Lys Thr Ala Gly Val Glu Glu Glu Leu Trp
        435                 440                 445
acc ttc acc ggc ccg gcc cgc gtc gtc gac agc cag gag gag gcc gtc     1692
Thr Phe Thr Gly Pro Ala Arg Val Val Asp Ser Gln Glu Glu Ala Val
    450                 455                 460
tcc atc atc ctc aag cgc gag gtc cag ccg ggt gag gtc gtc gtc atc     1740
Ser Ile Ile Leu Lys Arg Glu Val Gln Pro Gly Glu Val Val Val Ile
465                 470                 475                 480
cgt tac gag ggt cct tcc ggt ggc ccg ggc atg cag gag atg ctg cac     1788
Arg Tyr Glu Gly Pro Ser Gly Gly Pro Gly Met Gln Glu Met Leu His
                485                 490                 495
ccg acg tcc ttc ctc aag ggt gcc ggc ctg ggc aag aag tgc gcc ctc     1836
Pro Thr Ser Phe Leu Lys Gly Ala Gly Leu Gly Lys Lys Cys Ala Leu
            500                 505                 510
```

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atc acc gac ggc cgt ttc tcc ggc ggc acc tcc ggc ttg tcg atc ggc       1884
Ile Thr Asp Gly Arg Phe Ser Gly Gly Thr Ser Gly Leu Ser Ile Gly
        515                 520                 525
cac atc tcc ccg gag gcc gcc cac ggt ggt ctc atc ggc ctg atc cgc       1932
His Ile Ser Pro Glu Ala Ala His Gly Gly Leu Ile Gly Leu Ile Arg
    530                 535                 540
aac ggt gac ccg atc acc atc gac gtc cac acc cgt cgt ctc tcc ctc       1980
Asn Gly Asp Pro Ile Thr Ile Asp Val His Thr Arg Arg Leu Ser Leu
545                 550                 555                 560
gac ctg ccg gac gag gag atc gag gcc cgc cgc gcc gag atg gag gcc       2028
Asp Leu Pro Asp Glu Glu Ile Glu Ala Arg Arg Ala Glu Met Glu Ala
                565                 570                 575
tcc gag aag ccg tgg acc gcg aac cgc gag cgc aag gtc tcc aag gca       2076
Ser Glu Lys Pro Trp Thr Ala Asn Arg Glu Arg Lys Val Ser Lys Ala
            580                 585                 590
ctg cgt gcg tac gcc gcc atg gcc acc tcc gcc gat aag ggc gcc gtc       2124
Leu Arg Ala Tyr Ala Ala Met Ala Thr Ser Ala Asp Lys Gly Ala Val
        595                 600                 605
cgc cag gtg gac taa cattgtccgc gtgaccacga caaacaagcc cgcgatcctg       2179
Arg Gln Val Asp
    610
ccccacaccg ccatcctgag gatggtggtg gccctggggc tgatcgcggg cttcggcgtc     2239
accggacgcc agatgatgat caccgacttc cccatcgaca tgatcatcta catggagggc     2299
gtgcgggcct tcctcgacgg cgccgagatg tacgccgtgc cgatgtacgc cggctccctg     2359
gccctgccgt tcatctatcc cccgttcggc gccctcgtca tggtgccgct cacccgttac     2419
gagcatgacc tggccggcga                                                2439
<210>  102
<211>  612
<212>  PRT
<213>  Corynebacterium humireducens
<400>  102
Val Phe Pro Leu Arg Ser Lys Val Thr Thr Val Gly Arg Asn Ala Ala
1               5                   10                  15
Gly Ala Arg Ala Leu Trp Arg Ala Thr Gly Thr Lys Glu His Glu Phe
            20                  25                  30
Gly Lys Pro Ile Val Ala Ile Val Asn Ser Tyr Thr Gln Phe Val Pro
        35                  40                  45
Gly His Val His Leu Lys Asn Val Gly Asp Ile Val Ala Asp Ala Val
    50                  55                  60
Arg Ala Ala Gly Gly Val Pro Lys Glu Phe His Thr Ile Ala Val Asp
65                  70                  75                  80
Asp Gly Ile Ala Met Gly His Gly Gly Met Leu Tyr Ser Leu Pro Ser
                85                  90                  95
Arg Glu Ile Ile Ala Asp Ser Val Glu Tyr Met Val Asn Ala His Thr
            100                 105                 110
Ala Asp Ala Met Val Cys Ile Ser Asn Cys Asp Lys Ile Thr Pro Gly
        115                 120                 125
Met Leu Asn Ala Ala Leu Arg Leu Asn Ile Pro Ala Val Phe Val Ser
    130                 135                 140
Gly Gly Pro Met Glu Ala Gly Lys Ala Val Val Val Asp Gly Val Ala
145                 150                 155                 160
Gln Thr Pro Thr Asp Leu Ile Thr Ala Ile Ala Ala Ser Ala Asp Asp
                165                 170                 175
Asn Val Ser Asp Glu Gly Leu Ala Thr Ile Glu Glu Ser Ala Cys Pro
            180                 185                 190
Thr Cys Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys
        195                 200                 205
Leu Thr Glu Ala Leu Gly Leu Ser Leu Pro Gly Asn Gly Thr Thr Leu
    210                 215                 220
Ala Thr His Ser Ala Arg Arg Arg Leu Phe Glu Gln Ala Gly Glu Thr
225                 230                 235                 240
Ile Val Glu Leu Cys Arg Arg Tyr Tyr Gly Glu Glu Asp Glu Ser Val
                245                 250                 255
Leu Pro Arg Asn Ile Ala Thr Lys Asp Ala Phe Arg Asn Ala Met Ala
            260                 265                 270
Leu Asp Met Ala Met Gly Gly Ser Thr Asn Thr Ile Leu His Thr Leu
        275                 280                 285
Ala Ala Ala Gln Glu Gly Glu Val Asp Phe Thr Leu Ala Asp Ile Glu
    290                 295                 300
Glu Ile Ser His Gln Val Pro Cys Ile Ser Lys Val Ala Pro Asn Gly
305                 310                 315                 320
Ile Tyr His Ile Glu Asp Val His Arg Ala Gly Gly Ile Pro Ala Ile
                325                 330                 335
Leu Gly Glu Leu Arg Arg Ala Asn Leu Leu Asn Glu Asp Val His Ser
            340                 345                 350
Ile Thr Tyr Asp Ser Leu Asp Glu Trp Leu Gly Asp Trp Asp Ile Arg
        355                 360                 365
Gly Gly Arg Ala Ile Asp Ala Ala Thr Glu Leu Phe His Ala Ala Pro
```

```
    370                 375                 380
Gly Gly Val Arg Thr Thr Glu Pro Phe Ser Thr Asp Asn Arg Trp Asp
385                 390                 395                 400
Ser Leu Asp Thr Asp Pro Val Asn Gly Cys Ile His Asp Val Glu His
                405                 410                 415
Ala His Ser Ala Asp Gly Gly Leu Val Val Leu Arg Gly Asn Leu Ala
            420                 425                 430
Pro Asp Gly Ser Val Leu Lys Thr Ala Gly Val Glu Glu Glu Leu Trp
        435                 440                 445
Thr Phe Thr Gly Pro Ala Arg Val Val Asp Ser Gln Glu Glu Ala Val
    450                 455                 460
Ser Ile Ile Leu Lys Arg Glu Val Gln Pro Gly Glu Val Val Val Ile
465                 470                 475                 480
Arg Tyr Glu Gly Pro Ser Gly Gly Pro Gly Met Gln Glu Met Leu His
                485                 490                 495
Pro Thr Ser Phe Leu Lys Gly Ala Gly Leu Gly Lys Lys Cys Ala Leu
            500                 505                 510
Ile Thr Asp Gly Arg Phe Ser Gly Gly Thr Ser Gly Leu Ser Ile Gly
        515                 520                 525
His Ile Ser Pro Glu Ala Ala His Gly Gly Leu Ile Gly Leu Ile Arg
    530                 535                 540
Asn Gly Asp Pro Ile Thr Ile Asp Val His Thr Arg Arg Leu Ser Leu
545                 550                 555                 560
Asp Leu Pro Asp Glu Glu Ile Glu Ala Arg Arg Ala Glu Met Glu Ala
                565                 570                 575
Ser Glu Lys Pro Trp Thr Ala Asn Arg Glu Arg Lys Val Ser Lys Ala
            580                 585                 590
Leu Arg Ala Tyr Ala Ala Met Ala Thr Ser Ala Asp Lys Gly Ala Val
        595                 600                 605
Arg Gln Val Asp
    610
<210>  103
<211>  1725
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<213>  Corynebacterium humireducens
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<221>  CDS
<222>  (301)..(1425)
<223>  gen ilvE
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ggcggcgtcg tcgagaagga cggaggccgg cagctccggg ccgtcctcac cgcagaggac     120
ggggacgagc agtgcgtcgg gggtcttcgg ggccttcttg gccagctcga cggcgggggt     180
ggtgccgcgg gcgggaaggg tgaaagtggg gttcgccatg gaaagtacct cctgagattg     240
acaagcgatg aacccagctt atagagatca cctctgggtc gtcggtgtag cgtgttcccc     300
atg acg tct ctc aat ttc acc gtg aac cgt acg agc acc ccg acg tcc       348
Met Thr Ser Leu Asn Phe Thr Val Asn Arg Thr Ser Thr Pro Thr Ser
1               5                  10                  15
gat gag gcg cgc gag gag att ctg cag aat ccg cgg ttc ggc aag aac       396
Asp Glu Ala Arg Glu Glu Ile Leu Gln Asn Pro Arg Phe Gly Lys Asn
            20                  25                  30
ttc acc gat cac atg gtc acc atc gag tgg tcc gag gac aag ggc tgg       444
Phe Thr Asp His Met Val Thr Ile Glu Trp Ser Glu Asp Lys Gly Trp
        35                  40                  45
cac gac gcc cgc gtg cgt ccc tac gag gcc atc ccg atg gat ccc gcg       492
His Asp Ala Arg Val Arg Pro Tyr Glu Ala Ile Pro Met Asp Pro Ala
    50                  55                  60
acc acg gtg ttc cac tac ggc cag gcg atc ttc gag ggc atc aag gcc       540
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
65                  70                  75                  80
tac cgt cag ccg gac ggc tcc atc gcc acc ttc cgc ccg gag cgc aac       588
Tyr Arg Gln Pro Asp Gly Ser Ile Ala Thr Phe Arg Pro Glu Arg Asn
                85                  90                  95
gcc gag cgc atg cag cgt tcc gcc gag cgc atg gcc atg ccg ccg ctg       636
Ala Glu Arg Met Gln Arg Ser Ala Glu Arg Met Ala Met Pro Pro Leu
            100                 105                 110
ccg acc gag gac ttc ctc gag acg ctc cgc ctg ctt gtc gac gtc gac       684
Pro Thr Glu Asp Phe Leu Glu Thr Leu Arg Leu Leu Val Asp Val Asp
        115                 120                 125
cgt gac tgg gtc ccc gcc gcc ggc ggc gag gcc agc ctc tac ctg cgt       732
Arg Asp Trp Val Pro Ala Ala Gly Gly Glu Ala Ser Leu Tyr Leu Arg
    130                 135                 140
ccc ttc atg atc tcc acc gag gtc tcc ctg ggc gtc agc ccg gcc aac       780
Pro Phe Met Ile Ser Thr Glu Val Ser Leu Gly Val Ser Pro Ala Asn
145                 150                 155                 160
cgg tac acc ttc ttc gtc atc gcc tcc ccg gtc ggg gcg tac ttc acc       828
Arg Tyr Thr Phe Phe Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
                165                 170                 175
```

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ggt ggc gtc aag ccg gtc tcc gtg tgg ctg agc gag gac tac gtc cgt        876
Gly Gly Val Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
            180                 185                 190
gcc gcc ccg ggt ggc acc ggt gcc gcg aag ttc gcc ggc aac tac gcc        924
Ala Ala Pro Gly Gly Thr Gly Ala Ala Lys Phe Ala Gly Asn Tyr Ala
        195                 200                 205
gcc tcc ctg ctc gcg cag gcg cag gcg gag gag aag ggc tgc gac cag        972
Ala Ser Leu Leu Ala Gln Ala Gln Ala Glu Glu Lys Gly Cys Asp Gln
    210                 215                 220
gtc gtg tgg ctc gac gcc atc gag cac acc tac atc gag gag atg ggt       1020
Val Val Trp Leu Asp Ala Ile Glu His Thr Tyr Ile Glu Glu Met Gly
225                 230                 235                 240
ggc atg aac ctg ttc ttc gtg tac ggc tcg ggt gac gac gtc acc gtg       1068
Gly Met Asn Leu Phe Phe Val Tyr Gly Ser Gly Asp Asp Val Thr Val
                245                 250                 255
gcc acc ccc gag ctc tcc ggc tcc ctc ctg ccg ggc gtc acc cgc gac       1116
Ala Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Val Thr Arg Asp
            260                 265                 270
tcc ctc ctg cag gtc gcc cgc gat ctc ggc cac cgc acc gag gag cgg       1164
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly His Arg Thr Glu Glu Arg
        275                 280                 285
agg atc tcc aag ttc gac tgg cgc gac gac gtc gcc tcc ggt gcg atg       1212
Arg Ile Ser Lys Phe Asp Trp Arg Asp Asp Val Ala Ser Gly Ala Met
    290                 295                 300
acc gag gcc atg gcc tgc ggc aca gcc gcc gtg atc acc ccg gtc ggc       1260
Thr Glu Ala Met Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
305                 310                 315                 320
cgg gtc ctg tcc aac gac ggc gag ttc cag atc aat gac aac cag ccg       1308
Arg Val Leu Ser Asn Asp Gly Glu Phe Gln Ile Asn Asp Asn Gln Pro
                325                 330                 335
ggt gag gtc acc atg gcc atg cgc gag cgt ctc acc gac atc cag cgc       1356
Gly Glu Val Thr Met Ala Met Arg Glu Arg Leu Thr Asp Ile Gln Arg
            340                 345                 350
ggc ctg tac gag gac acc cac ggc tgg gtg cac acc ctc gtc ccg gct       1404
Gly Leu Tyr Glu Asp Thr His Gly Trp Val His Thr Leu Val Pro Ala
        355                 360                 365
gag gac cag ccg gcg gac tag tcggccagca gctcggcggc ggcccgcacc           1455
Glu Asp Gln Pro Ala Asp
    370
agcgggagcg ccgctagcgc gccggtgccc tggccggcgt tcatgtccag ggcgacgaga     1515
ggcgtgagtt cgagggcctg cagcgcgatg aggtgcgcgg gctccggggt cagctgccct     1575
gcctggcacc agggggcggt gccgggggag agacgttccg cgaggtaggc ggcgacggtg     1635
acgggggcgc cgtcgagaag cacgggggtg cggcgtgccg cggcctgcgc gatgaaggcc     1695
accagtgcca ccaggtccgg ggaggcgatc                                      1725
<210>  104
<211>  374
<212>  PRT
<213>  Corynebacterium humireducens
<400>  104
Met Thr Ser Leu Asn Phe Thr Val Asn Arg Thr Ser Thr Pro Thr Ser
1               5                   10                  15
Asp Glu Ala Arg Glu Glu Ile Leu Gln Asn Pro Arg Phe Gly Lys Asn
            20                  25                  30
Phe Thr Asp His Met Val Thr Ile Glu Trp Ser Glu Asp Lys Gly Trp
        35                  40                  45
His Asp Ala Arg Val Arg Pro Tyr Glu Ala Ile Pro Met Asp Pro Ala
    50                  55                  60
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
65                  70                  75                  80
Tyr Arg Gln Pro Asp Gly Ser Ile Ala Thr Phe Arg Pro Glu Arg Asn
                85                  90                  95
Ala Glu Arg Met Gln Arg Ser Ala Glu Arg Met Ala Met Pro Pro Leu
            100                 105                 110
Pro Thr Glu Asp Phe Leu Glu Thr Leu Arg Leu Leu Val Asp Val Asp
        115                 120                 125
Arg Asp Trp Val Pro Ala Ala Gly Gly Glu Ala Ser Leu Tyr Leu Arg
    130                 135                 140
Pro Phe Met Ile Ser Thr Glu Val Ser Leu Gly Val Ser Pro Ala Asn
145                 150                 155                 160
Arg Tyr Thr Phe Phe Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
                165                 170                 175
Gly Gly Val Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
            180                 185                 190
Ala Ala Pro Gly Gly Thr Gly Ala Ala Lys Phe Ala Gly Asn Tyr Ala
        195                 200                 205
Ala Ser Leu Leu Ala Gln Ala Gln Ala Glu Glu Lys Gly Cys Asp Gln
    210                 215                 220
Val Val Trp Leu Asp Ala Ile Glu His Thr Tyr Ile Glu Glu Met Gly
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225                 230                 235                 240
Gly Met Asn Leu Phe Phe Val Tyr Gly Ser Gly Asp Asp Val Thr Val
                245                 250                 255
Ala Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Val Thr Arg Asp
            260                 265                 270
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly His Arg Thr Glu Glu Arg
        275                 280                 285
Arg Ile Ser Lys Phe Asp Trp Arg Asp Asp Val Ala Ser Gly Ala Met
    290                 295                 300
Thr Glu Ala Met Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
305                 310                 315                 320
Arg Val Leu Ser Asn Asp Gly Glu Phe Gln Ile Asn Asp Asn Gln Pro
                325                 330                 335
Gly Glu Val Thr Met Ala Met Arg Glu Arg Leu Thr Asp Ile Gln Arg
            340                 345                 350
Gly Leu Tyr Glu Asp Thr His Gly Trp Val His Thr Leu Val Pro Ala
        355                 360                 365
Glu Asp Gln Pro Ala Asp
    370
<210>  105
<211>  1896
<212>  AND
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1596)
<223>  gen ilvA
<400>  105
gccgatcggg gccagcgaga gggccgcacc cggggccgag tggacgacgg ggttgtccac       60
gacagcggcg tgggccgggg cgatgaggga gacactggtg gcgagcgccg cgcacagcgc      120
gacagcggaa cggcgaaggg acacggggag aactcctgtg gtcggtgggg tgcagatcgt      180
gtgacatggt ggaccagtga catgacacca atctcaattc cggaccacct gcaggtgaac      240
agtcggtgaa gtgggctgca acgccgtggc cggtggacag ggggactaca ctgagtcccc      300
atg agt gac acc cgg tct gcc gta acc acc ttc gag cct gtc cgc gcc        348
Met Ser Asp Thr Arg Ser Ala Val Thr Thr Phe Glu Pro Val Arg Ala
1               5                   10                  15
tcg gac att cag ctg gcg cag gca cgg atc tcc tcc gtc atc gag ccc        396
Ser Asp Ile Gln Leu Ala Gln Ala Arg Ile Ser Ser Val Ile Glu Pro
            20                  25                  30
acc ccg ctc cag tac tgc ccc cgc ctc tcc gag gag acc ggc tgc gag        444
Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu Glu Thr Gly Cys Glu
        35                  40                  45
gtg tac ctc aaa cgc gag gac ctg cag gac gtg cgc tcc tac aag atc        492
Val Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile
    50                  55                  60
cgc ggc gcc tac tac gcc atg gcc aac ctc gac gag cag cag cgg gac        540
Arg Gly Ala Tyr Tyr Ala Met Ala Asn Leu Asp Glu Gln Gln Arg Asp
65                  70                  75                  80
gcc ggc atc gtc gcc gcc tcc gcc ggc aac cac gca cag ggt gtc gcc        588
Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala
                85                  90                  95
tac gcc tgc cgc acg atg ggc atc cgg ggt cgc atc ttc gtc ccc aac        636
Tyr Ala Cys Arg Thr Met Gly Ile Arg Gly Arg Ile Phe Val Pro Asn
            100                 105                 110
cag acg ccg aag cag aag cgt gac cgc atc atg gtc cac ggc ggt gac        684
Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met Val His Gly Gly Asp
        115                 120                 125
atg gtg gag ctg gtc gtc acc ggc aac aac ttc gac gag gcc gcc gag        732
Met Val Glu Leu Val Val Thr Gly Asn Asn Phe Asp Glu Ala Ala Glu
    130                 135                 140
gcc gcg cgt gcc gac gcc gcc gag cgc ggc gcc acc atg atc gag ccc        780
Ala Ala Arg Ala Asp Ala Ala Glu Arg Gly Ala Thr Met Ile Glu Pro
145                 150                 155                 160
ttc gac gcc cgc gac acc gtc atc ggt cag ggg acc atc gcg gcg gag        828
Phe Asp Ala Arg Asp Thr Val Ile Gly Gln Gly Thr Ile Ala Ala Glu
                165                 170                 175
atc ctc acg cag ctc acg tcc atc ggc aag tcc ctc gac acg gtg ctc        876
Ile Leu Thr Gln Leu Thr Ser Ile Gly Lys Ser Leu Asp Thr Val Leu
            180                 185                 190
gtg ccg gtc ggc ggc ggt ggc ctc ctg gcc ggt gtc gcc agc tac ctc        924
Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly Val Ala Ser Tyr Leu
        195                 200                 205
gcc gac atg gcg ccg cgc acc gcg atc gtc ggc gtc gag ccg ggc ggt        972
Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly Val Glu Pro Gly Gly
    210                 215                 220
gcc gcc tcc ctc cag gcc gcc ctg cgt gcc gac gcc ccc gtc acc ctc       1020
Ala Ala Ser Leu Gln Ala Ala Leu Arg Ala Asp Ala Pro Val Thr Leu
225                 230                 235                 240
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tcc gcg gtc gac ccc ttc gtc gac ggc gcc gcc gtc aag cgc atc ggt      1068
Ser Ala Val Asp Pro Phe Val Asp Gly Ala Ala Val Lys Arg Ile Gly
                245                 250                 255
gac ctg ccc ttc gac atc atc gaa cgc aac aag ggc cgc atc cac gtc      1116
Asp Leu Pro Phe Asp Ile Ile Glu Arg Asn Lys Gly Arg Ile His Val
            260                 265                 270
atg gac gtc tcc gag ggc gcc gtg tgc acc gag atg ctc gac ctg tac      1164
Met Asp Val Ser Glu Gly Ala Val Cys Thr Glu Met Leu Asp Leu Tyr
        275                 280                 285
cag aac gag ggc atc atc acc gag ccc gcc ggt gca ctg tcg gtc acg      1212
Gln Asn Glu Gly Ile Ile Thr Glu Pro Ala Gly Ala Leu Ser Val Thr
    290                 295                 300
ggc ctg aag gag atg aag ctc cag cag gac tcc atc gtg gtg tgc atc      1260
Gly Leu Lys Glu Met Lys Leu Gln Gln Asp Ser Ile Val Val Cys Ile
305                 310                 315                 320
atc tcc ggc ggc aac aac gac gtg ctg cgc tac gcc gag atc atg gag      1308
Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr Ala Glu Ile Met Glu
                325                 330                 335
cgc tcc ctg gtg cac cgc ggc ctc aag cac tac ttc ctg gtg aac ttc      1356
Arg Ser Leu Val His Arg Gly Leu Lys His Tyr Phe Leu Val Asn Phe
            340                 345                 350
ccg cag gag ccg ggc cag ctg cgc cac ttc ctc aac gac atc ctc ggc      1404
Pro Gln Glu Pro Gly Gln Leu Arg His Phe Leu Asn Asp Ile Leu Gly
        355                 360                 365

ccc gac gac gac atc acc ctc ttc gag tac ctc aag cgc aac aac cgg      1452
Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg
    370                 375                 380
gag acc ggt gcc gcg ctc gtc ggc ctc gag ctc ggc cgg gcc agc gac      1500
Glu Thr Gly Ala Ala Leu Val Gly Leu Glu Leu Gly Arg Ala Ser Asp
385                 390                 395                 400
ctc gac ccg ctg ctc gag cgg atg aac gcc tcc cgc atc gag tgc cag      1548
Leu Asp Pro Leu Leu Glu Arg Met Asn Ala Ser Arg Ile Glu Cys Gln
                405                 410                 415
cac ctc aag ccg aac acc ccc gag tac gag tac ctg gtc aac acc tag      1596
His Leu Lys Pro Asn Thr Pro Glu Tyr Glu Tyr Leu Val Asn Thr
            420                 425                 430
gggtctctac ctgcgcagga gcgcgaactc ccacgggccc aggcgcgtgt cgtcgaggcc    1656
gacctccggt tccgtgaagg agtagatgag ctcgccgccg taggggcgc ggacctccgc     1716
gtcggagagg ttggccacga ggatcacgtc ctcccagccc atcgccagcc agccgtcccc    1776
ggtctcgacg gtgaggcggg agagatcggc gcgggagagg ccgagctcgc ggcgcagacg    1836
cagcagctcc cggtaggcgg cgtggatctc ctgctgctcc tccgtgaagt cccagtccag    1896
<210>  106
<211>  431
<212>  PRT
<213>  Corynebacterium humireducens
<400>  106
Met Ser Asp Thr Arg Ser Ala Val Thr Thr Phe Glu Pro Val Arg Ala
1               5                   10                  15
Ser Asp Ile Gln Leu Ala Gln Ala Arg Ile Ser Ser Val Ile Glu Pro
            20                  25                  30
Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu Glu Thr Gly Cys Glu
        35                  40                  45
Val Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile
    50                  55                  60
Arg Gly Ala Tyr Tyr Ala Met Ala Asn Leu Asp Glu Gln Gln Arg Asp
65                  70                  75                  80
Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala
                85                  90                  95
Tyr Ala Cys Arg Thr Met Gly Ile Arg Gly Arg Ile Phe Val Pro Asn
            100                 105                 110
Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met Val His Gly Gly Asp
        115                 120                 125
Met Val Glu Leu Val Val Thr Gly Asn Asn Phe Asp Glu Ala Ala Glu
    130                 135                 140
Ala Ala Arg Ala Asp Ala Ala Glu Arg Gly Ala Thr Met Ile Glu Pro
145                 150                 155                 160
Phe Asp Ala Arg Asp Thr Val Ile Gly Gln Gly Thr Ile Ala Ala Glu
                165                 170                 175
Ile Leu Thr Gln Leu Thr Ser Ile Gly Lys Ser Leu Asp Thr Val Leu
            180                 185                 190
Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly Val Ala Ser Tyr Leu
        195                 200                 205
Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly Val Glu Pro Gly Gly
    210                 215                 220
Ala Ala Ser Leu Gln Ala Ala Leu Arg Ala Asp Ala Pro Val Thr Leu
225                 230                 235                 240
Ser Ala Val Asp Pro Phe Val Asp Gly Ala Ala Val Lys Arg Ile Gly
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                245                 250                 255
Asp Leu Pro Phe Asp Ile Ile Glu Arg Asn Lys Gly Arg Ile His Val
            260                 265                 270
Met Asp Val Ser Glu Gly Ala Val Cys Thr Glu Met Leu Asp Leu Tyr
        275                 280                 285
Gln Asn Glu Gly Ile Ile Thr Glu Pro Ala Gly Ala Leu Ser Val Thr
    290                 295                 300
Gly Leu Lys Glu Met Lys Leu Gln Gln Asp Ser Ile Val Val Cys Ile
305                 310                 315                 320
Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr Ala Glu Ile Met Glu
                325                 330                 335
Arg Ser Leu Val His Arg Gly Leu Lys His Tyr Phe Leu Val Asn Phe
            340                 345                 350
Pro Gln Glu Pro Gly Gln Leu Arg His Phe Leu Asn Asp Ile Leu Gly
        355                 360                 365
Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg
    370                 375                 380
Glu Thr Gly Ala Ala Leu Val Gly Leu Glu Leu Gly Arg Ala Ser Asp
385                 390                 395                 400
Leu Asp Pro Leu Leu Glu Arg Met Asn Ala Ser Arg Ile Glu Cys Gln
                405                 410                 415
His Leu Lys Pro Asn Thr Pro Glu Tyr Glu Tyr Leu Val Asn Thr
            420                 425                 430

<210>  107
<211>  2043
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1743)
<223>  gen thrC
<400>  107
cggggcagca ccgcgatggc cacgacgagg acgagcagga ccgcggtgac ggtggctacg       60
gtacgtgtgt tacctcggga ggccacgggg cgctcactcc tctgtgcgac tctctgcgac      120
tctgtacgac tctgtgcgac gcggcgtgga caacgccgcc cggcaggggc gtgcggccgc      180
agtaccccgt agcgtactca actgcttttc ccgggaaagg ggaattcacc gggatccccg      240
ccccggcgtg cgggtgggat gttgcgcatg cttccagccc cgccacgtat ggttgtccac      300
gtg gat tac att tcg acg cgc gac tcc tcc cgt act ccc gcc acc ttc        348
Val Asp Tyr Ile Ser Thr Arg Asp Ser Ser Arg Thr Pro Ala Thr Phe
1               5                  10                  15
acc gac atc ctg ctc ggt gga ctg gcc ccc gac ggc ggc ctc tac ctg        396
Thr Asp Ile Leu Leu Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu
            20                  25                  30
ccc gcc gag tac ccg cag atc agc gat gag cag ctg acg cag tgg cgg        444
Pro Ala Glu Tyr Pro Gln Ile Ser Asp Glu Gln Leu Thr Gln Trp Arg
        35                  40                  45
tct ctc ctg cag gag aag ggg tac gcc gcc ctg gcg gcg gag atc ctc        492
Ser Leu Leu Gln Glu Lys Gly Tyr Ala Ala Leu Ala Ala Glu Ile Leu
    50                  55                  60
aag ctc ttc gtc gac gac atc ccg gcg gag gat ctc gag ggc atc gcc        540
Lys Leu Phe Val Asp Asp Ile Pro Ala Glu Asp Leu Glu Gly Ile Ala
65                  70                  75                  80
gcc cgc gcc tac acc tcc ccg aag ttc gcg cac gag gag atc gtc ccc        588
Ala Arg Ala Tyr Thr Ser Pro Lys Phe Ala His Glu Glu Ile Val Pro
                85                  90                  95
gtg acc gag ctc gag gac ggc ctg tgg atc ggc cac ctc tcc gag ggc        636
Val Thr Glu Leu Glu Asp Gly Leu Trp Ile Gly His Leu Ser Glu Gly
            100                 105                 110
ccg acc gcc gcg ttc aag gac atg gcg atg cag ctg ctc ggc gag ctc        684
Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu
        115                 120                 125
ttc gag tac gag ctg gcc cgt cgc ggg gag acc ctc aac atc ctg ggt        732
Phe Glu Tyr Glu Leu Ala Arg Arg Gly Glu Thr Leu Asn Ile Leu Gly
    130                 135                 140
gcg acc tcg ggt gac acg ggt tcc tcc gcc gag tac gcg atg cgc ggc        780
Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly
145                 150                 155                 160
cgt aag ggc atc cgt gtc ttc atg ctg acc ccg gcc ggt cgc atg acc        828
Arg Lys Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr
                165                 170                 175
ccg ttc cag cag gcg cag atg ttc ggc ctg cag gac ccc aac atc ttc        876
Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Gln Asp Pro Asn Ile Phe
            180                 185                 190
aac atc gcc ctg gac ggc gtc ttc gac gac tgc cag gac gtg gtc aag        924
Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys
        195                 200                 205
gcg gtg tcc gcc gac gcc ggg ttc aag gcc gag aac cgt atc ggt gcg        972
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Ala Val Ser Ala Asp Ala Gly Phe Lys Ala Glu Asn Arg Ile Gly Ala
    210                 215                 220
gtc aac tcg atc aac tgg gcc cgc ctc atg gcg cag atc gtc tac tac      1020
Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Ile Val Tyr Tyr
225                 230                 235                 240
gtc tcc tcc tgg ctg agg atc acc gag agc aac gac cag aag gtc tcc      1068
Val Ser Ser Trp Leu Arg Ile Thr Glu Ser Asn Asp Gln Lys Val Ser
                245                 250                 255
ttc tcc gtg ccg acc ggc aac ttc ggt gac atc tgc gcc ggc cac atc      1116
Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile
            260                 265                 270
gcc cgt cag atg ggt ctg ccg atc gac cgt ctc atc gtc gcc acc aac      1164
Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn
        275                 280                 285
gag aac gac gtc ctc gac gag ttc ttc cgc acc ggc aac tac cgt ccg      1212
Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asn Tyr Arg Pro
    290                 295                 300
cgc ccg gcg gag gag acc ctg gag acg tcc tcg ccg tcg atg gac atc      1260
Arg Pro Ala Glu Glu Thr Leu Glu Thr Ser Ser Pro Ser Met Asp Ile
305                 310                 315                 320
tcc cgt gcc tcc aac ttc gag cgt ttc gtc ttc gac ctg ctg ggc cgt      1308
Ser Arg Ala Ser Asn Phe Glu Arg Phe Val Phe Asp Leu Leu Gly Arg
                325                 330                 335
gac gcc gcg cgc gtc gcg cag cac ttc ggc gtc gac gtc cgc gcc gac      1356
Asp Ala Ala Arg Val Ala Gln His Phe Gly Val Asp Val Arg Ala Asp
            340                 345                 350
ggt ttc tcg ctt gcc gac gac ccc gcg ttc ccg gcc gcc gca gag aag      1404
Gly Phe Ser Leu Ala Asp Asp Pro Ala Phe Pro Ala Ala Ala Glu Lys
        355                 360                 365
tac ggc ttc gcc tcc ggt cgt tcc acc cac cag gac cgc ctc gac acg      1452
Tyr Gly Phe Ala Ser Gly Arg Ser Thr His Gln Asp Arg Leu Asp Thr
    370                 375                 380
atc agg gac gtg tgg gag cgc ctg ggc atc atg ctc gac ccg cac acc      1500
Ile Arg Asp Val Trp Glu Arg Leu Gly Ile Met Leu Asp Pro His Thr
385                 390                 395                 400
gcc gac ggc gtg aag gtc gcc cgc gag tgg cgt tcc gag atc gac ggc      1548
Ala Asp Gly Val Lys Val Ala Arg Glu Trp Arg Ser Glu Ile Asp Gly
                405                 410                 415
ccg atc gtg tgc ctg gag acc gcc ctg ccg gtg aag ttc tcc gag acc      1596
Pro Ile Val Cys Leu Glu Thr Ala Leu Pro Val Lys Phe Ser Glu Thr
            420                 425                 430
atc gag gag gcc acc ggc gtg cag ccg gag acc ccg gag cgt ttc gcc      1644
Ile Glu Glu Ala Thr Gly Val Gln Pro Glu Thr Pro Glu Arg Phe Ala
        435                 440                 445
ggc atc ctc gac gcc gag cgc cac gtg acg gac ctg ccg aac gac gcg      1692
Gly Ile Leu Asp Ala Glu Arg His Val Thr Asp Leu Pro Asn Asp Ala
    450                 455                 460
gag acc gtc aag aag ttc atc acc gac tcc atc cgc acc acc gag gtg      1740
Glu Thr Val Lys Lys Phe Ile Thr Asp Ser Ile Arg Thr Thr Glu Val
465                 470                 475                 480
taa ccgtcgtggc catggagttc aagatgggtc aggagtactt ccaggacttc           1793
gacccggaga agttcgccgc gatgatcaag gcgcaggccg aggctgaggc tgacgctgcg    1853
gccggggaag acggcgtcga caagcagtga acatccgcgt ctgggcgggt ctggtcgcac    1913
tgaccaccgc cggcgtgggg tcgctcatcg cctggtccgt cgaggaccag cggcagcacc    1973
ccacgcccat cgccgaggtg atcgcggcgg cgccgacgca ggtcccgacg gagttccgtg    2033
cccctgcggt                                                          2043
<210>  108
<211>  480
<212>  PRT
<213>  Corynebacterium humireducens
<400>  108
Val Asp Tyr Ile Ser Thr Arg Asp Ser Ser Arg Thr Pro Ala Thr Phe
1               5                   10                  15
Thr Asp Ile Leu Leu Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu
            20                  25                  30
Pro Ala Glu Tyr Pro Gln Ile Ser Asp Glu Gln Leu Thr Gln Trp Arg
        35                  40                  45
Ser Leu Leu Gln Glu Lys Gly Tyr Ala Ala Leu Ala Ala Glu Ile Leu
    50                  55                  60
Lys Leu Phe Val Asp Asp Ile Pro Ala Glu Asp Leu Glu Gly Ile Ala
65                  70                  75                  80
Ala Arg Ala Tyr Thr Ser Pro Lys Phe Ala His Glu Glu Ile Val Pro
                85                  90                  95
Val Thr Glu Leu Glu Asp Gly Leu Trp Ile Gly His Leu Ser Glu Gly
            100                 105                 110
Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu
        115                 120                 125
Phe Glu Tyr Glu Leu Ala Arg Arg Gly Glu Thr Leu Asn Ile Leu Gly
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    130                 135                 140
Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly
145                 150                 155                 160
Arg Lys Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr
                165                 170                 175
Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Gln Asp Pro Asn Ile Phe
            180                 185                 190
Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys
        195                 200                 205
Ala Val Ser Ala Asp Ala Gly Phe Lys Ala Glu Asn Arg Ile Gly Ala
    210                 215                 220
Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Ile Val Tyr Tyr
225                 230                 235                 240
Val Ser Ser Trp Leu Arg Ile Thr Glu Ser Asn Asp Gln Lys Val Ser
                245                 250                 255
Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile
            260                 265                 270
Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn
        275                 280                 285
Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asn Tyr Arg Pro
    290                 295                 300
Arg Pro Ala Glu Glu Thr Leu Glu Thr Ser Ser Pro Ser Met Asp Ile
305                 310                 315                 320
Ser Arg Ala Ser Asn Phe Glu Arg Phe Val Phe Asp Leu Leu Gly Arg
                325                 330                 335
Asp Ala Ala Arg Val Ala Gln His Phe Gly Val Asp Val Arg Ala Asp
            340                 345                 350
Gly Phe Ser Leu Ala Asp Asp Pro Ala Phe Pro Ala Ala Ala Glu Lys
        355                 360                 365
Tyr Gly Phe Ala Ser Gly Arg Ser Thr His Gln Asp Arg Leu Asp Thr
    370                 375                 380
Ile Arg Asp Val Trp Glu Arg Leu Gly Ile Met Leu Asp Pro His Thr
385                 390                 395                 400
Ala Asp Gly Val Lys Val Ala Arg Glu Trp Arg Ser Glu Ile Asp Gly
                405                 410                 415
Pro Ile Val Cys Leu Glu Thr Ala Leu Pro Val Lys Phe Ser Glu Thr
            420                 425                 430
Ile Glu Glu Ala Thr Gly Val Gln Pro Glu Thr Pro Glu Arg Phe Ala
        435                 440                 445
Gly Ile Leu Asp Ala Glu Arg His Val Thr Asp Leu Pro Asn Asp Ala
    450                 455                 460
Glu Thr Val Lys Lys Phe Ile Thr Asp Ser Ile Arg Thr Thr Glu Val
465                 470                 475                 480
<210>  109
<211>  2448
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(2148)
<223>  gen leuA
<400>  109
gggtcgatgc cgtggagcag ggcttttcac gtttcttcac aaaactgcgt tgcgccgggg       60
gagggagtgt gtagacttca cagcatgttc tcccgcgcga acctccttct tcttcgccgc      120
ggcgggtccc aggtccagta acgaagcgac cggcaccccg tcgcggagtt tggtgttgcc      180
ggtcgctgct cccgctgaat agcccattca tcagcggtga gacctcgcag gctactacag      240
tgaaggccgt tgtcggcccc tggtagtccg cagccacaga cagacccgaa aaggaaactc      300
atg tcc ccg aac gac tcc ttc atc tcc gcc ccc tcc gag atc cgc acc        348
Met Ser Pro Asn Asp Ser Phe Ile Ser Ala Pro Ser Glu Ile Arg Thr
1               5                   10                  15
ccg gac gga ccg cgc cgc gag ggc cag ccc ttc tgg aac aag cag cgc        396
Pro Asp Gly Pro Arg Arg Glu Gly Gln Pro Phe Trp Asn Lys Gln Arg
            20                  25                  30
aac tcc tcc atg ccg gta cac cgc tac cgc ccc ttc gcc gag gcc gtc        444
Asn Ser Ser Met Pro Val His Arg Tyr Arg Pro Phe Ala Glu Ala Val
        35                  40                  45
gag gac atc gtt ctg ccg gac cgc acc tgg ccg gac aag aag atc acc        492
Glu Asp Ile Val Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr
    50                  55                  60
gcc gcc ccg cag tgg tgt gcg gtc gac ctg cgt gac ggc aac cag gcg        540
Ala Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala
65                  70                  75                  80
ctc atc gac ccg atg agc ccg gaa cgc aag cgc cgc atg ttc aac ctg        588
Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Asn Leu
                85                  90                  95
ctg gtg cag atg ggc tac aag gag atc gag gtt ggt ttc ccg tcc gcc        636
Leu Val Gln Met Gly Tyr Lys Glu Ile Glu Val Gly Phe Pro Ser Ala
            100                 105                 110
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tcc cag acc gac ttc gac ttc gtc cgc gag atc atc gag cag gac atg        684
Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Gln Asp Met
        115                 120                 125
atc ccg gag gac gtc acc atc cag gtc ctg gtc cag gcc cgt gag cac        732
Ile Pro Glu Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His
    130                 135                 140
ctg atc cgc cgc acc ttc gag gcg tgc gag ggc gcg aag aac gtc atc        780
Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile
145                 150                 155                 160
gtc cac ttc tac aac tcc acc tcc gag ctg cag cgc cgc gtc gtg ttc        828
Val His Phe Tyr Asn Ser Thr Ser Glu Leu Gln Arg Arg Val Val Phe
                165                 170                 175
cgc aag gat aag ccg gcc atc aag cag ctg gcc gtc gac gcc gcc gag        876
Arg Lys Asp Lys Pro Ala Ile Lys Gln Leu Ala Val Asp Ala Ala Glu
            180                 185                 190
ctg atc cag acc atc gcc cag gac tac ccg ggc acc aac tgg cgt tgg        924
Leu Ile Gln Thr Ile Ala Gln Asp Tyr Pro Gly Thr Asn Trp Arg Trp
        195                 200                 205
cag tac tcc ccg gag tcc ttc acc ggc acc gag ctg gag ttc gcc ctc        972
Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Leu Glu Phe Ala Leu
    210                 215                 220
gag gtc tgc aac gcc gtc atc gag gtc atg gcg ccc acc ccg gac aac       1020
Glu Val Cys Asn Ala Val Ile Glu Val Met Ala Pro Thr Pro Asp Asn
225                 230                 235                 240
ccg atc aac atc aac ctg ccg tcc acc gtc gag atg atc acc ccg aac       1068
Pro Ile Asn Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn
                245                 250                 255

gtc tac gcc gac tcc atc gag tgg atg cac cgc aac ctg gac cgc cgt       1116
Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asp Arg Arg
            260                 265                 270
gac tcc gtc atc ctg tcg ctg cac ccc cac aac gac cgt ggt gag ggc       1164
Asp Ser Val Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Glu Gly
        275                 280                 285
gtc gcc gcc gcc gag ctg ggc tac ctg gcc ggc gcc gac cgc atc gag       1212
Val Ala Ala Ala Glu Leu Gly Tyr Leu Ala Gly Ala Asp Arg Ile Glu
    290                 295                 300
ggc tgc ctg ttc ggc aac ggt gag cgc acc ggt aac gtc tgc ctg gtc       1260
Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val
305                 310                 315                 320
acc ctg ggc ctg aac atg ctc acc cag ggc gtc gac ccg cag atc gac       1308
Thr Leu Gly Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Ile Asp
                325                 330                 335
ttc tcc gac atc cgc cag atc cgc agc acc gtc gag tac tgc aac cag       1356
Phe Ser Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln
            340                 345                 350
ctg cga gtc ccg gag cgt cac ccc tac ggc ggc gac ctg gtc ttc acc       1404
Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr
        355                 360                 365
gcc ttc tcc ggc tcc cac cag gac gcc gtc aac aag ggc ctc gac gcc       1452
Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
    370                 375                 380
atg gcc gcc aag gtc aag ccg ggc gcc aac aac acc gag gtc acc tgg       1500
Met Ala Ala Lys Val Lys Pro Gly Ala Asn Asn Thr Glu Val Thr Trp
385                 390                 395                 400
gag gag ctg ggc aag gcc gtc tgg gag gtt ccc tac ctg ccc atc gac       1548
Glu Glu Leu Gly Lys Ala Val Trp Glu Val Pro Tyr Leu Pro Ile Asp
                405                 410                 415
ccg aag gac gtc ggc cgc gac tac gag gcc gtc atc cgc gtc aac tcc       1596
Pro Lys Asp Val Gly Arg Asp Tyr Glu Ala Val Ile Arg Val Asn Ser
            420                 425                 430
cag tcc ggt aag ggc ggc gtc gcc tac atc atg aag acg gat cac ggc       1644
Gln Ser Gly Lys Gly Gly Val Ala Tyr Ile Met Lys Thr Asp His Gly
        435                 440                 445
atc aac ctg ccg cgt cag atg cag gcc gag ttc tcc tcc gtc gtc cag       1692
Ile Asn Leu Pro Arg Gln Met Gln Ala Glu Phe Ser Ser Val Val Gln
    450                 455                 460
gcg atc acc gac tcc gag ggc gga gag gtc aac tcc aag gag atg tgg       1740
Ala Ile Thr Asp Ser Glu Gly Gly Glu Val Asn Ser Lys Glu Met Trp
465                 470                 475                 480
gac gtc ttc gcc acc gag tac ctg gat gtc acc gag ccg gtg gag gag       1788
Asp Val Phe Ala Thr Glu Tyr Leu Asp Val Thr Glu Pro Val Glu Glu
                485                 490                 495
gtc tcc atc cgc atc gtc aac gcc gag acc gac acc gac gag gcc acc       1836
Val Ser Ile Arg Ile Val Asn Ala Glu Thr Asp Thr Asp Glu Ala Thr
            500                 505                 510
gtc acc gcc acc gtc atc cac aag ggc tcc gag aag gag atc acc ggc       1884
Val Thr Ala Thr Val Ile His Lys Gly Ser Glu Lys Glu Ile Thr Gly
```

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        515                 520                 525
acc ggc aac ggc ccc gtc gcc gcc tac gcc aac gcc ctg gag cag ctg      1932
Thr Gly Asn Gly Pro Val Ala Ala Tyr Ala Asn Ala Leu Glu Gln Leu
    530                 535                 540
ggc atc gac gcg gag gtc cag ttc tac tcc cag cag gcc cgc tcc tcg      1980
Gly Ile Asp Ala Glu Val Gln Phe Tyr Ser Gln Gln Ala Arg Ser Ser
545                 550                 555                 560
ggc gat gac gcc gag gcc gcc tgc tac atc tac gcc acg gtc aac ggc      2028
Gly Asp Asp Ala Glu Ala Ala Cys Tyr Ile Tyr Ala Thr Val Asn Gly
                565                 570                 575
tcc gcc gcc tgg ggc gtc ggt atc gcg ggc tcc atc acc cgc gcc tcc      2076
Ser Ala Ala Trp Gly Val Gly Ile Ala Gly Ser Ile Thr Arg Ala Ser
            580                 585                 590
atc aag gca ctg acc tcc gcg gtc aac cgt gcc atc aag gtc gag gcc      2124
Ile Lys Ala Leu Thr Ser Ala Val Asn Arg Ala Ile Lys Val Glu Ala
        595                 600                 605
tcc gtg ctg gcc ggc ggc gtc tag accgcctgag tcacgggagg ggagtgcgcg      2178
Ser Val Leu Ala Gly Gly Val
    610                 615
gccgcgcact cccctccttc cgtatctcac cgcccctacc ggcccctacc agcacagtcc      2238
ccgcaggaga ggcactagac tctgaacaat gaccacgacc ccagaccacg gcgattccgc      2298
agctgagacc ccgcctgccg tcgagccggc gttccccttc gtcgctctga cggtccaggc      2358
cacggggatc catccgtcga ccgcccgcct ggtggccgtc gacgtcctga ccttcgacga      2418
ggacggggag atcggcgagg agttccacac                                      2448
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<212>  PRT
<213>  Corynebacterium humireducens

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1               5                  10                  15
Pro Asp Gly Pro Arg Arg Glu Gly Gln Pro Phe Trp Asn Lys Gln Arg
            20                  25                  30
Asn Ser Ser Met Pro Val His Arg Tyr Arg Pro Phe Ala Glu Ala Val
        35                  40                  45
Glu Asp Ile Val Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr
    50                  55                  60
Ala Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala
65                  70                  75                  80
Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Asn Leu
                85                  90                  95
Leu Val Gln Met Gly Tyr Lys Glu Ile Glu Val Gly Phe Pro Ser Ala
            100                 105                 110
Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Gln Asp Met
        115                 120                 125
Ile Pro Glu Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His
    130                 135                 140
Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile
145                 150                 155                 160
Val His Phe Tyr Asn Ser Thr Ser Glu Leu Gln Arg Arg Val Val Phe
                165                 170                 175
Arg Lys Asp Lys Pro Ala Ile Lys Gln Leu Ala Val Asp Ala Ala Glu
            180                 185                 190
Leu Ile Gln Thr Ile Ala Gln Asp Tyr Pro Gly Thr Asn Trp Arg Trp
        195                 200                 205
Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Leu Glu Phe Ala Leu
    210                 215                 220
Glu Val Cys Asn Ala Val Ile Glu Val Met Ala Pro Thr Pro Asp Asn
225                 230                 235                 240
Pro Ile Asn Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn
                245                 250                 255
Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asp Arg Arg
            260                 265                 270
Asp Ser Val Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Glu Gly
        275                 280                 285
Val Ala Ala Ala Glu Leu Gly Tyr Leu Ala Gly Ala Asp Arg Ile Glu
    290                 295                 300
Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val
305                 310                 315                 320
Thr Leu Gly Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Ile Asp
                325                 330                 335
Phe Ser Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln
            340                 345                 350
Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr
        355                 360                 365
Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
    370                 375                 380
```

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Met Ala Ala Lys Val Lys Pro Gly Ala Asn Asn Thr Glu Val Thr Trp
385                 390                 395                 400
Glu Glu Leu Gly Lys Ala Val Trp Glu Val Pro Tyr Leu Pro Ile Asp
                405                 410                 415
Pro Lys Asp Val Gly Arg Asp Tyr Glu Ala Val Ile Arg Val Asn Ser
            420                 425                 430
Gln Ser Gly Lys Gly Gly Val Ala Tyr Ile Met Lys Thr Asp His Gly
        435                 440                 445
Ile Asn Leu Pro Arg Gln Met Gln Ala Glu Phe Ser Ser Val Val Gln
    450                 455                 460
Ala Ile Thr Asp Ser Glu Gly Gly Glu Val Asn Ser Lys Glu Met Trp
465                 470                 475                 480
Asp Val Phe Ala Thr Glu Tyr Leu Asp Val Thr Glu Pro Val Glu Glu
                485                 490                 495
Val Ser Ile Arg Ile Val Asn Ala Glu Thr Asp Thr Asp Glu Ala Thr
            500                 505                 510
Val Thr Ala Thr Val Ile His Lys Gly Ser Glu Lys Glu Ile Thr Gly
        515                 520                 525
Thr Gly Asn Gly Pro Val Ala Ala Tyr Ala Asn Ala Leu Glu Gln Leu
    530                 535                 540
Gly Ile Asp Ala Glu Val Gln Phe Tyr Ser Gln Gln Ala Arg Ser Ser
545                 550                 555                 560
Gly Asp Asp Ala Glu Ala Ala Cys Tyr Ile Tyr Ala Thr Val Asn Gly
                565                 570                 575
Ser Ala Ala Trp Gly Val Gly Ile Ala Gly Ser Ile Thr Arg Ala Ser
            580                 585                 590
Ile Lys Ala Leu Thr Ser Ala Val Asn Arg Ala Ile Lys Val Glu Ala
        595                 600                 605
Ser Val Leu Ala Gly Gly Val
    610                 615
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cggggaaccg gtgacggcgg cgacgagctc gacgtcgtcg agactgcgga gcgccgggag      120
gaaggcctgc tgggtgatct ggccgacacc gacgacagcg aaacggacag gggagtcata      180
tgcgtgtgtg ctcatggccc caggctacgg actcgaaacg tgcggcgttg agcgcacgag      240
gggaggggtg ggctgataga atcgccgcca gttcagcagg tgagaaagga atcccacaga      300
atg aaa ctt gca gtc att ggc gga gac ggc atc ggc ccg gag gtc acc         348
Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
1               5                   10                  15
gaa gag gcg ctc aag gtc ctc cgc acc gtc cgc gac gac atc gag acc         396
Glu Glu Ala Leu Lys Val Leu Arg Thr Val Arg Asp Asp Ile Glu Thr
            20                  25                  30
acc gac tac gat ctc ggc gca cgt cgc tac ctg cgc aac ggt gag ctg         444
Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Arg Asn Gly Glu Leu
        35                  40                  45
ctc acc gac gcc gac ctc gac tcc ctc cgc gag cac gac gcc atc ctc         492
Leu Thr Asp Ala Asp Leu Asp Ser Leu Arg Glu His Asp Ala Ile Leu
    50                  55                  60
ctc ggc gcc atc ggc gcc ccg gac acc gtc gcg ccg ggc gtc ctc gag         540
Leu Gly Ala Ile Gly Ala Pro Asp Thr Val Ala Pro Gly Val Leu Glu
65                  70                  75                  80
cgt ggc ctg ctg ctc aag atg cgt ttc gcc ctc gac cac cac gtc aac         588
Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
                85                  90                  95
ctg cgt ccc tcc aag ctc tac gag ggc gtc gag tcc ccg ctg aag aac         636
Leu Arg Pro Ser Lys Leu Tyr Glu Gly Val Glu Ser Pro Leu Lys Asn
            100                 105                 110
ccg ggc gag atc gac ttc gtc gtc gtc cgc gag ggc acc gag ggc gcc         684
Pro Gly Glu Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala
        115                 120                 125
tac acc ggc aac ggc ggc gcc atc cgc gtg ggc acc ccg cac gag gtc         732
Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Val
    130                 135                 140
gcc aac gag acc tcc gtc aac acc cgc tac ggc gcc gag cgc gtc gtc         780
Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Val
145                 150                 155                 160
cgc tac gcc ttc gag ctg gcc atg acc cgc cgc aag cac gtc acc ctg         828
Arg Tyr Ala Phe Glu Leu Ala Met Thr Arg Arg Lys His Val Thr Leu
                165                 170                 175
gtc cac aag acc aac gtg ctc gtc cac ggc ggc ggc atg tgg cag cgc         876
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Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Met Trp Gln Arg
            180                 185                 190
acc gtc gac gag gtc gcc acg gag tac cct gag gtc acc gtc gac tac      924
Thr Val Asp Glu Val Ala Thr Glu Tyr Pro Glu Val Thr Val Asp Tyr
        195                 200                 205
gcg cac atc gac gcc gcg acg atc tac atg atc acc gac ccc tcc cgc      972
Ala His Ile Asp Ala Ala Thr Ile Tyr Met Ile Thr Asp Pro Ser Arg
    210                 215                 220
ttc gac gtc atc gtc acc gac aac ctc ttc ggc gac atc atc acc gat     1020
Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Ile Thr Asp
225                 230                 235                 240
gag gcc ggt gcc gtc tcc ggt ggc atc ggc ctc gcc gcc tcc ggc aac     1068
Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn
                245                 250                 255
atc gac gcc acc cgc acc aac ccg tcc atg ttc gag ccg gtc cac ggc     1116
Ile Asp Ala Thr Arg Thr Asn Pro Ser Met Phe Glu Pro Val His Gly
            260                 265                 270
tcc gca ccg gac atc gcc ggc cag ggc atc gcc gac ccg acc gcc gcc     1164
Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala
        275                 280                 285
atc ctc tcc gcc gcg atg ctg ctg cgt cac ctc ggt gac gag gac aac     1212
Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn
    290                 295                 300
gcc gca cgg atc gag gcc gcg gtg gcc gag gac gtc gcc aag cgt gag     1260
Ala Ala Arg Ile Glu Ala Ala Val Ala Glu Asp Val Ala Lys Arg Glu
305                 310                 315                 320
ggg cag atc cgc acc acc gag gtc ggc gac cgc atc gcc gcc gcc ctc     1308
Gly Gln Ile Arg Thr Thr Glu Val Gly Asp Arg Ile Ala Ala Ala Leu
                325                 330                 335
aag tag tctgtcggca gcagacagac gccatatata taaggagcat tcgtgaggcg      1364
Lys

acgtacagca ctactggccc tggccaccac cctggccatg gtcaccggat gctccacctc    1424
ggcggacacc ggtgacgggg acgaccggaa gcccggcacc cccgccctgg agatgacctc    1484
ctccgaggtc atcgccgacg ccgccggcaa cggcgtcgac acctccgccc gcctcttcga    1544
ggaggcggag accgtcgtgg tcgccgccga cacccctgag gaccaggccc ggggcgccca    1604
cctggcgatc                                                          1614
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<213>  Corynebacterium humireducens
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Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
1               5                   10                  15
Glu Glu Ala Leu Lys Val Leu Arg Thr Val Arg Asp Asp Ile Glu Thr
            20                  25                  30
Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Arg Asn Gly Glu Leu
        35                  40                  45
Leu Thr Asp Ala Asp Leu Asp Ser Leu Arg Glu His Asp Ala Ile Leu
    50                  55                  60
Leu Gly Ala Ile Gly Ala Pro Asp Thr Val Ala Pro Gly Val Leu Glu
65                  70                  75                  80
Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
                85                  90                  95
Leu Arg Pro Ser Lys Leu Tyr Glu Gly Val Glu Ser Pro Leu Lys Asn
            100                 105                 110
Pro Gly Glu Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala
        115                 120                 125
Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Val
    130                 135                 140
Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Val
145                 150                 155                 160
Arg Tyr Ala Phe Glu Leu Ala Met Thr Arg Arg Lys His Val Thr Leu
                165                 170                 175
Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Met Trp Gln Arg
            180                 185                 190
Thr Val Asp Glu Val Ala Thr Glu Tyr Pro Glu Val Thr Val Asp Tyr
        195                 200                 205
Ala His Ile Asp Ala Ala Thr Ile Tyr Met Ile Thr Asp Pro Ser Arg
    210                 215                 220
Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Ile Thr Asp
225                 230                 235                 240
Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn
                245                 250                 255
Ile Asp Ala Thr Arg Thr Asn Pro Ser Met Phe Glu Pro Val His Gly
            260                 265                 270
Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala
        275                 280                 285
```

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Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn
    290                 295                 300
Ala Ala Arg Ile Glu Ala Ala Val Ala Glu Asp Val Ala Lys Arg Glu
305                 310                 315                 320
Gly Gln Ile Arg Thr Thr Glu Val Gly Asp Arg Ile Ala Ala Ala Leu
                325                 330                 335
Lys
<210>  113
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<212>  ADN
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cgtcgccgcg ggcgaggatg cggtgtgtct cgagggcggt ggcgaggcgg tgggcggtgg      120
cgcggggcag gccggtggtc tcgcacagtt cggtgaggga gaggggatgg ggggcgacgg      180
ccatcatgat ggcgacggcc cgatcgagca ccttgatccc tgacactgcg ctatactgtc      240
ccataccacg atactaacat ctcaccttgt gagatttcac agatggaaag gtggacatcc      300
atg gcc gag aag ctc acg ctg gcc gag aag gtg tgg aac gac cat att         348
Met Ala Glu Lys Leu Thr Leu Ala Glu Lys Val Trp Asn Asp His Ile
1               5                   10                  15
gtc gcg aag ggc gag aac ggc gag ccc gat ctc ctc tac att gac ctg        396
Val Ala Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu Tyr Ile Asp Leu
            20                  25                  30
cag ctc ctg cac gag gtg acc tcc ccg cag gcc ttc gac gga ctg cgc        444
Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe Asp Gly Leu Arg
        35                  40                  45
ctc gcc ggc cgc aag ctc cgc cgc ccg gac ctg cac ctg gcc acc gag        492
Leu Ala Gly Arg Lys Leu Arg Arg Pro Asp Leu His Leu Ala Thr Glu
    50                  55                  60
gac cac aac gtg ccc acc gag ggc atc gtc tcc ggc tcc ctc ctg gag        540
Asp His Asn Val Pro Thr Glu Gly Ile Val Ser Gly Ser Leu Leu Glu
65                  70                  75                  80
atc aag gag gcc acc tcc cgc acg cag gtc gag acc ctg cgc aag aac        588
Ile Lys Glu Ala Thr Ser Arg Thr Gln Val Glu Thr Leu Arg Lys Asn
                85                  90                  95
tgc gag gag ttc ggc atc cgc ctg cac ccg atg ggc gac gtc aag cag        636
Cys Glu Glu Phe Gly Ile Arg Leu His Pro Met Gly Asp Val Lys Gln
            100                 105                 110
ggc atc gtc cac acc gtc ggc ccg cag ctg ggc gcc acc cag ccg ggc        684
Gly Ile Val His Thr Val Gly Pro Gln Leu Gly Ala Thr Gln Pro Gly
        115                 120                 125
atg acc atc gtc tgc ggc gac tcc cac acc tcc acc cac ggt gcc ttc        732
Met Thr Ile Val Cys Gly Asp Ser His Thr Ser Thr His Gly Ala Phe
    130                 135                 140
ggc tcc atc gcc atg ggc atc ggc acc tcc gag gtc gag cac gtc atg        780
Gly Ser Ile Ala Met Gly Ile Gly Thr Ser Glu Val Glu His Val Met
145                 150                 155                 160
gcg acc cag acc ctg ccg ctc aag ccg ttc aag acc atg gcc atc gag        828
Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe Lys Thr Met Ala Ile Glu
                165                 170                 175
gtc tcc ggc gag ctg cag gag ggc gtc acc gcc aag gac ctc atc ttg        876
Val Ser Gly Glu Leu Gln Glu Gly Val Thr Ala Lys Asp Leu Ile Leu
            180                 185                 190
gcg atc atc gcc aag atc ggc acc ggc ggc ggc cag ggc cac atc atc        924
Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly Gly Gln Gly His Ile Ile
        195                 200                 205
gag tac cgc ggc gag gcc atc gag aag ctc tcg atg gag gcc cgg atg        972
Glu Tyr Arg Gly Glu Ala Ile Glu Lys Leu Ser Met Glu Ala Arg Met
    210                 215                 220
acc atc tgc aac atg tcc atc gag gcc ggt gcc cgt gcc ggc atg gtc       1020
Thr Ile Cys Asn Met Ser Ile Glu Ala Gly Ala Arg Ala Gly Met Val
225                 230                 235                 240
gcc ccc gac cag aag acc ttc gac tac gtc cag ggc cgc gag ttc gcc       1068
Ala Pro Asp Gln Lys Thr Phe Asp Tyr Val Gln Gly Arg Glu Phe Ala
                245                 250                 255
ccc acc ggc gag gac tgg gac gcc gcc gtc gcc tac tgg aag acc ctg       1116
Pro Thr Gly Glu Asp Trp Asp Ala Ala Val Ala Tyr Trp Lys Thr Leu
            260                 265                 270
ccg acc gac gag ggc gcc gag ttc gac acc gtc gtc gag atc gac ggc       1164
Pro Thr Asp Glu Gly Ala Glu Phe Asp Thr Val Val Glu Ile Asp Gly
        275                 280                 285
tcc gcg ctg acc ccg ttc gtc acc tgg ggc acc aac ccg ggc cag ggc       1212
Ser Ala Leu Thr Pro Phe Val Thr Trp Gly Thr Asn Pro Gly Gln Gly
    290                 295                 300
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ctg ccc ctg tcc gcg aac gtc ccg gac ccg gag gac ttc acc aac gag       1260
Leu Pro Leu Ser Ala Asn Val Pro Asp Pro Glu Asp Phe Thr Asn Glu
305                 310                 315                 320
gcc gac aag gcc gcc gcg gag aag gcc ctg gcc tac atg gac ctc acc       1308
Ala Asp Lys Ala Ala Ala Glu Lys Ala Leu Ala Tyr Met Asp Leu Thr
                325                 330                 335
ccg ggc acc ccg ctg cgg gac atc aag atc gac acc gtc ttc ctc ggc       1356
Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr Val Phe Leu Gly
            340                 345                 350
tcc tgc acc aac gcc cgc atc gag gac ctg cgc gct gcc gcc gag gtc       1404
Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Arg Ala Ala Ala Glu Val
        355                 360                 365
gtc gag ggc cgc acg atc gcc ccg aac acc cgc atg ctc gtc gtc ccg       1452
Val Glu Gly Arg Thr Ile Ala Pro Asn Thr Arg Met Leu Val Val Pro
    370                 375                 380
tcc tcg acg ctg gtc aag cag cag gcc gag gag gag ggg ctg gac aag       1500
Ser Ser Thr Leu Val Lys Gln Gln Ala Glu Glu Glu Gly Leu Asp Lys
385                 390                 395                 400
atc ttc acc gac ttc ggc gcc gag tgg cgc acc gcc ggc tgc tcc atg       1548
Ile Phe Thr Asp Phe Gly Ala Glu Trp Arg Thr Ala Gly Cys Ser Met
                405                 410                 415
tgc ctg ggc atg aac ccg gac cag ctg gcc ccg ggc gag cgc tcc gcc       1596
Cys Leu Gly Met Asn Pro Asp Gln Leu Ala Pro Gly Glu Arg Ser Ala
            420                 425                 430
tcc acc tcg aac cgt aac ttc gag ggc cgg cag ggc ccg ggc ggc cgc       1644
Ser Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly Pro Gly Gly Arg
        435                 440                 445
acc cac ctg gtg tcc ccg ccg gtc gcc gcc gcc acc gcc gtc ctc ggc       1692
Thr His Leu Val Ser Pro Pro Val Ala Ala Ala Thr Ala Val Leu Gly
    450                 455                 460
cac ctg gct tcc ccc gca gac ctc tga ccacgccgac caccaaggag             1739
His Leu Ala Ser Pro Ala Asp Leu
465                 470
ataaaaacag tggagaagtt caccacccac accggcgtcg gcgtcccgct gacccgctcg      1799
aacgtcgaca ccgaccagat catccccgcc gtctacctca agcgcgtcac ccgcacgggc      1859
ttcgatgacg gcctgttcgc cgagtggcgc aaggacgatt ccttcgtcct caaccaggag      1919
ccctaccgca acggctccgt cctggtcgcc ggccccgact tcggcaccgg ctcctcccgt      1979
gagcacgccg tctgggccct catggactac ggcttccgcg                            2019
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<211>  472
<212>  PRT
<213>  Corynebacterium humireducens
<400>  114
Met Ala Glu Lys Leu Thr Leu Ala Glu Lys Val Trp Asn Asp His Ile
1               5                   10                  15
Val Ala Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu Tyr Ile Asp Leu
            20                  25                  30
Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe Asp Gly Leu Arg
        35                  40                  45
Leu Ala Gly Arg Lys Leu Arg Arg Pro Asp Leu His Leu Ala Thr Glu
    50                  55                  60
Asp His Asn Val Pro Thr Glu Gly Ile Val Ser Gly Ser Leu Leu Glu
65                  70                  75                  80
Ile Lys Glu Ala Thr Ser Arg Thr Gln Val Glu Thr Leu Arg Lys Asn
                85                  90                  95
Cys Glu Glu Phe Gly Ile Arg Leu His Pro Met Gly Asp Val Lys Gln
            100                 105                 110
Gly Ile Val His Thr Val Gly Pro Gln Leu Gly Ala Thr Gln Pro Gly
        115                 120                 125
Met Thr Ile Val Cys Gly Asp Ser His Thr Ser Thr His Gly Ala Phe
    130                 135                 140
Gly Ser Ile Ala Met Gly Ile Gly Thr Ser Glu Val Glu His Val Met
145                 150                 155                 160
Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe Lys Thr Met Ala Ile Glu
                165                 170                 175
Val Ser Gly Glu Leu Gln Glu Gly Val Thr Ala Lys Asp Leu Ile Leu
            180                 185                 190
Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly Gly Gln Gly His Ile Ile
        195                 200                 205
Glu Tyr Arg Gly Glu Ala Ile Glu Lys Leu Ser Met Glu Ala Arg Met
    210                 215                 220
Thr Ile Cys Asn Met Ser Ile Glu Ala Gly Ala Arg Ala Gly Met Val
225                 230                 235                 240
Ala Pro Asp Gln Lys Thr Phe Asp Tyr Val Gln Gly Arg Glu Phe Ala
                245                 250                 255
Pro Thr Gly Glu Asp Trp Asp Ala Ala Val Ala Tyr Trp Lys Thr Leu
            260                 265                 270
Pro Thr Asp Glu Gly Ala Glu Phe Asp Thr Val Val Glu Ile Asp Gly
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        275                 280                 285
Ser Ala Leu Thr Pro Phe Val Thr Trp Gly Thr Asn Pro Gly Gln Gly
    290                 295                 300
Leu Pro Leu Ser Ala Asn Val Pro Asp Pro Glu Asp Phe Thr Asn Glu
305                 310                 315                 320
Ala Asp Lys Ala Ala Ala Glu Lys Ala Leu Ala Tyr Met Asp Leu Thr
                325                 330                 335
Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr Val Phe Leu Gly
            340                 345                 350
Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Arg Ala Ala Ala Glu Val
        355                 360                 365
Val Glu Gly Arg Thr Ile Ala Pro Asn Thr Arg Met Leu Val Val Pro
    370                 375                 380
Ser Ser Thr Leu Val Lys Gln Gln Ala Glu Glu Glu Gly Leu Asp Lys
385                 390                 395                 400
Ile Phe Thr Asp Phe Gly Ala Glu Trp Arg Thr Ala Gly Cys Ser Met
                405                 410                 415
Cys Leu Gly Met Asn Pro Asp Gln Leu Ala Pro Gly Glu Arg Ser Ala
            420                 425                 430
Ser Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly Pro Gly Gly Arg
        435                 440                 445
Thr His Leu Val Ser Pro Pro Val Ala Ala Ala Thr Ala Val Leu Gly
    450                 455                 460
His Leu Ala Ser Pro Ala Asp Leu
465                 470
<210>  115
<211>  1197
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(897)
<223>  gen leuD
<400>  115
cccgtcctcg acgctggtca agcagcaggc cgaggaggag gggctggaca agatcttcac       60
cgacttcggc gccgagtggc gcaccgccgg ctgctccatg tgcctgggca tgaacccgga      120
ccagctggcc ccgggcgagc gctccgcctc cacctcgaac cgtaacttcg agggccggca      180
gggcccgggc ggccgcaccc acctggtgtc cccgccggtc gccgccgcca ccgccgtcct      240
cggccacctg gcttcccccg cagacctctg accacgccga ccaccaagga gataaaaaca      300
gtg gag aag ttc acc acc cac acc ggc gtc ggc gtc ccg ctg acc cgc         348
Val Glu Lys Phe Thr Thr His Thr Gly Val Gly Val Pro Leu Thr Arg
1               5                   10                  15
tcg aac gtc gac acc gac cag atc atc ccc gcc gtc tac ctc aag cgc         396
Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg
            20                  25                  30
gtc acc cgc acg ggc ttc gat gac ggc ctg ttc gcc gag tgg cgc aag         444
Val Thr Arg Thr Gly Phe Asp Asp Gly Leu Phe Ala Glu Trp Arg Lys
        35                  40                  45
gac gat tcc ttc gtc ctc aac cag gag ccc tac cgc aac ggc tcc gtc         492
Asp Asp Ser Phe Val Leu Asn Gln Glu Pro Tyr Arg Asn Gly Ser Val
    50                  55                  60
ctg gtc gcc ggc ccc gac ttc ggc acc ggc tcc tcc cgt gag cac gcc         540
Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala
65                  70                  75                  80
gtc tgg gcc ctc atg gac tac ggc ttc cgc gtc gtg ctg tcc tcc cgc         588
Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Val Val Leu Ser Ser Arg
                85                  90                  95
ttc gcc gac atc ttc cgc ggc aac tcc ggc aag gcc ggc ctg ctg gcc         636
Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Leu Leu Ala
            100                 105                 110
gcc cag atg gag gag gcc gat atc gag ctg ctg tgg aag cag ctc gag         684
Ala Gln Met Glu Glu Ala Asp Ile Glu Leu Leu Trp Lys Gln Leu Glu
        115                 120                 125
gct gag ccg ggc ctg gag atc acc gtc gac ctc gag tcc cgc acc gtc         732
Ala Glu Pro Gly Leu Glu Ile Thr Val Asp Leu Glu Ser Arg Thr Val
    130                 135                 140
acc gcc ggc gag aac acc tac cag ttc tcc gtc gac gac tac acc cgc         780
Thr Ala Gly Glu Asn Thr Tyr Gln Phe Ser Val Asp Asp Tyr Thr Arg
145                 150                 155                 160
tgg cgc ctc atg gag ggc ctc gac gac atc ggc ctg acc ctg cgc gac         828
Trp Arg Leu Met Glu Gly Leu Asp Asp Ile Gly Leu Thr Leu Arg Asp
                165                 170                 175
gag cag gcc atc acc gac tac gag gcg aag cgc ccc gtg tac aag ccg         876
Glu Gln Ala Ile Thr Asp Tyr Glu Ala Lys Arg Pro Val Tyr Lys Pro
            180                 185                 190
acc atc acc gcg gag gtg tga gtcatgtccg acaaccgttt cgacgaggga           927
Thr Ile Thr Ala Glu Val
        195
```

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atccgcatcc gccgcgaggt catgggcgac gatttcgtcg acgccgccct gacccgcaac      987
gccggcaccg acggcgagga cctgcagcac cacatcaccg ccaccgtctg gggttcggtg     1047
tggacccgcg agggcctgtc caagcgtgac cgcagcctgc tcaacatcgg catgctcgtc     1107
gccctgcgcg cgaccgagga actgcgcgga catgtccgcg gcggcctgcg taacggcctg     1167
acccgcgagg agatcaccga ggcgatcatc                                      1197
<210>  116
<211>  198
<212>  PRT
<213>  Corynebacterium humireducens
<400>  116
Val Glu Lys Phe Thr Thr His Thr Gly Val Gly Val Pro Leu Thr Arg
1               5                  10                  15
Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg
            20                  25                  30
Val Thr Arg Thr Gly Phe Asp Asp Gly Leu Phe Ala Glu Trp Arg Lys
        35                  40                  45
Asp Asp Ser Phe Val Leu Asn Gln Glu Pro Tyr Arg Asn Gly Ser Val
    50                  55                  60
Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala
65                  70                  75                  80
Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Val Val Leu Ser Ser Arg
                85                  90                  95
Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Leu Leu Ala
            100                 105                 110
Ala Gln Met Glu Glu Ala Asp Ile Glu Leu Leu Trp Lys Gln Leu Glu
        115                 120                 125
Ala Glu Pro Gly Leu Glu Ile Thr Val Asp Leu Glu Ser Arg Thr Val
    130                 135                 140
Thr Ala Gly Glu Asn Thr Tyr Gln Phe Ser Val Asp Asp Tyr Thr Arg
145                 150                 155                 160
Trp Arg Leu Met Glu Gly Leu Asp Asp Ile Gly Leu Thr Leu Arg Asp
                165                 170                 175


Glu Gln Ala Ile Thr Asp Tyr Glu Ala Lys Arg Pro Val Tyr Lys Pro
            180                 185                 190
Thr Ile Thr Ala Glu Val
        195
<210>  117
<211>  1398
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1098)
<223>  gen panB
<400>  117
ccgggcgcaa ggcggacgta ctcgtcattc cgccaacccc ggatgattct ctgacgctct       60
gccccggtgg cacgcgtggt gctgatcacc ggccccccga cctggttcat gtccgcagtc      120
tcccatcagc gcctgcggca cgcacctcca cacgtcggtg gcgttgtgag gcacccgctt      180
gttcgcgagc tccgggagtt ttcccaggtc aggttttcct ggggtgaaca agagggtact      240
tccgcacaca tgccttccgt gggaacaggg gggcatatac tcttgcccat ggtttcccgg      300
atg cgt acc cgc cat ttc gcc cag gcc aag gcc gag ggc cgc aag atc         348
Met Arg Thr Arg His Phe Ala Gln Ala Lys Ala Glu Gly Arg Lys Ile
1               5                  10                  15
tcc tgc ctg acc gcc tac gac gcg ccc acc gcc gcg atc ttc gat gag         396
Ser Cys Leu Thr Ala Tyr Asp Ala Pro Thr Ala Ala Ile Phe Asp Glu
            20                  25                  30
gcg ggc atc gac ctg ctc ctc gtc ggc gat tcc gcc gcc aac gtc gtc         444
Ala Gly Ile Asp Leu Leu Leu Val Gly Asp Ser Ala Ala Asn Val Val
        35                  40                  45
ctg ggc cag gac tcg acc ctg tcg atc acg gtc gag gag atg atg acc         492
Leu Gly Gln Asp Ser Thr Leu Ser Ile Thr Val Glu Glu Met Met Thr
    50                  55                  60
atg gcg acc gcc gtc gcc cgc ggc acc gaa cgc gcc ttc gtg gtc acc         540
Met Ala Thr Ala Val Ala Arg Gly Thr Glu Arg Ala Phe Val Val Thr
65                  70                  75                  80
gac ctg ccc ttc ggc tcc tac gag gtc tcc ccc gcc cag gcg ctg gag         588
Asp Leu Pro Phe Gly Ser Tyr Glu Val Ser Pro Ala Gln Ala Leu Glu
                85                  90                  95
acg gcc gcc cgg ttc atg aag cag acc ggt gtc gcc gcg gtg aag atc         636
Thr Ala Ala Arg Phe Met Lys Gln Thr Gly Val Ala Ala Val Lys Ile
            100                 105                 110
gag ggc ggc gtc gag atc gcc ccg acg atc cgc acg ctc gtc gac gcc         684
Glu Gly Gly Val Glu Ile Ala Pro Thr Ile Arg Thr Leu Val Asp Ala
        115                 120                 125
ggc atc ccc gtc atg gcc cac atc ggc tac acc ccg cag tcc gag cac         732
Gly Ile Pro Val Met Ala His Ile Gly Tyr Thr Pro Gln Ser Glu His
```

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    130                 135                 140
gcc ctc ggc ggc tac gtc gtc cag ggt cgc ggg gag gcc gcg gag aag        780
Ala Leu Gly Gly Tyr Val Val Gln Gly Arg Gly Glu Ala Ala Glu Lys
145                 150                 155                 160
ctg cgc gcc gac gcc ctc gcc gtc cag gag gcc ggc gcc ttc gcc gtc        828
Leu Arg Ala Asp Ala Leu Ala Val Gln Glu Ala Gly Ala Phe Ala Val
                165                 170                 175
gtc ctc gag atg gtc ccc gcc ggc atc gcc ggg gag atc acc cgc gag        876
Val Leu Glu Met Val Pro Ala Gly Ile Ala Gly Glu Ile Thr Arg Glu
            180                 185                 190
ctc acc atc ccg acg atc ggc atc ggc gcc ggc gcc gac acc gac ggc        924
Leu Thr Ile Pro Thr Ile Gly Ile Gly Ala Gly Ala Asp Thr Asp Gly
        195                 200                 205
cag gtc ctc gtg tgg acc gac gcc ttc ggt ctc acg cgc ggc cgt acg        972
Gln Val Leu Val Trp Thr Asp Ala Phe Gly Leu Thr Arg Gly Arg Thr
    210                 215                 220
ccg cgt ttc gcg cgt cgt tac gcg gag atc ggg gac atg ctc ctc gac       1020
Pro Arg Phe Ala Arg Arg Tyr Ala Glu Ile Gly Asp Met Leu Leu Asp
225                 230                 235                 240
gcc gcc cgt gcc tac cgc acc gac gtc gag tcc ggc tcc ttc ccg gac       1068
Ala Ala Arg Ala Tyr Arg Thr Asp Val Glu Ser Gly Ser Phe Pro Asp
                245                 250                 255
gag tcc gag tcc ttc cgg gac gag cag tga ccgtcgtcgc gcgcactgtc         1118
Glu Ser Glu Ser Phe Arg Asp Glu Gln
            260                 265
gcgcagctgc gttccgccgt cgccgatctg cagggttccg tcggcctcgt gccgaccatg     1178
ggtgcgctcc acgagggtca cggccgtctg gtgtccctgg ccgccgagga gaactcctcg     1238
gtggtggtga gcatcttcgt caacccgttg cagttcaccg acctcggcga ctgcgacgac     1298
ttccgccact acccgcgtga cctggacaag gacgtcgcct tcctggagaa gctcggcgtc     1358
gacgtcgtgt tcgcgccgac cgacgaggcg atgtacccgg                           1398
<210>  118
<211>  265
<212>  PRT
<213>  Corynebacterium humireducens
<400>  118
Met Arg Thr Arg His Phe Ala Gln Ala Lys Ala Glu Gly Arg Lys Ile
1               5                   10                  15
Ser Cys Leu Thr Ala Tyr Asp Ala Pro Thr Ala Ala Ile Phe Asp Glu
            20                  25                  30
Ala Gly Ile Asp Leu Leu Leu Val Gly Asp Ser Ala Ala Asn Val Val
        35                  40                  45
Leu Gly Gln Asp Ser Thr Leu Ser Ile Thr Val Glu Glu Met Met Thr
    50                  55                  60
Met Ala Thr Ala Val Ala Arg Gly Thr Glu Arg Ala Phe Val Val Thr
65                  70                  75                  80
Asp Leu Pro Phe Gly Ser Tyr Glu Val Ser Pro Ala Gln Ala Leu Glu
                85                  90                  95
Thr Ala Ala Arg Phe Met Lys Gln Thr Gly Val Ala Ala Val Lys Ile
            100                 105                 110
Glu Gly Gly Val Glu Ile Ala Pro Thr Ile Arg Thr Leu Val Asp Ala
        115                 120                 125
Gly Ile Pro Val Met Ala His Ile Gly Tyr Thr Pro Gln Ser Glu His
    130                 135                 140
Ala Leu Gly Gly Tyr Val Val Gln Gly Arg Gly Glu Ala Ala Glu Lys
145                 150                 155                 160
Leu Arg Ala Asp Ala Leu Ala Val Gln Glu Ala Gly Ala Phe Ala Val
                165                 170                 175
Val Leu Glu Met Val Pro Ala Gly Ile Ala Gly Glu Ile Thr Arg Glu
            180                 185                 190
Leu Thr Ile Pro Thr Ile Gly Ile Gly Ala Gly Ala Asp Thr Asp Gly
        195                 200                 205
Gln Val Leu Val Trp Thr Asp Ala Phe Gly Leu Thr Arg Gly Arg Thr
    210                 215                 220
Pro Arg Phe Ala Arg Arg Tyr Ala Glu Ile Gly Asp Met Leu Leu Asp
225                 230                 235                 240
Ala Ala Arg Ala Tyr Arg Thr Asp Val Glu Ser Gly Ser Phe Pro Asp
                245                 250                 255
Glu Ser Glu Ser Phe Arg Asp Glu Gln
            260                 265
<210>  119
<211>  1452
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1152)
<223>  gen panC
<400>  119
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cctcgccgtc caggaggccg gcgccttcgc cgtcgtcctc gagatggtcc ccgccggcat       60
cgccggggag atcacccgcg agctcaccat cccgacgatc ggcatcggcg ccggcgccga      120
caccgacggc caggtcctcg tgtggaccga cgccttcggt ctcacgcgcg gccgtacgcc      180
gcgtttcgcg cgtcgttacg cggagatcgg ggacatgctc ctcgacgccg cccgtgccta      240
ccgcaccgac gtcgagtccg gctccttccc ggacgagtcc gagtccttcc gggacgagca      300
gtg acc gtc gtc gcg cgc act gtc gcg cag ctg cgt tcc gcc gtc gcc         348
Val Thr Val Val Ala Arg Thr Val Ala Gln Leu Arg Ser Ala Val Ala
1               5                  10                  15
gat ctg cag ggt tcc gtc ggc ctc gtg ccg acc atg ggt gcg ctc cac       396
Asp Leu Gln Gly Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His
            20                  25                  30
gag ggt cac ggc cgt ctg gtg tcc ctg gcc gcc gag gag aac tcc tcg       444
Glu Gly His Gly Arg Leu Val Ser Leu Ala Ala Glu Glu Asn Ser Ser
        35                  40                  45
gtg gtg gtg agc atc ttc gtc aac ccg ttg cag ttc acc gac ctc ggc       492
Val Val Val Ser Ile Phe Val Asn Pro Leu Gln Phe Thr Asp Leu Gly
    50                  55                  60
gac tgc gac gac ttc cgc cac tac ccg cgt gac ctg gac aag gac gtc       540
Asp Cys Asp Asp Phe Arg His Tyr Pro Arg Asp Leu Asp Lys Asp Val
65                  70                  75                  80
gcc ttc ctg gag aag ctc ggc gtc gac gtc gtg ttc gcg ccg acc gac       588
Ala Phe Leu Glu Lys Leu Gly Val Asp Val Val Phe Ala Pro Thr Asp
                85                  90                  95
gag gcg atg tac ccg gac ggc ctg ccc cag gtg tgg gtg cgg gcc ggc       636
Glu Ala Met Tyr Pro Asp Gly Leu Pro Gln Val Trp Val Arg Ala Gly
            100                 105                 110
gag atg ggt gag cgc ctc gag ggc gcc tcc cgt ccc ggc cac ttc gac       684
Glu Met Gly Glu Arg Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp
        115                 120                 125
ggc gtg acc acc gtg gtg gcc aag ctg ttc cag ctc atc cag ccg gac       732
Gly Val Thr Thr Val Val Ala Lys Leu Phe Gln Leu Ile Gln Pro Asp
    130                 135                 140
cgc gcc tac ttc ggt gag aag gac gcg cag cag ctg gcg atc atc cag       780
Arg Ala Tyr Phe Gly Glu Lys Asp Ala Gln Gln Leu Ala Ile Ile Gln
145                 150                 155                 160
cgc atg gtc atg gac ctg gac ttc ccg ctg cag atc cgc ccg gtg ccg       828
Arg Met Val Met Asp Leu Asp Phe Pro Leu Gln Ile Arg Pro Val Pro
                165                 170                 175
atc atc cgc ggt gcc gac ggc ctg gcc gag tcc tcc cgc aac cag cac       876
Ile Ile Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln His
            180                 185                 190
ctc acc ccc gag gcg cgg gag cag gcg ctc gtc ctg ccg cgc acc ctg       924
Leu Thr Pro Glu Ala Arg Glu Gln Ala Leu Val Leu Pro Arg Thr Leu
        195                 200                 205
gcc gcg ctg cgt gac cgc gcc gcc gcc ggt gac ccc ctc gac gtc gag       972
Ala Ala Leu Arg Asp Arg Ala Ala Ala Gly Asp Pro Leu Asp Val Glu
    210                 215                 220
ggt gcc cgc gag gcg ctg cgc tcc gcc gag ggc gtg gaa ctc gac cac      1020
Gly Ala Arg Glu Ala Leu Arg Ser Ala Glu Gly Val Glu Leu Asp His
225                 230                 235                 240
ctc gag gtc gtc gac gcc gcg acg ctg ctg ccg gtc tcc gag gtc ggc      1068
Leu Glu Val Val Asp Ala Ala Thr Leu Leu Pro Val Ser Glu Val Gly
                245                 250                 255
gcc ggc gcg ctg gcc gtc gcc gcg atc cac gtg ggt ggc acg cgg ctc      1116
Ala Gly Ala Leu Ala Val Ala Ala Ile His Val Gly Gly Thr Arg Leu
            260                 265                 270
atc gac aac gtg cga ctg ctt ccg ccg cgc gct tag cgtaggggcc           1162
Ile Asp Asn Val Arg Leu Leu Pro Pro Arg Ala
        275                 280
gacgccgacg atcgtcgccg aaccggggcc gagccagtcc ccgtagccca ccaggtgcag     1222
cggcagcccc cggtcgagga cccgccggaa gggacgcagc gccgggcgga agccggtgca     1282
ccagatgagg tgctccgcgt ccacctcgtc gaggctgcgg aacagcggcg tcgcccgcag     1342
gcggccggag tcccgcgcgg ccttcaccgc gggcaggacc acgatgtccc cgagctcgga     1402
gtccgccccc gggtcctcct ccccgcgcag gatcgccagg gcccgcaggc                1452
<210>  120
<211>  283
<212>  PRT
<213>  Corynebacterium humireducens
<400>  120
Val Thr Val Val Ala Arg Thr Val Ala Gln Leu Arg Ser Ala Val Ala
1               5                  10                  15
Asp Leu Gln Gly Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His
            20                  25                  30
Glu Gly His Gly Arg Leu Val Ser Leu Ala Ala Glu Glu Asn Ser Ser
        35                  40                  45
Val Val Val Ser Ile Phe Val Asn Pro Leu Gln Phe Thr Asp Leu Gly
    50                  55                  60
Asp Cys Asp Asp Phe Arg His Tyr Pro Arg Asp Leu Asp Lys Asp Val
```

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65                  70                  75                  80
Ala Phe Leu Glu Lys Leu Gly Val Asp Val Val Phe Ala Pro Thr Asp
                85                  90                  95
Glu Ala Met Tyr Pro Asp Gly Leu Pro Gln Val Trp Val Arg Ala Gly
            100                 105                 110
Glu Met Gly Glu Arg Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp
        115                 120                 125
Gly Val Thr Thr Val Val Ala Lys Leu Phe Gln Leu Ile Gln Pro Asp
    130                 135                 140
Arg Ala Tyr Phe Gly Glu Lys Asp Ala Gln Gln Leu Ala Ile Ile Gln
145                 150                 155                 160
Arg Met Val Met Asp Leu Asp Phe Pro Leu Gln Ile Arg Pro Val Pro
                165                 170                 175
Ile Ile Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln His
            180                 185                 190
Leu Thr Pro Glu Ala Arg Glu Gln Ala Leu Val Leu Pro Arg Thr Leu
        195                 200                 205
Ala Ala Leu Arg Asp Arg Ala Ala Ala Gly Asp Pro Leu Asp Val Glu
    210                 215                 220
Gly Ala Arg Glu Ala Leu Arg Ser Ala Glu Gly Val Glu Leu Asp His
225                 230                 235                 240
Leu Glu Val Val Asp Ala Ala Thr Leu Leu Pro Val Ser Glu Val Gly
                245                 250                 255
Ala Gly Ala Leu Ala Val Ala Ala Ile His Val Gly Gly Thr Arg Leu
            260                 265                 270
Ile Asp Asn Val Arg Leu Leu Pro Pro Arg Ala
        275                 280
<210>  121
<211>  1116
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(816)
<223>  gen ilvH
<400>  121
gcgtcacccg cgaggaggac gtcctgccga cgatccagaa ggcacgcgag atcaacgacc       60
gcccggtcgt catcgacttc atcgtcggtg aggacgccca ggtctggccg atggtcgccg      120
ccggcgcctc caactcggac atcgagtacg cacgtggtct gcgccccttc ttcgagggtg      180
acgagtccgc gggtgagtcc ccggccgaca tccacggtgt catggagaac gcccaggagg      240
agaccgtcga ggaagtcctc gaggagcgcg cgaacgacag cgagaaggag aactaggaca      300
atg gcg aac acc gac atc atc cgc aac acc ctc agc gtc ctg gtc cag         348
Met Ala Asn Thr Asp Ile Ile Arg Asn Thr Leu Ser Val Leu Val Gln
1               5                   10                  15
gac gtc gac ggc atc atc tcc cgc gtc gca ggc atg ttc acc cgc cgt         396
Asp Val Asp Gly Ile Ile Ser Arg Val Ala Gly Met Phe Thr Arg Arg
            20                  25                  30
ggc tac aac ctg gtg tcc atc gtc tcg gcg cac acc gac acc ccg ggc         444
Gly Tyr Asn Leu Val Ser Ile Val Ser Ala His Thr Asp Thr Pro Gly
        35                  40                  45
atc agc cgc atc acc atc gtg gtc gac gcc aac gag ctg gtc atc gag         492
Ile Ser Arg Ile Thr Ile Val Val Asp Ala Asn Glu Leu Val Ile Glu
    50                  55                  60
cag gtc acc aag cag ctc aac aag atc atc ccg gtg ctc aag gtc gtc         540
Gln Val Thr Lys Gln Leu Asn Lys Ile Ile Pro Val Leu Lys Val Val
65                  70                  75                  80
cgc ctc gag gag gac acc acc atc gcc cgc gcc atc atg ctg gtg aag         588
Arg Leu Glu Glu Asp Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
                85                  90                  95
gtc aac gcc gac aac acc aac cgc ccg cag gtc gtc gac gcc gcg aac         636
Val Asn Ala Asp Asn Thr Asn Arg Pro Gln Val Val Asp Ala Ala Asn
            100                 105                 110
atc ttc cgc gcc cgc atc gtc gac gtg gcc cag gag tcc gtg gtc atc         684
Ile Phe Arg Ala Arg Ile Val Asp Val Ala Gln Glu Ser Val Val Ile
        115                 120                 125
gag gcc acc ggt acc ccg ggc aag ctg cgc gcc ctg ctg gag gtc ctc         732
Glu Ala Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Glu Val Leu
    130                 135                 140
gag ccc ttc ggt atc cgt gag ctc atc cag tcc ggt cag atc gcc ctc         780
Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
145                 150                 155                 160
aac cgc ggt ccg aag acg atg gca ccg tcc aag taa caccccctca               826
Asn Arg Gly Pro Lys Thr Met Ala Pro Ser Lys
                165                 170
tcccacctgg tgagacaaca cgcatgaaag tcccaccagg tggggtaccc ctgtctcatg      886
ttgtggtaca aacaacaaca gcacttgtat aagacgaaag gcgagttttt ctcccatggc      946
tattgaactg ctttacgacg ccgacgctga cctctccctc atccagggcc gcaaggtcgc     1006
catcatcggc tacggctccc agggccacgc ccacgcccag aacctgcgtg actccggcgt     1066
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cgaggtctgc atcggcctgc gcgacggctc caagtccgcg gagaaggcca 1116

<210> 122
<211> 171
<212> PRT
<213> Corynebacterium humireducens
<400> 122

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Met Ala Asn Thr Asp Ile Ile Arg Asn Thr Leu Ser Val Leu Val Gln
1               5                  10                  15
Asp Val Asp Gly Ile Ile Ser Arg Val Ala Gly Met Phe Thr Arg Arg
            20                  25                  30
Gly Tyr Asn Leu Val Ser Ile Val Ser Ala His Thr Asp Thr Pro Gly
        35                  40                  45
Ile Ser Arg Ile Thr Ile Val Val Asp Ala Asn Glu Leu Val Ile Glu
    50                  55                  60
Gln Val Thr Lys Gln Leu Asn Lys Ile Ile Pro Val Leu Lys Val Val
65                  70                  75                  80
Arg Leu Glu Glu Asp Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
                85                  90                  95
Val Asn Ala Asp Asn Thr Asn Arg Pro Gln Val Val Asp Ala Ala Asn
            100                 105                 110
Ile Phe Arg Ala Arg Ile Val Asp Val Ala Gln Glu Ser Val Val Ile
        115                 120                 125
Glu Ala Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Glu Val Leu
    130                 135                 140
Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
145                 150                 155                 160
Asn Arg Gly Pro Lys Thr Met Ala Pro Ser Lys
                165                 170
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<210> 123
<211> 1944
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1644)
<223> gen gdh
<400> 123

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gaaggtggcg gcggtgccct caccccgtc ggccatggga gcgagggtga tctcggcgtc       60
ccggatgatc gagcggacac cctcgccgat cagccgtgcg gcctgatcgg cggtggcagt      120
gcccttgaag gagtcggggg cgatgatgat gtggaccatg ggaagcagtc taggggtagt      180
gggagtgaca tattcaactc cggagtgact tgcatgaacc gcgccgcccg tgaaaactat      240
aggccgttag aaaacccccat cccccgggct gcccgcgact gcgggccgga aaggactcgt      300
atg tct att gac gag cag gtc tcc tcc tac tac aac atg ctg ctc aag         348
Met Ser Ile Asp Glu Gln Val Ser Ser Tyr Tyr Asn Met Leu Leu Lys
1               5                  10                  15
cgg aac gca gga gag ccg gag ttc cac cag gca gtc gca gaa gtt ctc         396
Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
            20                  25                  30
gcc tcc ctc aag atc gtc ctg gag aag gat ccg cac tac gcg gac tac         444
Ala Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
        35                  40                  45
ggc ctc atc cag cgc ctg tgc gag ccg gag cgc cag ctc atc ttc cgt         492
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
    50                  55                  60
gtg ccg tgg atc gac gac aac ggc gtg gta cag gtc aac cgt ggt ttc         540
Val Pro Trp Ile Asp Asp Asn Gly Val Val Gln Val Asn Arg Gly Phe
65                  70                  75                  80
cga gta cag ttc aac tcc gcc ctc ggc ccg tac aag ggc ggc cta cgc         588
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
                85                  90                  95
ttc cac ccg tcc gtc aac ctg ggc atc atc aag ttc ctc ggc ttc gag         636
Phe His Pro Ser Val Asn Leu Gly Ile Ile Lys Phe Leu Gly Phe Glu
            100                 105                 110
cag atc ttc aag aac tcc ctc acc ggc ctg ccc atc ggc ggc ggc aag         684
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
        115                 120                 125
ggc ggc tcc gac ttc gac ccg aag ggc aag tcc gag ctc gag atc atg         732
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Leu Glu Ile Met
    130                 135                 140
cgt ttc tgc cag tcc ttc atg acc gag ctg cac aag cac atc ggc gag         780
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Lys His Ile Gly Glu
145                 150                 155                 160
tac aag gac gtc ccc gcc ggt gac atc ggc gtc ggc ggc cgg gag atc         828
Tyr Lys Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
                165                 170                 175
ggt ttc ctc ttc ggc cag tac cgt cgt ctg gcc ggc cag cac gag tcc         876
Gly Phe Leu Phe Gly Gln Tyr Arg Arg Leu Ala Gly Gln His Glu Ser
            180                 185                 190
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ggc gtc ctc acc ggc aag ggc ctc gcc tgg ggt ggc tcc ctc gtg cgc        924
Gly Val Leu Thr Gly Lys Gly Leu Ala Trp Gly Gly Ser Leu Val Arg
        195                 200                 205
acc gag gcc acc ggc tac ggc gcc gtc tac ctc acg cag gag atg atg        972
Thr Glu Ala Thr Gly Tyr Gly Ala Val Tyr Leu Thr Gln Glu Met Met
    210                 215                 220
aag gcc cac ggc gac tcc ctc tcc ggt tcg aag gtc atc gtc tcc ggc       1020
Lys Ala His Gly Asp Ser Leu Ser Gly Ser Lys Val Ile Val Ser Gly
225                 230                 235                 240
tcc ggc aac gtc gcc atc tac gcc atc gag aag gcc cag gag ctc ggc       1068
Ser Gly Asn Val Ala Ile Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly
                245                 250                 255
gcc acc gtc gtc ggc ttc tcc gac tcc tcc ggc tgg gtc tcc acc ccg       1116
Ala Thr Val Val Gly Phe Ser Asp Ser Ser Gly Trp Val Ser Thr Pro
            260                 265                 270
aac ggc gtc gac gtc gag ctg ctc cac gac gtc aag gag aag cgc cgc       1164
Asn Gly Val Asp Val Glu Leu Leu His Asp Val Lys Glu Lys Arg Arg
        275                 280                 285
gag cgc gtc tcc tgc tac gcc gag gag gcc acc ggc gcg acc ttc cac       1212
Glu Arg Val Ser Cys Tyr Ala Glu Glu Ala Thr Gly Ala Thr Phe His
    290                 295                 300
gcc gag ggc tcc atc tgg gac ctc gcc gcc gac gtc gcc ctc ccg tgc       1260
Ala Glu Gly Ser Ile Trp Asp Leu Ala Ala Asp Val Ala Leu Pro Cys
305                 310                 315                 320
gcc acc cag aac gag ctc aac ggc gac cac gcc cgc acc ctg gcc gac       1308
Ala Thr Gln Asn Glu Leu Asn Gly Asp His Ala Arg Thr Leu Ala Asp
                325                 330                 335
aac ggc atc cgc tac gtc gcc gag ggc gcc aac atg ccc tcc acc ccg       1356
Asn Gly Ile Arg Tyr Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
            340                 345                 350
gag gcc atc gag gtc ttc cgt gag cgc ggt atc ttc ttc gcc ccg ggc       1404
Glu Ala Ile Glu Val Phe Arg Glu Arg Gly Ile Phe Phe Ala Pro Gly
        355                 360                 365
aag gcc gcc aac gcc ggt ggc gtg gcc acc tcc gcc ctg gag atg cag       1452
Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
    370                 375                 380
cag aac gcc tcc cgt gac tcc tgg tcc ttc gag tac acg gac cag cgc       1500
Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Gln Arg
385                 390                 395                 400

ctg cac aag atc atg tcc aag atc ttc cgc acc atg tcc cgc act gcc       1548
Leu His Lys Ile Met Ser Lys Ile Phe Arg Thr Met Ser Arg Thr Ala
                405                 410                 415
gca gag tac ggc cac gag ggc aac tac gtc gtc ggc tcc aac atc gcc       1596
Ala Glu Tyr Gly His Glu Gly Asn Tyr Val Val Gly Ser Asn Ile Ala
            420                 425                 430
ggc ttc aag aag gtc gcc gac gcg atg ctc gcg cag ggc gtc atc taa       1644
Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
        435                 440                 445
ggctctccac aggattccct gacccctgg ccctgccgca ccacacattg tgcggcaggg      1704
ccagtaatct ttgagtcatg tatagagtct tcgaagccct ggacgagctc aaccagaccg      1764
tggagcaggc ctacggcgtg cccatgacct ccaactgcat ggtgccgcgc aacgacaccc      1824
tcgcgcttct cgacgatctg cgtaacgccc tgcccgtcga gatcgacgac gcccaggatg      1884
tcctggacca gcgcgacgag atcctccgcg gggccgagga ccgggcccgc gacatgatcg      1944
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<212>  PRT
<213>  Corynebacterium humireducens
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1               5                   10                  15
Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
            20                  25                  30
Ala Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
        35                  40                  45
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
    50                  55                  60
Val Pro Trp Ile Asp Asp Asn Gly Val Val Gln Val Asn Arg Gly Phe
65                  70                  75                  80
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
                85                  90                  95
Phe His Pro Ser Val Asn Leu Gly Ile Ile Lys Phe Leu Gly Phe Glu
            100                 105                 110
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
        115                 120                 125
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Leu Glu Ile Met
    130                 135                 140
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Lys His Ile Gly Glu
```

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145                 150                 155                 160
Tyr Lys Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
                165                 170                 175
Gly Phe Leu Phe Gly Gln Tyr Arg Arg Leu Ala Gly Gln His Glu Ser
            180                 185                 190
Gly Val Leu Thr Gly Lys Gly Leu Ala Trp Gly Gly Ser Leu Val Arg
        195                 200                 205
Thr Glu Ala Thr Gly Tyr Gly Ala Val Tyr Leu Thr Gln Glu Met Met
    210                 215                 220
Lys Ala His Gly Asp Ser Leu Ser Gly Ser Lys Val Ile Val Ser Gly
225                 230                 235                 240
Ser Gly Asn Val Ala Ile Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly
                245                 250                 255
Ala Thr Val Val Gly Phe Ser Asp Ser Ser Gly Trp Val Ser Thr Pro
            260                 265                 270
Asn Gly Val Asp Val Glu Leu Leu His Asp Val Lys Glu Lys Arg Arg
        275                 280                 285
Glu Arg Val Ser Cys Tyr Ala Glu Glu Ala Thr Gly Ala Thr Phe His
    290                 295                 300
Ala Glu Gly Ser Ile Trp Asp Leu Ala Ala Asp Val Ala Leu Pro Cys
305                 310                 315                 320
Ala Thr Gln Asn Glu Leu Asn Gly Asp His Ala Arg Thr Leu Ala Asp
                325                 330                 335
Asn Gly Ile Arg Tyr Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
            340                 345                 350
Glu Ala Ile Glu Val Phe Arg Glu Arg Gly Ile Phe Phe Ala Pro Gly
        355                 360                 365
Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
    370                 375                 380
Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Gln Arg
385                 390                 395                 400
Leu His Lys Ile Met Ser Lys Ile Phe Arg Thr Met Ser Arg Thr Ala
                405                 410                 415
Ala Glu Tyr Gly His Glu Gly Asn Tyr Val Val Gly Ser Asn Ile Ala
            420                 425                 430
Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
        435                 440                 445
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<213>  Corynebacterium humireducens
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aaggggtcct cgtgttcgcc ggggatctgg gggccgtcga gccagctacg cttggggttc      120
gccataccgt agacattagc cgggggcgtg cgggcagggg aaactcgagt ttcctgcgac      180
tattgatcgg tcaacagata gcagtttaga atgagcgaca ggtaataggg agcggtgccc      240
gcacctgtag actggctgag ataccgcacg acctagagcg tcaacaacca aggagtcatc      300
gtg gcc ttc aac acg atc gaa gaa gtc gtc aag tac atc aag gat gaa          348
Val Ala Phe Asn Thr Ile Glu Glu Val Val Lys Tyr Ile Lys Asp Glu
1               5                  10                  15
aac gtc gag ttc gtc gac gtc cgc ttc acg gac gtc ccg ggc acc gag         396
Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Val Pro Gly Thr Glu
            20                  25                  30
cac cac ttc acc atc ccc gcc tcg atg ttc gac gag gag gcg gcg gag         444
His His Phe Thr Ile Pro Ala Ser Met Phe Asp Glu Glu Ala Ala Glu
        35                  40                  45
gaa ggc ctc gcc ttc gac ggc tcc tcc atc cgc ggc ttc acc acg atc         492
Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile
    50                  55                  60
gac gag tcc gac atg aac ctc ctg ccg gac ctc aag acc gcc aag ctc         540
Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Lys Thr Ala Lys Leu
65                  70                  75                  80
gac ccc ttc cgc gag gcc aag acg ctg aac atc aag ttc ttc gtc cac         588
Asp Pro Phe Arg Glu Ala Lys Thr Leu Asn Ile Lys Phe Phe Val His
                85                  90                  95
gac ccc ttc acc cgc gag ccc ttc tcc cgc gac ccc cgc aac gtc gcc         636
Asp Pro Phe Thr Arg Glu Pro Phe Ser Arg Asp Pro Arg Asn Val Ala
            100                 105                 110
cgc aag gcc gag gag tac ctc gcc tcc acc ggc atc gcc gac acc tgc         684
Arg Lys Ala Glu Glu Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
        115                 120                 125
ttc ttc ggc gcc gag gcc gag ttc tac ctc ttc gac acc gtc cgg ttc         732
Phe Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Thr Val Arg Phe
    130                 135                 140
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gag acc tcc acc aac ggc ggc ttc tac gag gtc gac tcc gac gag ggc        780
Glu Thr Ser Thr Asn Gly Gly Phe Tyr Glu Val Asp Ser Asp Glu Gly
145                 150                 155                 160
tgg tgg aac cgc ggc aag gag gag cgt ctc gac ggc cgc cgc aac ctc        828
Trp Trp Asn Arg Gly Lys Glu Glu Arg Leu Asp Gly Arg Arg Asn Leu
                165                 170                 175
ggc tac acc aac cgc gtc aag ggc gga tac ttc ccg gtc gcc ccc tac        876
Gly Tyr Thr Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
            180                 185                 190
gac cag acc gtg gac atc cgt gac tcc atg gtg cgc cac ctg cag aac        924
Asp Gln Thr Val Asp Ile Arg Asp Ser Met Val Arg His Leu Gln Asn
        195                 200                 205
gcc gac ttc cac atc gag cgc ttc cac aag gag gtg ggc acg ggc ggc        972
Ala Asp Phe His Ile Glu Arg Phe His Lys Glu Val Gly Thr Gly Gly
    210                 215                 220
cag cag gag atc aac tac cgc ttc aac acc ctg ctc cac gcc gcc gat       1020
Gln Gln Glu Ile Asn Tyr Arg Phe Asn Thr Leu Leu His Ala Ala Asp
225                 230                 235                 240
gat ctg cag acc ttc aag tac atc atc aag aac acc gcc ttc aac gcc       1068
Asp Leu Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Phe Asn Ala
                245                 250                 255
ggc aag acg gcc acg ttc atg ccc aag ccc atc gcc ggc gac aac ggt       1116
Gly Lys Thr Ala Thr Phe Met Pro Lys Pro Ile Ala Gly Asp Asn Gly
            260                 265                 270
tcc ggc atg cac gcc cac cag tcg ctg tgg aag gac ggc gag ccg ctc       1164
Ser Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Glu Pro Leu
        275                 280                 285
ttc cac gac gag tcc ggc tac gcc ggc ctg tcc gac atg gcc cgc tac       1212
Phe His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Met Ala Arg Tyr
    290                 295                 300
tac atc ggc ggc atc ctc cac cac gcc ggc gcc gtc ctg gcc ttc acc       1260
Tyr Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr
305                 310                 315                 320
aac ccg acg ctg aac tcc tac cac cgc ctg gtc aag ggc ttc gag gca       1308
Asn Pro Thr Leu Asn Ser Tyr His Arg Leu Val Lys Gly Phe Glu Ala
                325                 330                 335
ccg atc aac ctg gtg tac tcc cag cgc aac cgc tcc gcc gcg atc cgc       1356
Pro Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Ile Arg
            340                 345                 350
atc ccg atc acc ggc tcc aac ccg aag gcc aag cgc atc gag ttc cgc       1404
Ile Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg
        355                 360                 365
gcc ccg gac ccg tcc ggc aac ccg tac ctc ggc ttc gcc gcg atg atg       1452
Ala Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met
    370                 375                 380
ctc gcc ggc ctc gac ggc atc aag aac cgc atc gag ccg atg gcc ccg       1500
Leu Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro Met Ala Pro
385                 390                 395                 400
gtg gac aag gac ctc tac gag ctc ccg ccg gag gag gcc gcc gcc atc       1548
Val Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ala Ile
                405                 410                 415
ccg cag gcc ccg acc tcc ctc gag gcc tcc ctg gcc gcc ctg cag gag       1596
Pro Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Ala Ala Leu Gln Glu
            420                 425                 430
gac aac gac ttc ctc acc gag ggt gac gtg ttc acc gag gac ctc atc       1644
Asp Asn Asp Phe Leu Thr Glu Gly Asp Val Phe Thr Glu Asp Leu Ile
        435                 440                 445
gag gcc tac atc cag ctc aag tac gac aac gag atc acc ccg gcc cgt       1692
Glu Ala Tyr Ile Gln Leu Lys Tyr Asp Asn Glu Ile Thr Pro Ala Arg
    450                 455                 460
ctg cgc ccg acg ccg ctg gag ttc gag ctg tac tac gac tgc tga           1737
Leu Arg Pro Thr Pro Leu Glu Phe Glu Leu Tyr Tyr Asp Cys
465                 470                 475
ccatgccccc accgcaaccc ccgcgccgga gctttccgac gcgggggttg cgcgcctctc     1797
ccctgtcagc taactgacag taactatact ttccaccgtg aacatatccc tggcaggccc     1857
ccgtcgcctc gcatccctca tcctgtcact gttcctggcg ttgtccctgg cccccgcggc     1917
acacgccgcc accggcagcc cccaggaatt cgtcccctac accgacagcc acggcacaag     1977
ttcgaactac cacttctacc cctccggccg cgagaacgcc ggactcctcg tccacctcga     2037
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1               5                   10                  15
Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Val Pro Gly Thr Glu
            20                  25                  30
His His Phe Thr Ile Pro Ala Ser Met Phe Asp Glu Glu Ala Ala Glu
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        35                  40                  45
Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile
    50                  55                  60
Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Lys Thr Ala Lys Leu
65                  70                  75                  80
Asp Pro Phe Arg Glu Ala Lys Thr Leu Asn Ile Lys Phe Phe Val His
                85                  90                  95
Asp Pro Phe Thr Arg Glu Pro Phe Ser Arg Asp Pro Arg Asn Val Ala
            100                 105                 110
Arg Lys Ala Glu Glu Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
        115                 120                 125
Phe Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Thr Val Arg Phe
    130                 135                 140
Glu Thr Ser Thr Asn Gly Gly Phe Tyr Glu Val Asp Ser Asp Glu Gly
145                 150                 155                 160
Trp Trp Asn Arg Gly Lys Glu Glu Arg Leu Asp Gly Arg Arg Asn Leu
                165                 170                 175
Gly Tyr Thr Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
            180                 185                 190
Asp Gln Thr Val Asp Ile Arg Asp Ser Met Val Arg His Leu Gln Asn
        195                 200                 205
Ala Asp Phe His Ile Glu Arg Phe His Lys Glu Val Gly Thr Gly Gly
    210                 215                 220
Gln Gln Glu Ile Asn Tyr Arg Phe Asn Thr Leu Leu His Ala Ala Asp
225                 230                 235                 240
Asp Leu Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Phe Asn Ala
                245                 250                 255
Gly Lys Thr Ala Thr Phe Met Pro Lys Pro Ile Ala Gly Asp Asn Gly
            260                 265                 270
Ser Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Glu Pro Leu
        275                 280                 285
Phe His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Met Ala Arg Tyr
    290                 295                 300
Tyr Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr
305                 310                 315                 320
Asn Pro Thr Leu Asn Ser Tyr His Arg Leu Val Lys Gly Phe Glu Ala
                325                 330                 335
Pro Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Ile Arg
            340                 345                 350
Ile Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg
        355                 360                 365
Ala Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met
    370                 375                 380
Leu Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro Met Ala Pro
385                 390                 395                 400
Val Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ala Ile
                405                 410                 415
Pro Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Ala Ala Leu Gln Glu
            420                 425                 430
Asp Asn Asp Phe Leu Thr Glu Gly Asp Val Phe Thr Glu Asp Leu Ile
        435                 440                 445
Glu Ala Tyr Ile Gln Leu Lys Tyr Asp Asn Glu Ile Thr Pro Ala Arg
    450                 455                 460
Leu Arg Pro Thr Pro Leu Glu Phe Glu Leu Tyr Tyr Asp Cys
465                 470                 475
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cttctgctac tccatcggcg gcatgcccgt ggaggacgtc gcctgggcct gggacgtcta      180
ccacaacgcc ctggagaagg gcatcggcac caggctcaac ctgtgggaca cccccaccct      240
caagtaagcc cctcaagcaa gacacctgaa cacaacaatc taggagccct gacacctgtc      300
gtg tcc ttc cag tcc acc acc gac ctg atc gac ttc atg cgc gat gag        348
Val Ser Phe Gln Ser Thr Thr Asp Leu Ile Asp Phe Met Arg Asp Glu
1               5                   10                  15
ggg gtg gag tac ctg gac atc cgt ttc acc gat gtc ccc ggc aca gaa        396
Gly Val Glu Tyr Leu Asp Ile Arg Phe Thr Asp Val Pro Gly Thr Glu
            20                  25                  30
cac gcg ctg acg gtt ccc gcc gcg gcg ctg acc gag gag acc gcg gcg        444
His Ala Leu Thr Val Pro Ala Ala Ala Leu Thr Glu Glu Thr Ala Ala
        35                  40                  45
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gag ggc ttc gcc ttc gac ggc tcg tcg atc gca ggt ttc acc tcg gtc        492
Glu Gly Phe Ala Phe Asp Gly Ser Ser Ile Ala Gly Phe Thr Ser Val
    50                  55                  60
gac gag tcc gac atg acc ctc atg ccg gac gtc tcg acg gcc tac gtg        540
Asp Glu Ser Asp Met Thr Leu Met Pro Asp Val Ser Thr Ala Tyr Val
65                  70                  75                  80
gac ccc ttc cgt cac cgg aag acg gtg aac atg cag ttc ttc gtc cac        588
Asp Pro Phe Arg His Arg Lys Thr Val Asn Met Gln Phe Phe Val His
                85                  90                  95
gac ccc ttc acc cgc gag gcg ttc tcc cgc gat ccg cgc aac atc gcc        636
Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Ile Ala
            100                 105                 110
cgc aag gcg gag gag tac atg cgt gcc tcc ggc atc gcc gac gag tgc        684
Arg Lys Ala Glu Glu Tyr Met Arg Ala Ser Gly Ile Ala Asp Glu Cys
        115                 120                 125
tac atc ggc gcc gag gcc gag ttc ttc gtc ttc gac tcg gtc cgc tac        732
Tyr Ile Gly Ala Glu Ala Glu Phe Phe Val Phe Asp Ser Val Arg Tyr
    130                 135                 140
tcc acc gac gtc cac cgt tcc ttc cac cag gtc gac tcc gac gag ggc        780
Ser Thr Asp Val His Arg Ser Phe His Gln Val Asp Ser Asp Glu Gly
145                 150                 155                 160
tgg tgg aac tcc gac gcg gag acc atg atc gac ggt tcc ccg aac ctg        828
Trp Trp Asn Ser Asp Ala Glu Thr Met Ile Asp Gly Ser Pro Asn Leu
                165                 170                 175
ggc aac aag atc cgc gtc aac gac ggc tac ttc ccc gtc gcc ccc tac        876
Gly Asn Lys Ile Arg Val Asn Asp Gly Tyr Phe Pro Val Ala Pro Tyr
            180                 185                 190
gac aag acg atc ccg gtg cgc gac gag atc gcg cac aac ctc tcg cag        924
Asp Lys Thr Ile Pro Val Arg Asp Glu Ile Ala His Asn Leu Ser Gln
        195                 200                 205
gtc ggt ttc gag atc gag cgt ttc cac cac gag gtc tcc acg ggt ggc        972
Val Gly Phe Glu Ile Glu Arg Phe His His Glu Val Ser Thr Gly Gly
    210                 215                 220
atc cag gag gtg aac tac cgc ttc aac acc ctc ctg cac gcg gcg gat       1020
Ile Gln Glu Val Asn Tyr Arg Phe Asn Thr Leu Leu His Ala Ala Asp
225                 230                 235                 240
gac ctg cag aag ttc aag tac atc gtg aag aac acc gcc gac gcc cac       1068
Asp Leu Gln Lys Phe Lys Tyr Ile Val Lys Asn Thr Ala Asp Ala His
                245                 250                 255
ggc aag gtc gcc acc ttc atg ccg aag ccg ctt ctc gac gac ggc ggc       1116
Gly Lys Val Ala Thr Phe Met Pro Lys Pro Leu Leu Asp Asp Gly Gly
            260                 265                 270
tgc ggc atg cac gcc cac cag tcc ctg tgg aag gac ggc cga ccg ctg       1164
Cys Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Arg Pro Leu
        275                 280                 285
ttc cac gac gag gaa ggt tac gcc ggc ctc tcc gag acc gcc cgc cac       1212
Phe His Asp Glu Glu Gly Tyr Ala Gly Leu Ser Glu Thr Ala Arg His
    290                 295                 300
tac atc ggt ggc ctg ctg gcc cac gcc ccg gcg gtc ctg gcg ttc acc       1260
Tyr Ile Gly Gly Leu Leu Ala His Ala Pro Ala Val Leu Ala Phe Thr
305                 310                 315                 320
aac ccg acg gtc aac tcc tac cgt cgc ctc tac tcc ggt ttc gag gcc       1308
Asn Pro Thr Val Asn Ser Tyr Arg Arg Leu Tyr Ser Gly Phe Glu Ala
                325                 330                 335
ccg gtg aac ctg gtg tac tcc cag cgc aac cgt tcc gcc gcg atc cgt       1356
Pro Val Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Ile Arg
            340                 345                 350
atc ccg gtg acc ggc ccc tcc gcc gcc gcc aag cgc atc gag ttc cgc       1404
Ile Pro Val Thr Gly Pro Ser Ala Ala Ala Lys Arg Ile Glu Phe Arg
        355                 360                 365
gcc ccg gac ccc tcc ggc aac ccc tac ctc ggt ttc gcg gcc cag ctg       1452
Ala Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Gln Leu
    370                 375                 380
ctg gcc ggt ctg gac ggc atc aag aac cgc atc gag ccg ggc gac ccg       1500
Leu Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro Gly Asp Pro
385                 390                 395                 400
gtg gac aag gac ctc tac gag ctg gag ccg gag gag gcc gac aag gtg       1548
Val Asp Lys Asp Leu Tyr Glu Leu Glu Pro Glu Glu Ala Asp Lys Val
                405                 410                 415
ccg cgc gtc ccg cac tcc ctg gag tcc tcg ctg tac gcc ctg gag aac       1596
Pro Arg Val Pro His Ser Leu Glu Ser Ser Leu Tyr Ala Leu Glu Asn
            420                 425                 430
gac cac gag ttc ctc acc gag ggc gac gtg ttc acc gag gac ctc atc       1644
Asp His Glu Phe Leu Thr Glu Gly Asp Val Phe Thr Glu Asp Leu Ile
        435                 440                 445
gag gcc tac atc cag ctg aag tac gac aac gag atc aac ccg atg cgc       1692
Glu Ala Tyr Ile Gln Leu Lys Tyr Asp Asn Glu Ile Asn Pro Met Arg
    450                 455                 460
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caa ggc ccg acg ccg aag gag ttc gag ctc tac ttc aac tgc tag 1737
Gln Gly Pro Thr Pro Lys Glu Phe Glu Leu Tyr Phe Asn Cys
465 470 475
gttcagcagg catgcggcgc agttacgtcc tcggggcgac agagcacacg gacctccggg 1797
gcatccggcg ggtgctcgca cgctaccgct acgacgcgcc gtgggtgctt ctcgacgccc 1857
gccccgtcct cgaggtctcc tggttcgggg agggcgcggt gtcgttctac gccaccactc 1917
ccccgctgcc tcccgacccc gccctggccc gcctcctctt cgacctcggg tcctgcggac 1977
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Gly Val Glu Tyr Leu Asp Ile Arg Phe Thr Asp Val Pro Gly Thr Glu
20 25 30
His Ala Leu Thr Val Pro Ala Ala Ala Leu Thr Glu Glu Thr Ala Ala
35 40 45
Glu Gly Phe Ala Phe Asp Gly Ser Ser Ile Ala Gly Phe Thr Ser Val
50 55 60
Asp Glu Ser Asp Met Thr Leu Met Pro Asp Val Ser Thr Ala Tyr Val
65 70 75 80
Asp Pro Phe Arg His Arg Lys Thr Val Asn Met Gln Phe Phe Val His
85 90 95
Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Ile Ala
100 105 110
Arg Lys Ala Glu Glu Tyr Met Arg Ala Ser Gly Ile Ala Asp Glu Cys
115 120 125
Tyr Ile Gly Ala Glu Ala Glu Phe Phe Val Phe Asp Ser Val Arg Tyr
130 135 140
Ser Thr Asp Val His Arg Ser Phe His Gln Val Asp Ser Asp Glu Gly
145 150 155 160
Trp Trp Asn Ser Asp Ala Glu Thr Met Ile Asp Gly Ser Pro Asn Leu
165 170 175
Gly Asn Lys Ile Arg Val Asn Asp Gly Tyr Phe Pro Val Ala Pro Tyr
180 185 190
Asp Lys Thr Ile Pro Val Arg Asp Glu Ile Ala His Asn Leu Ser Gln
195 200 205
Val Gly Phe Glu Ile Glu Arg Phe His His Glu Val Ser Thr Gly Gly
210 215 220
Ile Gln Glu Val Asn Tyr Arg Phe Asn Thr Leu Leu His Ala Ala Asp
225 230 235 240

Asp Leu Gln Lys Phe Lys Tyr Ile Val Lys Asn Thr Ala Asp Ala His
245 250 255
Gly Lys Val Ala Thr Phe Met Pro Lys Pro Leu Leu Asp Asp Gly Gly
260 265 270
Cys Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Arg Pro Leu
275 280 285
Phe His Asp Glu Glu Gly Tyr Ala Gly Leu Ser Glu Thr Ala Arg His
290 295 300
Tyr Ile Gly Gly Leu Leu Ala His Ala Pro Ala Val Leu Ala Phe Thr
305 310 315 320
Asn Pro Thr Val Asn Ser Tyr Arg Arg Leu Tyr Ser Gly Phe Glu Ala
325 330 335
Pro Val Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Ile Arg
340 345 350
Ile Pro Val Thr Gly Pro Ser Ala Ala Ala Lys Arg Ile Glu Phe Arg
355 360 365
Ala Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Gln Leu
370 375 380
Leu Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro Gly Asp Pro
385 390 395 400
Val Asp Lys Asp Leu Tyr Glu Leu Glu Pro Glu Glu Ala Asp Lys Val
405 410 415
Pro Arg Val Pro His Ser Leu Glu Ser Ser Leu Tyr Ala Leu Glu Asn
420 425 430
Asp His Glu Phe Leu Thr Glu Gly Asp Val Phe Thr Glu Asp Leu Ile
435 440 445
Glu Ala Tyr Ile Gln Leu Lys Tyr Asp Asn Glu Ile Asn Pro Met Arg
450 455 460
Gln Gly Pro Thr Pro Lys Glu Phe Glu Leu Tyr Phe Asn Cys
465 470 475
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<211> 2241
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<213> Corynebacterium humireducens

<220>
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<222> (301)..(1941)
<223> gen glutamate synthase
<400> 129

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gttccccgtg tacgaggcgg agtacggcga gatcacctcg gtgaagaaga tccgccgccc      120
cgccccggtc gaggactacc tccgcctcca gcgccgctac gcgcacctgt tccggaagga      180
cgcggacccg tccgtcatcg agcggctcca ggcgctggcg gaccgcaaca tccgccgcta      240
caacctcatc gacgaagaga ccctcgacga gttcgtcagg ttcgaaggag acgacgcaca      300
gtg agt acc ggt aac cac gtc aac atc ggc atg ccc ttc gcc atc acc         348
Val Ser Thr Gly Asn His Val Asn Ile Gly Met Pro Phe Ala Ile Thr
1               5                  10                  15
ctg cag acc ggc tcc tcc ctg gcg aac aag acc ggc tcc tgg cgc agc        396
Leu Gln Thr Gly Ser Ser Leu Ala Asn Lys Thr Gly Ser Trp Arg Ser
            20                  25                  30
gag cgg ccc gtg tac gtc gac ctg ctg ccg ccc tgc aac aag gcg tgt        444
Glu Arg Pro Val Tyr Val Asp Leu Leu Pro Pro Cys Asn Lys Ala Cys
        35                  40                  45
ccc gcc ggc ggg aac atc cag ggc tgg ctg tac cac gcc gag gag ggc        492
Pro Ala Gly Gly Asn Ile Gln Gly Trp Leu Tyr His Ala Glu Glu Gly
    50                  55                  60
gac tac gag tcc gcc tgg cgc gag atc atg gtg gac aac ccg ctg ccc        540
Asp Tyr Glu Ser Ala Trp Arg Glu Ile Met Val Asp Asn Pro Leu Pro
65                  70                  75                  80
gcc gtc atg ggg cgt gtc tgc tac cac acc tgc cag acc gcc tgt aac        588
Ala Val Met Gly Arg Val Cys Tyr His Thr Cys Gln Thr Ala Cys Asn
                85                  90                  95
cgc gcg gag gtc gac gag gcc gtc ggc atc aac gcg gtc gag cgc ttc        636
Arg Ala Glu Val Asp Glu Ala Val Gly Ile Asn Ala Val Glu Arg Phe
            100                 105                 110
ctc ggg gac cgt gcc atc gag gag ggg tgg cag gtc gaa ccc gtc aag        684
Leu Gly Asp Arg Ala Ile Glu Glu Gly Trp Gln Val Glu Pro Val Lys
        115                 120                 125
gac ccc tcc ggc cgg agg gtc ctc gtc gtg ggt tcc ggc ccc tcc ggc        732
Asp Pro Ser Gly Arg Arg Val Leu Val Val Gly Ser Gly Pro Ser Gly
    130                 135                 140
ctg tcc gcg gcc tac cac ctc gcc cga ctc ggc cac gag gtg acg gtc        780
Leu Ser Ala Ala Tyr His Leu Ala Arg Leu Gly His Glu Val Thr Val
145                 150                 155                 160
cgc gac cgg ggt gag cgg ccg ggc ggc atg atg cgc tac ggc atc ccc        828
Arg Asp Arg Gly Glu Arg Pro Gly Gly Met Met Arg Tyr Gly Ile Pro
                165                 170                 175
tcc tac cgc ctg ccc cgc cac atc ctc gac gcc gag atc gcg cgc atc        876
Ser Tyr Arg Leu Pro Arg His Ile Leu Asp Ala Glu Ile Ala Arg Ile
            180                 185                 190
gcg gcc ctg ggc gtc acc ttc gag cag ggg gtc acc gtc acc gac gtc        924
Ala Ala Leu Gly Val Thr Phe Glu Gln Gly Val Thr Val Thr Asp Val
        195                 200                 205
gag tcc gaa ctc gag ctt ttc gac gcc gtc ttc acc gcc gtc ggt gcc        972
Glu Ser Glu Leu Glu Leu Phe Asp Ala Val Phe Thr Ala Val Gly Ala
    210                 215                 220
cag ctg ggc cgc aac gtg gag gtg ccc gcc ggg tcg gcg gcg acc atc       1020
Gln Leu Gly Arg Asn Val Glu Val Pro Ala Gly Ser Ala Ala Thr Ile
225                 230                 235                 240
atg aac gcc gtt gac ctg ctg cgt gac acc gag gcc ggg gag gcg ccg       1068
Met Asn Ala Val Asp Leu Leu Arg Asp Thr Glu Ala Gly Glu Ala Pro
                245                 250                 255
ctg ctc ggt cgt cgg gtc gtg gtc tac ggc ggc ggc aac aca gcc gtc       1116
Leu Leu Gly Arg Arg Val Val Val Tyr Gly Gly Gly Asn Thr Ala Val
            260                 265                 270
gac gcc gcc cgc acc gcg cgt cgt ctc ggg gcg acc gag tcg gtc atc       1164
Asp Ala Ala Arg Thr Ala Arg Arg Leu Gly Ala Thr Glu Ser Val Ile
        275                 280                 285
ctc tac cgc cgc acc cgc gac cac atg agc gcc cac gac tcc gag gtc       1212
Leu Tyr Arg Arg Thr Arg Asp His Met Ser Ala His Asp Ser Glu Val
    290                 295                 300
atg gag gcc gag gag gag ggc atc acc atg cgc tgg ctg tcc acc gtc       1260
Met Glu Ala Glu Glu Glu Gly Ile Thr Met Arg Trp Leu Ser Thr Val
305                 310                 315                 320
gac cac gtc gag gag ggc tcc atc agg atc gag aag atg gac atc gac       1308
Asp His Val Glu Glu Gly Ser Ile Arg Ile Glu Lys Met Asp Ile Asp
                325                 330                 335
gcc gac ggc cac ctc acc ccg acc ggt gag tac gag gag ctc gcc gcc       1356
Ala Asp Gly His Leu Thr Pro Thr Gly Glu Tyr Glu Glu Leu Ala Ala
            340                 345                 350
gac tcc ctc gtc atg gcg ctg ggc cag gag tcg gac ctc tcc ctg ctc       1404
Asp Ser Leu Val Met Ala Leu Gly Gln Glu Ser Asp Leu Ser Leu Leu
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        355                 360                 365
gag ggc gtg gag ggg gtg gag atc tcc cgc ggc gtc gtc gcc gtc gac      1452
Glu Gly Val Glu Gly Val Glu Ile Ser Arg Gly Val Val Ala Val Asp
    370                 375                 380
gag cag atg atg acc gga cgt gcg ggc gtc ttc gcc ggc ggc gac atg      1500
Glu Gln Met Met Thr Gly Arg Ala Gly Val Phe Ala Gly Gly Asp Met
385                 390                 395                 400
gtg ccg agc gag aag aac gtc acc gtc gcc atc ggc cac ggc aag aag      1548
Val Pro Ser Glu Lys Asn Val Thr Val Ala Ile Gly His Gly Lys Lys
                405                 410                 415
gcg gcc cgg tac atc gac ggt tgg ctc cgt ggc gaa ccc tac gtg ccc      1596
Ala Ala Arg Tyr Ile Asp Gly Trp Leu Arg Gly Glu Pro Tyr Val Pro
            420                 425                 430
gcc gtc aag cct gca gac gcg act ctc gac cgt atg gag acc tgg tac      1644
Ala Val Lys Pro Ala Asp Ala Thr Leu Asp Arg Met Glu Thr Trp Tyr
        435                 440                 445
tac tca gag gcc ccg cac cag gtg cgc gaa cgc ctc gag ggc gcc cgc      1692
Tyr Ser Glu Ala Pro His Gln Val Arg Glu Arg Leu Glu Gly Ala Arg
    450                 455                 460
cgc gcc tcc acc ttt gac gag gtc gtc cgg gga ctc gac gcc gac tcc      1740
Arg Ala Ser Thr Phe Asp Glu Val Val Arg Gly Leu Asp Ala Asp Ser
465                 470                 475                 480
gcc ctg ctc gag gca cgc cgc tgc atg tcg tgc ggc aac tgc ttc ggc      1788
Ala Leu Leu Glu Ala Arg Arg Cys Met Ser Cys Gly Asn Cys Phe Gly
                485                 490                 495
tgc gac aac tgc ttc ggc gtc tgc ccg gac aac gcg gtc acc aaa ttg      1836
Cys Asp Asn Cys Phe Gly Val Cys Pro Asp Asn Ala Val Thr Lys Leu
            500                 505                 510
gcg ccg ggt gag tac gag ttc aag tac gac tac tgc aag ggc tgc ggc      1884
Ala Pro Gly Glu Tyr Glu Phe Lys Tyr Asp Tyr Cys Lys Gly Cys Gly
        515                 520                 525
atc tgc gcg gag gag tgc ccg tgc ggc gcg atc tcc atg att ccc gag      1932
Ile Cys Ala Glu Glu Cys Pro Cys Gly Ala Ile Ser Met Ile Pro Glu
    530                 535                 540
gag aac tga ggagaactga ccgcccgcaa caagttagag tatgggcacc              1981
Glu Asn
545
aacgtcgtcc cctgaccaga aggatcccca tgcgccgcac cctcatcgcc ctcggcaccg     2041
ccaccgccct caccctgggg gcggtcccgg ccgcccacgc ccagcccgcg aacgccgtca     2101
ccgcccagat cgaggagctg ccggccgaca tgcgggcagg ctcctccggc gcggagaagc     2161
tctcctccgc ctccaccgag gccgagaagc aggagggtgc cctgctgctg ggacgcgact     2221
ggctgctcgg tttcgccgcg                                                2241
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Leu Gln Thr Gly Ser Ser Leu Ala Asn Lys Thr Gly Ser Trp Arg Ser
            20                  25                  30
Glu Arg Pro Val Tyr Val Asp Leu Leu Pro Pro Cys Asn Lys Ala Cys
        35                  40                  45
Pro Ala Gly Gly Asn Ile Gln Gly Trp Leu Tyr His Ala Glu Glu Gly
    50                  55                  60
Asp Tyr Glu Ser Ala Trp Arg Glu Ile Met Val Asp Asn Pro Leu Pro
65                  70                  75                  80
Ala Val Met Gly Arg Val Cys Tyr His Thr Cys Gln Thr Ala Cys Asn
                85                  90                  95
Arg Ala Glu Val Asp Glu Ala Val Gly Ile Asn Ala Val Glu Arg Phe
            100                 105                 110
Leu Gly Asp Arg Ala Ile Glu Glu Gly Trp Gln Val Glu Pro Val Lys
        115                 120                 125
Asp Pro Ser Gly Arg Arg Val Leu Val Val Gly Ser Gly Pro Ser Gly
    130                 135                 140
Leu Ser Ala Ala Tyr His Leu Ala Arg Leu Gly His Glu Val Thr Val
145                 150                 155                 160
Arg Asp Arg Gly Glu Arg Pro Gly Gly Met Met Arg Tyr Gly Ile Pro
                165                 170                 175
Ser Tyr Arg Leu Pro Arg His Ile Leu Asp Ala Glu Ile Ala Arg Ile
            180                 185                 190
Ala Ala Leu Gly Val Thr Phe Glu Gln Gly Val Thr Val Thr Asp Val
        195                 200                 205
Glu Ser Glu Leu Glu Leu Phe Asp Ala Val Phe Thr Ala Val Gly Ala
    210                 215                 220
Gln Leu Gly Arg Asn Val Glu Val Pro Ala Gly Ser Ala Ala Thr Ile
225                 230                 235                 240
Met Asn Ala Val Asp Leu Leu Arg Asp Thr Glu Ala Gly Glu Ala Pro
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                245                 250                 255
Leu Leu Gly Arg Arg Val Val Val Tyr Gly Gly Gly Asn Thr Ala Val
            260                 265                 270
Asp Ala Ala Arg Thr Ala Arg Arg Leu Gly Ala Thr Glu Ser Val Ile
        275                 280                 285
Leu Tyr Arg Arg Thr Arg Asp His Met Ser Ala His Asp Ser Glu Val
    290                 295                 300
Met Glu Ala Glu Glu Glu Gly Ile Thr Met Arg Trp Leu Ser Thr Val
305                 310                 315                 320
Asp His Val Glu Glu Gly Ser Ile Arg Ile Glu Lys Met Asp Ile Asp
                325                 330                 335
Ala Asp Gly His Leu Thr Pro Thr Gly Glu Tyr Glu Glu Leu Ala Ala
            340                 345                 350
Asp Ser Leu Val Met Ala Leu Gly Gln Glu Ser Asp Leu Ser Leu Leu
        355                 360                 365
Glu Gly Val Glu Gly Val Glu Ile Ser Arg Gly Val Val Ala Val Asp
    370                 375                 380
Glu Gln Met Met Thr Gly Arg Ala Gly Val Phe Ala Gly Gly Asp Met
385                 390                 395                 400
Val Pro Ser Glu Lys Asn Val Thr Val Ala Ile Gly His Gly Lys Lys
                405                 410                 415
Ala Ala Arg Tyr Ile Asp Gly Trp Leu Arg Gly Glu Pro Tyr Val Pro
            420                 425                 430
Ala Val Lys Pro Ala Asp Ala Thr Leu Asp Arg Met Glu Thr Trp Tyr
        435                 440                 445
Tyr Ser Glu Ala Pro His Gln Val Arg Glu Arg Leu Glu Gly Ala Arg
    450                 455                 460
Arg Ala Ser Thr Phe Asp Glu Val Val Arg Gly Leu Asp Ala Asp Ser
465                 470                 475                 480
Ala Leu Leu Glu Ala Arg Arg Cys Met Ser Cys Gly Asn Cys Phe Gly
                485                 490                 495
Cys Asp Asn Cys Phe Gly Val Cys Pro Asp Asn Ala Val Thr Lys Leu
            500                 505                 510
Ala Pro Gly Glu Tyr Glu Phe Lys Tyr Asp Tyr Cys Lys Gly Cys Gly
        515                 520                 525
Ile Cys Ala Glu Glu Cys Pro Cys Gly Ala Ile Ser Met Ile Pro Glu
    530                 535                 540
Glu Asn
545
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<213>  Corynebacterium humireducens
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<222>  (301)..(2517)
<223>  gen isoxitrat dehydrogenaza

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cggtcgcgcg cacctcctgc aggagcacca cgtcagccgg ggactgctcc agccaggcca      120
gcatgcccgg attgtcctcg ttgcgctgct tgacggcggc gcggattcca ttgacgttga      180
cggaggtgat ggtcagactc ataggaacca ccatatcgcc gttggtggca gggcccctgc      240
cccgccgggt atccttagcc gttgacactg ccgagattga agaaagcgtt agggagttac      300
atg gca aag atc atc tgg acc cgc acc gac gag gcc ccg ctg ctc gcg        348
Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala
1               5                   10                  15
acc tat tcg ttc aag cct gtt gtt gag gcc ttc gcc gcc acc gcg ggt        396
Thr Tyr Ser Phe Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly
            20                  25                  30
atc gat gtc gag acc cgc gac atc tcc ctg gcc ggc cgc atc ctg gcc        444
Ile Asp Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
        35                  40                  45
cag ttc ccg gac cgc ctc acc gag gag cag cga gtc gct gac gcc ctc        492
Gln Phe Pro Asp Arg Leu Thr Glu Glu Gln Arg Val Ala Asp Ala Leu
    50                  55                  60
acc gag ctc ggc gac ctg gcc aag acc ccg gaa gcc aac atc atc aag        540
Thr Glu Leu Gly Asp Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
65                  70                  75                  80
ctc ccg aac atc tcg gcg tcc gtc ccg cag ctc aag gca gcc atc aag        588
Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
                85                  90                  95
gag ctg cag gac cag gga tac gac ctc ccc gac tac gtc gac tcc ccg        636
Glu Leu Gln Asp Gln Gly Tyr Asp Leu Pro Asp Tyr Val Asp Ser Pro
            100                 105                 110
gag acc gac gag gag aag gac gcc cgc aag cgc tac gac gta gta aag        684
Glu Thr Asp Glu Glu Lys Asp Ala Arg Lys Arg Tyr Asp Val Val Lys
        115                 120                 125
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ggt tcc gct gtg aac ccg gta ctc cgt gag ggc aac tcc gac cgt cgt        732
Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
    130                 135                 140
gcc ccg gag gcc gtg aag aac ttc gtc cgc aag aac ccg cac cgc atg        780
Ala Pro Glu Ala Val Lys Asn Phe Val Arg Lys Asn Pro His Arg Met
145                 150                 155                 160
ggt gag tgg tcc gcc gac tcc aag acc aac gtc gcc acc atg gac tcc        828
Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ser
                165                 170                 175
gac gac ttc cgt cac aac gag cag tcc gtc atc ctc ccg gcc gag gac        876
Asp Asp Phe Arg His Asn Glu Gln Ser Val Ile Leu Pro Ala Glu Asp
            180                 185                 190
acc ctc tcc ttc gtc cac gtc gcc acc gac ggc acc gag acc aag ctc        924
Thr Leu Ser Phe Val His Val Ala Thr Asp Gly Thr Glu Thr Lys Leu
        195                 200                 205
cgc gac gac ctc aag gtc ctc gag ggc gag gtc gtc gac ggc acc gtc        972
Arg Asp Asp Leu Lys Val Leu Glu Gly Glu Val Val Asp Gly Thr Val
    210                 215                 220
atg cgc gcc gcc gcc ctg cag gag ttc ctg gcc gag cag gtc aag cgc       1020
Met Arg Ala Ala Ala Leu Gln Glu Phe Leu Ala Glu Gln Val Lys Arg
225                 230                 235                 240
gcc cag gac gag ggc atc ctg ttc tcc gtc cac ctc aag gcc acc atg       1068
Ala Gln Asp Glu Gly Ile Leu Phe Ser Val His Leu Lys Ala Thr Met
                245                 250                 255
atg aag gtc tcc gac ccg atc atc ttc ggc tac gtc gtc cgc gcc ttc       1116
Met Lys Val Ser Asp Pro Ile Ile Phe Gly Tyr Val Val Arg Ala Phe
            260                 265                 270
ttc gcc gac gtc tac gag aag tac ggc gag gag ctg ctg gcc gcc ggt       1164
Phe Ala Asp Val Tyr Glu Lys Tyr Gly Glu Glu Leu Leu Ala Ala Gly
        275                 280                 285
ctc gac ggc gag aac ggc ctc ggc gcc atc ttc tcc gga ctc gag gaa       1212
Leu Asp Gly Glu Asn Gly Leu Gly Ala Ile Phe Ser Gly Leu Glu Glu
    290                 295                 300
ctg gag aac ggc gag gag atc cgc cgt gcc ttc gac gag gcc ctc gag       1260
Leu Glu Asn Gly Glu Glu Ile Arg Arg Ala Phe Asp Glu Ala Leu Glu
305                 310                 315                 320
aac ggc cct gac ctg gcg atg gtg aac tcc gac aag ggc atc acc aac       1308
Asn Gly Pro Asp Leu Ala Met Val Asn Ser Asp Lys Gly Ile Thr Asn
                325                 330                 335
ctg cac gtc ccg tcc gac gtc atc gtc gac gcc tcc atg ccc gcc atg       1356
Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met
            340                 345                 350
atc cgc acc tcc ggc cag atg tgg aac aag gac gac aag acc cag gac       1404
Ile Arg Thr Ser Gly Gln Met Trp Asn Lys Asp Asp Lys Thr Gln Asp
        355                 360                 365
acc ctg gcc gtc atc ccg gac tcc tcc tac gcc ggc gtc ttc cag acc       1452
Thr Leu Ala Val Ile Pro Asp Ser Ser Tyr Ala Gly Val Phe Gln Thr
    370                 375                 380
gtc atc gac gac tgc aag gcc aac ggc gcc ttc gac ccg acc acc atg       1500
Val Ile Asp Asp Cys Lys Ala Asn Gly Ala Phe Asp Pro Thr Thr Met
385                 390                 395                 400
ggc acc gtc ccg aac gtc ggc ctc atg gcc cag aag gcc gag gag tac       1548
Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr
                405                 410                 415
ggc tcc cac gac aag acc ttc cgc atc gcc gcg gac ggc aag gtc gag       1596
Gly Ser His Asp Lys Thr Phe Arg Ile Ala Ala Asp Gly Lys Val Glu
            420                 425                 430
gtc cgc aac tcc gcc ggt gac gtc ctg ctc gag cac gag gtc tcc gag       1644
Val Arg Asn Ser Ala Gly Asp Val Leu Leu Glu His Glu Val Ser Glu
        435                 440                 445
ggc gac atc tgg cgc gcc tgc cag acc aag gac gcc ccg atc cag gac       1692
Gly Asp Ile Trp Arg Ala Cys Gln Thr Lys Asp Ala Pro Ile Gln Asp
    450                 455                 460
tgg gtc aag ctg gcc gtc gac cgc gcc cgc atc tcc ggc atg ccg gcc       1740
Trp Val Lys Leu Ala Val Asp Arg Ala Arg Ile Ser Gly Met Pro Ala
465                 470                 475                 480
gtc ttc tgg ctg gac ccg gag cgc gcc cac gac cgc aac ctc acc acc       1788
Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Thr Thr
                485                 490                 495
ctg gtg gag aag tac ctg gcc gac cac gac acc gag ggc ctg gac atc       1836
Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile
            500                 505                 510
cgc atc ctc tcc ccg gtc gag gcg acc cag ctg tcc gtc gac cgc atc       1884
Arg Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Val Asp Arg Ile
        515                 520                 525
cgc cgc ggc gag gac acc atc tcc gtg acc ggt aac gtc ctg cgt gac       1932
Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp
    530                 535                 540
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tac aac acc gac ctc ttc ccg atc ctc gag ctg ggc acc tcc gcc aag      1980
Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys
545                 550                 555                 560
atg ctc tcc gtc gtg ccg ctg atg gcc ggt ggc ggc ctc ttc gag acc      2028
Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr
                565                 570                 575
ggt gcc ggt ggc tcc gcc ccg aag cac gtc cag cag gtc gtc gag gag      2076
Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Val Glu Glu
            580                 585                 590
aac cac ctg cgc tgg gac tcc ctc ggt gag ttc ctc gcc ctg gcc gag      2124
Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu
        595                 600                 605
tcc ctg cgc cac gtc gcc cgc acc cag gac aac gcg aag gcc gcc gtc      2172
Ser Leu Arg His Val Ala Arg Thr Gln Asp Asn Ala Lys Ala Ala Val
    610                 615                 620
ctg gcc gac gcc ctg gac aag gcc acc gag aag gtc ctg tcc gag ggc      2220
Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Val Leu Ser Glu Gly
625                 630                 635                 640
aag tcc ccg tcc cgc aag gtc ggc gag atc gac aac cgt ggc tcc cac      2268
Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His
                645                 650                 655
ttc tac ctc gcg tcc tac tgg gcc gag gcc ctg gcc gca cag tcc gac      2316
Phe Tyr Leu Ala Ser Tyr Trp Ala Glu Ala Leu Ala Ala Gln Ser Asp
            660                 665                 670
gac gcc gag ctg gcc gcg acc ttc cag ccg gtc gcc gag gcc ctg gcc      2364
Asp Ala Glu Leu Ala Ala Thr Phe Gln Pro Val Ala Glu Ala Leu Ala
        675                 680                 685
gcc gac gcc gcg acc atc gac cag gag ctc atc gac aac cag ggt tcc      2412
Ala Asp Ala Ala Thr Ile Asp Gln Glu Leu Ile Asp Asn Gln Gly Ser
    690                 695                 700
gcc gtg gac ctc ggc ggc tac tac gcc ccg tcc gat gag aag acc tcc      2460
Ala Val Asp Leu Gly Gly Tyr Tyr Ala Pro Ser Asp Glu Lys Thr Ser
705                 710                 715                 720
gac gtg atg cgt ccg tcc gcg aag ttc aac gag atc atc gac ggt ctg      2508
Asp Val Met Arg Pro Ser Ala Lys Phe Asn Glu Ile Ile Asp Gly Leu
                725                 730                 735
aag aag taa cccccgcttt ccgacgccgc cctgccccgc caccggggca              2557
Lys Lys

gggcggcgtc gcctttgggc agggccccgg acgaaccact tggtctaccg tccctttatt     2617
tttattcatg cgccctgaac tgcggagaca gggtttggac agacagctcg gtttacgtcg     2677
aaaagcggtg cgccgtactc ttctcccatg acccgatacg acaactccgc agcagaccag     2737
tgggacttcg agacccgctc catccacgcc ggccagaacc cggaccccgc gaccggttcc     2797
cgtaaccagc cgatccacct                                                 2817
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<212>  PRT
<213>  Corynebacterium humireducens
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1                 5                  10                  15
Thr Tyr Ser Phe Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly
            20                  25                  30
Ile Asp Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
        35                  40                  45
Gln Phe Pro Asp Arg Leu Thr Glu Glu Gln Arg Val Ala Asp Ala Leu
    50                  55                  60
Thr Glu Leu Gly Asp Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
65                  70                  75                  80
Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
                85                  90                  95
Glu Leu Gln Asp Gln Gly Tyr Asp Leu Pro Asp Tyr Val Asp Ser Pro
            100                 105                 110
Glu Thr Asp Glu Glu Lys Asp Ala Arg Lys Arg Tyr Asp Val Val Lys
        115                 120                 125
Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
    130                 135                 140
Ala Pro Glu Ala Val Lys Asn Phe Val Arg Lys Asn Pro His Arg Met
145                 150                 155                 160
Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ser
                165                 170                 175
Asp Asp Phe Arg His Asn Glu Gln Ser Val Ile Leu Pro Ala Glu Asp
            180                 185                 190
Thr Leu Ser Phe Val His Val Ala Thr Asp Gly Thr Glu Thr Lys Leu
        195                 200                 205
Arg Asp Asp Leu Lys Val Leu Glu Gly Glu Val Val Asp Gly Thr Val
    210                 215                 220
Met Arg Ala Ala Ala Leu Gln Glu Phe Leu Ala Glu Gln Val Lys Arg
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225 230 235 240
Ala Gln Asp Glu Gly Ile Leu Phe Ser Val His Leu Lys Ala Thr Met
245 250 255
Met Lys Val Ser Asp Pro Ile Ile Phe Gly Tyr Val Val Arg Ala Phe
260 265 270
Phe Ala Asp Val Tyr Glu Lys Tyr Gly Glu Glu Leu Leu Ala Ala Gly
275 280 285
Leu Asp Gly Glu Asn Gly Leu Gly Ala Ile Phe Ser Gly Leu Glu Glu
290 295 300
Leu Glu Asn Gly Glu Glu Ile Arg Arg Ala Phe Asp Glu Ala Leu Glu
305 310 315 320
Asn Gly Pro Asp Leu Ala Met Val Asn Ser Asp Lys Gly Ile Thr Asn
325 330 335
Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met
340 345 350
Ile Arg Thr Ser Gly Gln Met Trp Asn Lys Asp Asp Lys Thr Gln Asp
355 360 365
Thr Leu Ala Val Ile Pro Asp Ser Ser Tyr Ala Gly Val Phe Gln Thr
370 375 380
Val Ile Asp Asp Cys Lys Ala Asn Gly Ala Phe Asp Pro Thr Thr Met
385 390 395 400
Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr
405 410 415
Gly Ser His Asp Lys Thr Phe Arg Ile Ala Ala Asp Gly Lys Val Glu
420 425 430
Val Arg Asn Ser Ala Gly Asp Val Leu Leu Glu His Glu Val Ser Glu
435 440 445
Gly Asp Ile Trp Arg Ala Cys Gln Thr Lys Asp Ala Pro Ile Gln Asp
450 455 460
Trp Val Lys Leu Ala Val Asp Arg Ala Arg Ile Ser Gly Met Pro Ala
465 470 475 480
Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Thr Thr
485 490 495
Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile
500 505 510
Arg Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Val Asp Arg Ile
515 520 525
Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp
530 535 540
Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys
545 550 555 560
Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr
565 570 575
Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Val Glu Glu
580 585 590
Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu
595 600 605
Ser Leu Arg His Val Ala Arg Thr Gln Asp Asn Ala Lys Ala Ala Val
610 615 620
Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Val Leu Ser Glu Gly
625 630 635 640
Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His
645 650 655
Phe Tyr Leu Ala Ser Tyr Trp Ala Glu Ala Leu Ala Ala Gln Ser Asp
660 665 670
Asp Ala Glu Leu Ala Ala Thr Phe Gln Pro Val Ala Glu Ala Leu Ala
675 680 685
Ala Asp Ala Ala Thr Ile Asp Gln Glu Leu Ile Asp Asn Gln Gly Ser
690 695 700
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Asp Val Met Arg Pro Ser Ala Lys Phe Asn Glu Ile Ile Asp Gly Leu
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Lys Lys

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cacacagcga aaagccacaa acaagacgct cgtactgtta gaattgcagc ggtcgttggt 180
ccgaatccct acacttgggg acgtaccacc gcgttctgcc ggtgcacgcc taccttgacc 240
ggggtagacg ggtgcgggta acgaacattc cagttcaatg aagaggaaat ggagctccct 300

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gtg acc gaa agc aag aac tcc ttc aac gcc aag cgc acc ctc gag gtc        348
Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Arg Thr Leu Glu Val
1               5                  10                  15
ggc gag aag tcc tac gac tac ttc gcc ctc gac gcc gtg ccg ggc atg        396
Gly Glu Lys Ser Tyr Asp Tyr Phe Ala Leu Asp Ala Val Pro Gly Met
            20                  25                  30
gag aag ctg ccg tac tcc ctg aag gtt ctc ggc gag aac ctt ctg cgt        444
Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
        35                  40                  45
acc gag gac ggc gca aac atc acc acc gag cac atc gag gca atc gcc        492
Thr Glu Asp Gly Ala Asn Ile Thr Thr Glu His Ile Glu Ala Ile Ala
    50                  55                  60
aac tgg gat ccg aag gct gag ccc tcc atc gag atc cag ttc acc ccg        540
Asn Trp Asp Pro Lys Ala Glu Pro Ser Ile Glu Ile Gln Phe Thr Pro
65                  70                  75                  80
gca cgt gtc ctc atg cag gac ttc acc ggt gtc gcc tgt gca gtc gac        588
Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Ala Cys Ala Val Asp
                85                  90                  95
ctg gcc acc atg cgc gag gcc gtg aag acc ctg ggc ggc gac ccg gac        636
Leu Ala Thr Met Arg Glu Ala Val Lys Thr Leu Gly Gly Asp Pro Asp
            100                 105                 110
gac gtc aac ccg ctg aac ccg gcc gag atg gtc atc gac cac tcc gtc        684
Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
        115                 120                 125
atc gtc gag gca ttc ggt acc tcc gcc gct ctg gag aag aac gtc gag        732
Ile Val Glu Ala Phe Gly Thr Ser Ala Ala Leu Glu Lys Asn Val Glu
    130                 135                 140
atc gag tac cag cgc aac gag gag cgc tac cag ttc ctc cgc tgg ggt        780
Ile Glu Tyr Gln Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
145                 150                 155                 160
gcc gag aac ttc tcc aac ttc cgc gtc gtt ccc ccg gga acc ggc atc        828
Ala Glu Asn Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
                165                 170                 175
gtc cac cag gtc aac atc gag tac ctg tcc cgc gtt gtc ttc gac aac        876
Val His Gln Val Asn Ile Glu Tyr Leu Ser Arg Val Val Phe Asp Asn
            180                 185                 190
aac ggc ctc gcc tac ccg gac acc tgc atc ggc acc gac tcc cac acc        924
Asn Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
        195                 200                 205
acc atg gag aac ggc ctg gga atc ctg ggc tgg ggc gtc ggc ggc atc        972
Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
    210                 215                 220
gag gcc gag gct gcc atg ctg ggc cag ccg gtc tcc atg ctc atc ccg       1020
Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro
225                 230                 235                 240
cgc gtc gtc ggc ttc aag ctg acc ggt gag atc ccg gcc ggc gtc acc       1068
Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Ala Gly Val Thr
                245                 250                 255
gcc acc gac gtg gtc ctc acc atc acc gag atg ctg cgt aac cac ggc       1116
Ala Thr Asp Val Val Leu Thr Ile Thr Glu Met Leu Arg Asn His Gly
            260                 265                 270

gtc gtc cag aag ttc gtc gag ttc tac ggc aac ggc gtc aag tcc gtc       1164
Val Val Gln Lys Phe Val Glu Phe Tyr Gly Asn Gly Val Lys Ser Val
        275                 280                 285
ccg ctg gcg aac cgc gcc acc atc ggc aac atg tcc ccg gag ttc ggc       1212
Pro Leu Ala Asn Arg Ala Thr Ile Gly Asn Met Ser Pro Glu Phe Gly
    290                 295                 300
tcc acc tgt gcc atg ttc ccg atc gac gag gag acc atc aag tac ctc       1260
Ser Thr Cys Ala Met Phe Pro Ile Asp Glu Glu Thr Ile Lys Tyr Leu
305                 310                 315                 320
gag ctc acc ggc cgc tcc gag gag gac atc gcc cgc gtc gag gca tac       1308
Glu Leu Thr Gly Arg Ser Glu Glu Asp Ile Ala Arg Val Glu Ala Tyr
                325                 330                 335
gcc aag gct cag ggc atg tgg ctc tac gag gac gcc ccg gag gcc gag       1356
Ala Lys Ala Gln Gly Met Trp Leu Tyr Glu Asp Ala Pro Glu Ala Glu
            340                 345                 350
tac tcc gag tac ctc gag ctg gac ctc tcc acc gtc gtc ccg tcc atc       1404
Tyr Ser Glu Tyr Leu Glu Leu Asp Leu Ser Thr Val Val Pro Ser Ile
        355                 360                 365
gcc ggc ccg aag cgc ccg cag gac cgc atc ctc ctc tcc gag gcc aag       1452
Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu Leu Ser Glu Ala Lys
    370                 375                 380
gca cag ttc cgc aag gac ctg ccg acc tac gcc tcc gac gag gtc gct       1500
Ala Gln Phe Arg Lys Asp Leu Pro Thr Tyr Ala Ser Asp Glu Val Ala
385                 390                 395                 400
gag ccg gtc cgc gcc acc aag gcc gtc ggc gac gac tac aac cag tcc       1548
Glu Pro Val Arg Ala Thr Lys Ala Val Gly Asp Asp Tyr Asn Gln Ser
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                405                 410                 415
ttc ccg ggc aac ggc gag tcc gct gcc gac tcc gcc gag ggc cgc gcc      1596
Phe Pro Gly Asn Gly Glu Ser Ala Ala Asp Ser Ala Glu Gly Arg Ala
            420                 425                 430
tcc aag ccg gtc atc gtc gag tcc ccg cag ggc ggc gag tac acc ctc      1644
Ser Lys Pro Val Ile Val Glu Ser Pro Gln Gly Gly Glu Tyr Thr Leu
        435                 440                 445
gac cac ggc atg gtg gcc atc gcc tcc atc acc tcc tgc acc aac acc      1692
Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys Thr Asn Thr
    450                 455                 460
tcc aac ccg tcc gtg ctg gtc gca gcc ggc ctg ctg gcc cgc aag gcc      1740
Ser Asn Pro Ser Val Leu Val Ala Ala Gly Leu Leu Ala Arg Lys Ala
465                 470                 475                 480
aac gag ctg ggc ctg aag tcc aag ccg tgg gtc aag acc atc tgc gcc      1788
Asn Glu Leu Gly Leu Lys Ser Lys Pro Trp Val Lys Thr Ile Cys Ala
                485                 490                 495
ccg ggc tcc cag gtc gtc gac ggt tac ttc aag cgc gcc gac ctc tgg      1836
Pro Gly Ser Gln Val Val Asp Gly Tyr Phe Lys Arg Ala Asp Leu Trp
            500                 505                 510
aag gat ctg gag gcc ctg ggc ttc tac ctc tcc ggc ttc ggc tgc acc      1884
Lys Asp Leu Glu Ala Leu Gly Phe Tyr Leu Ser Gly Phe Gly Cys Thr
        515                 520                 525
tcc tgc atc ggc aac tcc ggt ccg ctc ccg gct gag gtc tcc tcc gcc      1932
Ser Cys Ile Gly Asn Ser Gly Pro Leu Pro Ala Glu Val Ser Ser Ala
    530                 535                 540
atc aac gag cac gac ctg gcc gcc acc gca gtc ctg tcc ggc aac cgt      1980
Ile Asn Glu His Asp Leu Ala Ala Thr Ala Val Leu Ser Gly Asn Arg
545                 550                 555                 560
aac ttc gag ggt cgt atc tcc ccc gac gtc aag atg aac tac ctg gcc      2028
Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn Tyr Leu Ala
                565                 570                 575
tcc ccg ccg ctg gtc atc gcc tac gcc atc gcc ggc acc atg gac ttc      2076
Ser Pro Pro Leu Val Ile Ala Tyr Ala Ile Ala Gly Thr Met Asp Phe
            580                 585                 590
gac ttc gag acc gat gcc ctg ggt cag gac aag gac ggc aac gac gtc      2124
Asp Phe Glu Thr Asp Ala Leu Gly Gln Asp Lys Asp Gly Asn Asp Val
        595                 600                 605
ttc ctg aag gac atc tgg ccc tcc acc gag gag atc gag gag acc atc      2172
Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu Glu Thr Ile
    610                 615                 620
gcg gcc tcc atc tcc cgc gag ctg tac gag gcc gac tac gct gac gtc      2220
Ala Ala Ser Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr Ala Asp Val
625                 630                 635                 640
ttc aag ggc gac aag cag tgg cag gag ctc gac atc ccg acc ggc aag      2268
Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Ile Pro Thr Gly Lys
                645                 650                 655
acc ttc gag tgg gac gag aac tcc tcc tac atc cgt aag gca ccg tac      2316
Thr Phe Glu Trp Asp Glu Asn Ser Ser Tyr Ile Arg Lys Ala Pro Tyr
            660                 665                 670
ttc gac ggc atg ccg ctc gag ccg cag ccg gtc gag gac atc aag ggc      2364
Phe Asp Gly Met Pro Leu Glu Pro Gln Pro Val Glu Asp Ile Lys Gly
        675                 680                 685

gcc cgc gtc ctc gcc aag ctc ggc gac tcc gtg acc acc gac cac atc      2412
Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr Asp His Ile
    690                 695                 700
tcc ccg gcc tcc tcc atc aag ccg ggc acc ccg gca gcc cag tac ctg      2460
Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala Gln Tyr Leu
705                 710                 715                 720
gac tcc atg ggt gtc gag cgc aag gac tac aac tcc ctg ggc tcc cgt      2508
Asp Ser Met Gly Val Glu Arg Lys Asp Tyr Asn Ser Leu Gly Ser Arg
                725                 730                 735
cgt ggt aac cac gag gtc atg gtc cgc ggt acc ttc gcg aac atc cgc      2556
Arg Gly Asn His Glu Val Met Val Arg Gly Thr Phe Ala Asn Ile Arg
            740                 745                 750
ctg gcc aac cag ctg gtc gac gtc acc ggt ggc tac acc cgt gac ttc      2604
Leu Ala Asn Gln Leu Val Asp Val Thr Gly Gly Tyr Thr Arg Asp Phe
        755                 760                 765
acc cag gag ggt ggc ccg cag gcc tac atc tac gac gcc gcc atg aac      2652
Thr Gln Glu Gly Gly Pro Gln Ala Tyr Ile Tyr Asp Ala Ala Met Asn
    770                 775                 780
tac aag gag gcc ggc acc ccg ctg gtc gtc ctg ggt ggc aag gag tac      2700
Tyr Lys Glu Ala Gly Thr Pro Leu Val Val Leu Gly Gly Lys Glu Tyr
785                 790                 795                 800
ggc acc ggt tcc tcc cgt gac tgg gcc gcg aag ggc acc atc ctg ctc      2748
Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Ile Leu Leu
                805                 810                 815
ggc gtg aag gcc gtc atc acc gag tcc ttc gag cgt atc cac cgc tcg      2796
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Gly Val Lys Ala Val Ile Thr Glu Ser Phe Glu Arg Ile His Arg Ser
            820                 825                 830
aac ctg atc ggt atg ggt gtc atc ccg ctg cag ttc ccg gag ggc gag      2844
Asn Leu Ile Gly Met Gly Val Ile Pro Leu Gln Phe Pro Glu Gly Glu
        835                 840                 845
tcc cac gag tcc ctg ggc ctg gac ggc acc gag gtc ttc gac atc gag      2892
Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Val Phe Asp Ile Glu
    850                 855                 860
ggc atc acc gcc ctg aac gag ggc gag acc ccg aag acc gtc aag gtc      2940
Gly Ile Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr Val Lys Val
865                 870                 875                 880
acc gcc acc aag gag gac ggc tcc acc gtg gag ttc gac gcg att gtc      2988
Thr Ala Thr Lys Glu Asp Gly Ser Thr Val Glu Phe Asp Ala Ile Val
                885                 890                 895
cgc atc gac acc ccg ggt gag gcc gac tac tac cgc aac ggc ggc atc      3036
Arg Ile Asp Thr Pro Gly Glu Ala Asp Tyr Tyr Arg Asn Gly Gly Ile
            900                 905                 910
ctg cag tac gtc ctg cgt cag atg atc gct gct gcc aag taa              3078
Leu Gln Tyr Val Leu Arg Gln Met Ile Ala Ala Ala Lys
        915                 920                 925
gcgagcatcc tcccgcagtg tgaactgcct ctgagagggg gctgcatccc cggctaaggc     3138
gtcacgccac cggggagagc agccccctct ccccttttttc cctattcccc cgacaggagt     3198
cccctcatgc ccgtggtcag cgacaccgag ttgacgcgtc gtcagaccga gatcctcgaa     3258
ggcgcgcggc gttgcttcgc cgagtacggc tacgagggcg ccacggtgcg ccgcctcgag     3318
gaggccacgg gcaagtcgcg gggtgcgatc ttccaccact tcggtgacaa ggagaacctc     3378
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            20                  25                  30
Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
        35                  40                  45
Thr Glu Asp Gly Ala Asn Ile Thr Thr Glu His Ile Glu Ala Ile Ala
    50                  55                  60
Asn Trp Asp Pro Lys Ala Glu Pro Ser Ile Glu Ile Gln Phe Thr Pro
65                  70                  75                  80
Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Ala Cys Ala Val Asp
                85                  90                  95
Leu Ala Thr Met Arg Glu Ala Val Lys Thr Leu Gly Gly Asp Pro Asp
            100                 105                 110
Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
        115                 120                 125
Ile Val Glu Ala Phe Gly Thr Ser Ala Ala Leu Glu Lys Asn Val Glu
    130                 135                 140
Ile Glu Tyr Gln Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
145                 150                 155                 160
Ala Glu Asn Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
                165                 170                 175
Val His Gln Val Asn Ile Glu Tyr Leu Ser Arg Val Val Phe Asp Asn
            180                 185                 190
Asn Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
        195                 200                 205
Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
    210                 215                 220
Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro
225                 230                 235                 240
Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Ala Gly Val Thr
                245                 250                 255
Ala Thr Asp Val Val Leu Thr Ile Thr Glu Met Leu Arg Asn His Gly
            260                 265                 270
Val Val Gln Lys Phe Val Glu Phe Tyr Gly Asn Gly Val Lys Ser Val
        275                 280                 285
Pro Leu Ala Asn Arg Ala Thr Ile Gly Asn Met Ser Pro Glu Phe Gly
    290                 295                 300
Ser Thr Cys Ala Met Phe Pro Ile Asp Glu Glu Thr Ile Lys Tyr Leu
305                 310                 315                 320
Glu Leu Thr Gly Arg Ser Glu Glu Asp Ile Ala Arg Val Glu Ala Tyr
                325                 330                 335
Ala Lys Ala Gln Gly Met Trp Leu Tyr Glu Asp Ala Pro Glu Ala Glu
            340                 345                 350
Tyr Ser Glu Tyr Leu Glu Leu Asp Leu Ser Thr Val Val Pro Ser Ile
        355                 360                 365
Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu Leu Ser Glu Ala Lys
    370                 375                 380
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Ala Gln Phe Arg Lys Asp Leu Pro Thr Tyr Ala Ser Asp Glu Val Ala
385                 390                 395                 400
Glu Pro Val Arg Ala Thr Lys Ala Val Gly Asp Asp Tyr Asn Gln Ser
                405                 410                 415
Phe Pro Gly Asn Gly Glu Ser Ala Ala Asp Ser Ala Glu Gly Arg Ala
            420                 425                 430
Ser Lys Pro Val Ile Val Glu Ser Pro Gln Gly Gly Glu Tyr Thr Leu
        435                 440                 445
Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys Thr Asn Thr
    450                 455                 460
Ser Asn Pro Ser Val Leu Val Ala Ala Gly Leu Leu Ala Arg Lys Ala
465                 470                 475                 480
Asn Glu Leu Gly Leu Lys Ser Lys Pro Trp Val Lys Thr Ile Cys Ala
                485                 490                 495
Pro Gly Ser Gln Val Val Asp Gly Tyr Phe Lys Arg Ala Asp Leu Trp
            500                 505                 510
Lys Asp Leu Glu Ala Leu Gly Phe Tyr Leu Ser Gly Phe Gly Cys Thr
        515                 520                 525
Ser Cys Ile Gly Asn Ser Gly Pro Leu Pro Ala Glu Val Ser Ser Ala
    530                 535                 540
Ile Asn Glu His Asp Leu Ala Ala Thr Ala Val Leu Ser Gly Asn Arg
545                 550                 555                 560
Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn Tyr Leu Ala
                565                 570                 575
Ser Pro Pro Leu Val Ile Ala Tyr Ala Ile Ala Gly Thr Met Asp Phe
            580                 585                 590
Asp Phe Glu Thr Asp Ala Leu Gly Gln Asp Lys Asp Gly Asn Asp Val
        595                 600                 605
Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu Glu Thr Ile
    610                 615                 620
Ala Ala Ser Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr Ala Asp Val
625                 630                 635                 640
Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Ile Pro Thr Gly Lys
                645                 650                 655
Thr Phe Glu Trp Asp Glu Asn Ser Ser Tyr Ile Arg Lys Ala Pro Tyr
            660                 665                 670
Phe Asp Gly Met Pro Leu Glu Pro Gln Pro Val Glu Asp Ile Lys Gly
        675                 680                 685
Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr Asp His Ile
    690                 695                 700
Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala Gln Tyr Leu
705                 710                 715                 720
Asp Ser Met Gly Val Glu Arg Lys Asp Tyr Asn Ser Leu Gly Ser Arg
                725                 730                 735
Arg Gly Asn His Glu Val Met Val Arg Gly Thr Phe Ala Asn Ile Arg
            740                 745                 750
Leu Ala Asn Gln Leu Val Asp Val Thr Gly Gly Tyr Thr Arg Asp Phe
        755                 760                 765
Thr Gln Glu Gly Gly Pro Gln Ala Tyr Ile Tyr Asp Ala Ala Met Asn
    770                 775                 780
Tyr Lys Glu Ala Gly Thr Pro Leu Val Val Leu Gly Gly Lys Glu Tyr
785                 790                 795                 800
Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Ile Leu Leu
                805                 810                 815


Gly Val Lys Ala Val Ile Thr Glu Ser Phe Glu Arg Ile His Arg Ser
            820                 825                 830
Asn Leu Ile Gly Met Gly Val Ile Pro Leu Gln Phe Pro Glu Gly Glu
        835                 840                 845
Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Val Phe Asp Ile Glu
    850                 855                 860
Gly Ile Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr Val Lys Val
865                 870                 875                 880
Thr Ala Thr Lys Glu Asp Gly Ser Thr Val Glu Phe Asp Ala Ile Val
                885                 890                 895
Arg Ile Asp Thr Pro Gly Glu Ala Asp Tyr Tyr Arg Asn Gly Gly Ile
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Leu Gln Tyr Val Leu Arg Gln Met Ile Ala Ala Ala Lys
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gcacccagac cgggtgggtc gaccgcatgc agcaccgctc ccgcctctac gaactgctcc      180
gctacaacga gtacaacgcc ttcgaccagg aggttttcac gtactccgcc gacacctacc      240
agcccacctt ccagtagccc accagcaact cctgacattc cttgaaaggg gatgagtacc      300
atg tcc gac aac acc aac atc gag gtc cgc aag ggt ctc tac ggc gtg        348
Met Ser Asp Asn Thr Asn Ile Glu Val Arg Lys Gly Leu Tyr Gly Val
1               5                  10                  15
atc gcc gac tac acc gca gtc tcc aag gtc atg ccg gag acc aac tcc        396
Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
            20                  25                  30
ctg acc tac cgc gga tac gcc gtc cag gac ctc gtc gca gag tgc tcc        444
Leu Thr Tyr Arg Gly Tyr Ala Val Gln Asp Leu Val Ala Glu Cys Ser
        35                  40                  45
ttc gag gag gtc ttc tac ctc ctg tgg aac ggt gag ctg ccg aac gag        492
Phe Glu Glu Val Phe Tyr Leu Leu Trp Asn Gly Glu Leu Pro Asn Glu
    50                  55                  60
gag cag ctg gcg gag ttc aac agg cgc ggc cgt tcc tac cgc aag ctc        540
Glu Gln Leu Ala Glu Phe Asn Arg Arg Gly Arg Ser Tyr Arg Lys Leu
65                  70                  75                  80
gac gcc ggc ctg atc gca ctc atc cac tcc ctg ccg ctc gac tgt cac        588
Asp Ala Gly Leu Ile Ala Leu Ile His Ser Leu Pro Leu Asp Cys His
                85                  90                  95
ccg atg gac gtc atg cgc acc gcc gtg tcc tac atg ggc acc aag gac        636
Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
            100                 105                 110
tcc gag cac ttc acc ccg gac gcc gac cac atc acc cac gtc ggc cac        684
Ser Glu His Phe Thr Pro Asp Ala Asp His Ile Thr His Val Gly His
        115                 120                 125
aac ctc ctc gcc cag ctg ccg atg gtg ctg gcc atg gac atc cgc cgc        732
Asn Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
    130                 135                 140
cgt cag ggc ctc gac atc gtc gcc ccg gac ccg gac aag tcc gtc gcc        780
Arg Gln Gly Leu Asp Ile Val Ala Pro Asp Pro Asp Lys Ser Val Ala
145                 150                 155                 160
cac aac ctg ctg tcg atg gtc ttc ggc aac ggc ccg gag tcc ccg gcg        828
His Asn Leu Leu Ser Met Val Phe Gly Asn Gly Pro Glu Ser Pro Ala
                165                 170                 175
tcc aac ccg gac gac gtg cgt gac ttc gag aag tcg ctc atc ctc tac        876
Ser Asn Pro Asp Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
            180                 185                 190
gcc gag cac tcc ttc aac gcc tcg acc ttc acc tcg cgt gtg atc acc        924
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ser Arg Val Ile Thr
        195                 200                 205
tcg acc cgc tcg gac gtc tac tcc gcg atc acc ggt gcc atc ggc gcc        972
Ser Thr Arg Ser Asp Val Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala
    210                 215                 220
ctc aag ggc ccg ctg cac ggc ggc gcc aac gag ttc gtc atg cac acc       1020
Leu Lys Gly Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr
225                 230                 235                 240
atg ctg gag atc gac gac ccg gag aag gcc gcc gac tgg gtc aac aac       1068
Met Leu Glu Ile Asp Asp Pro Glu Lys Ala Ala Asp Trp Val Asn Asn
                245                 250                 255
gcc ctg gac aac aag gac ctc atc atg ggc ttc ggt cac cgc gtg tac       1116
Ala Leu Asp Asn Lys Asp Leu Ile Met Gly Phe Gly His Arg Val Tyr
            260                 265                 270
aag aag ggt gac tcg cgt gtc ccg tcc atg gag gcg tcc ttc cgt gac       1164
Lys Lys Gly Asp Ser Arg Val Pro Ser Met Glu Ala Ser Phe Arg Asp
        275                 280                 285
ctc gcc gag cgt cac gac ggc gcc aag tgg gtc gcc atg tac gag aac       1212
Leu Ala Glu Arg His Asp Gly Ala Lys Trp Val Ala Met Tyr Glu Asn
    290                 295                 300
atg cgc gac gcc atg gac gcc cgc acc ggc atc aag ccg aac ctg gac       1260
Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp
305                 310                 315                 320
ttc ccg gcc ggc ccg gcg tac cac ctg ctc ggc ttc ccg gtc gac ttc       1308
Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe Pro Val Asp Phe
                325                 330                 335
ttc acc ccg ctg ttc gtc gtc gcc cgc atc gcc ggc tgg acc gcc cac       1356
Phe Thr Pro Leu Phe Val Val Ala Arg Ile Ala Gly Trp Thr Ala His
            340                 345                 350
atc gtg gag cag tac aac gac aac tcc ctg att cgt ccg ctc tcc gcc       1404
Ile Val Glu Gln Tyr Asn Asp Asn Ser Leu Ile Arg Pro Leu Ser Ala
        355                 360                 365
tac aac ggc ccc gag cag cgc cag gtc acc ccg ctg gcc gcc cgt tag       1452
Tyr Asn Gly Pro Glu Gln Arg Gln Val Thr Pro Leu Ala Ala Arg
    370                 375                 380
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ccccacggcc ggcaccggac caccgcgacg cccacggcac tgcccacaca ttggggtggt 1512
gcgcgtgggt ttcgctgttc ggaacacctg tcggcccatt ccgcagggcg ggacagaaac 1572
ggcctttcgg gcgcccgtcc cgcggagtgc ggaaatggac cgcaccgggt ccaccacctg 1632
cagataccc ctgtgactag gggatactcc cccgaagaca accctctttc ttgcgatact 1692
gtggtgtgcc agagagctca cccgctctca gacacacccc cgacatgacg ttcggaaagg 1752

<210> 136
<211> 383
<212> PRT
<213> Corynebacterium humireducens
<400> 136

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1 5 10 15
Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
20 25 30
Leu Thr Tyr Arg Gly Tyr Ala Val Gln Asp Leu Val Ala Glu Cys Ser
35 40 45
Phe Glu Glu Val Phe Tyr Leu Leu Trp Asn Gly Glu Leu Pro Asn Glu
50 55 60
Glu Gln Leu Ala Glu Phe Asn Arg Arg Gly Arg Ser Tyr Arg Lys Leu
65 70 75 80
Asp Ala Gly Leu Ile Ala Leu Ile His Ser Leu Pro Leu Asp Cys His
85 90 95
Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
100 105 110
Ser Glu His Phe Thr Pro Asp Ala Asp His Ile Thr His Val Gly His
115 120 125
Asn Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
130 135 140
Arg Gln Gly Leu Asp Ile Val Ala Pro Asp Pro Asp Lys Ser Val Ala
145 150 155 160
His Asn Leu Leu Ser Met Val Phe Gly Asn Gly Pro Glu Ser Pro Ala
165 170 175
Ser Asn Pro Asp Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
180 185 190
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ser Arg Val Ile Thr
195 200 205
Ser Thr Arg Ser Asp Val Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala
210 215 220
Leu Lys Gly Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr
225 230 235 240
Met Leu Glu Ile Asp Asp Pro Glu Lys Ala Ala Asp Trp Val Asn Asn
245 250 255
Ala Leu Asp Asn Lys Asp Leu Ile Met Gly Phe Gly His Arg Val Tyr
260 265 270
Lys Lys Gly Asp Ser Arg Val Pro Ser Met Glu Ala Ser Phe Arg Asp
275 280 285
Leu Ala Glu Arg His Asp Gly Ala Lys Trp Val Ala Met Tyr Glu Asn
290 295 300
Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp
305 310 315 320
Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe Pro Val Asp Phe
325 330 335
Phe Thr Pro Leu Phe Val Val Ala Arg Ile Ala Gly Trp Thr Ala His
340 345 350

Ile Val Glu Gln Tyr Asn Asp Asn Ser Leu Ile Arg Pro Leu Ser Ala
355 360 365
Tyr Asn Gly Pro Glu Gln Arg Gln Val Thr Pro Leu Ala Ala Arg
370 375 380

<210> 137
<211> 3372
<212> ADN
<213> Corynebacterium humireducens
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<222> (301)..(3072)
<223> gen pepc
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tctcgtcggt ggcgcctcgc tcgacggcga ggagttcgcc aagctggcgg ccgccgcggc 120
gtccgtcgtc tagcatcacc tcatccaccg gccccgggca ctgaacattc agtgcccggg 180
gccggtgtcc tttctccggg gaatatggtg cgcaatcccc acgcacggcc gtcatatgcg 240
tcatgatggg gaggcgaacc gcatccccgc cttcttcgag tacgaacagg gagacactca 300
atg acc gtc cgc gat cat ctg cag gaa gac atc cgc tac ctc ggc cgt 348
Met Thr Val Arg Asp His Leu Gln Glu Asp Ile Arg Tyr Leu Gly Arg
1 5 10 15
atc ctc ggc cag gtc atc gcg gaa cag gag ggc gag gac gtg ttc aac 396

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Ile Leu Gly Gln Val Ile Ala Glu Gln Glu Gly Glu Asp Val Phe Asn
          20                  25                  30
ctc gtc gag cac gcc cgc cag cag gcc ttc gag gtg gcc aag ggc aac      444
Leu Val Glu His Ala Arg Gln Gln Ala Phe Glu Val Ala Lys Gly Asn
        35                  40                  45
gcc tcc ctg gag gtg ctc gtc gac ctg ttc cgg aac atc gag ccg gag      492
Ala Ser Leu Glu Val Leu Val Asp Leu Phe Arg Asn Ile Glu Pro Glu
    50                  55                  60
cgc gcg acc ccg gtg atc cgg gcg ttc agc cac ttc gcc ctg atg gcg      540
Arg Ala Thr Pro Val Ile Arg Ala Phe Ser His Phe Ala Leu Met Ala
65                  70                  75                  80
aac ctc gcg gag gac atc cac gac gac ttc cac cgg gag cgc atc ctc      588
Asn Leu Ala Glu Asp Ile His Asp Asp Phe His Arg Glu Arg Ile Leu
                85                  90                  95
gat gag ggc ggg gcc ccc gac tcc acc ctc aac gcc acg tgg gag aag      636
Asp Glu Gly Gly Ala Pro Asp Ser Thr Leu Asn Ala Thr Trp Glu Lys
            100                 105                 110
ttc cgg gag gcc ggc gtc agt gcc gcg gac atc gag agg tcg ctg tct      684
Phe Arg Glu Ala Gly Val Ser Ala Ala Asp Ile Glu Arg Ser Leu Ser
        115                 120                 125
gcc ggg ctc gtc gcc ccg gtg ctc acc gcc cac ccg acg gag acc cgc      732
Ala Gly Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg
    130                 135                 140
cgc cgc acc gtc ttc gac gcc cag aag cac atc acc gag ctc atg ctg      780
Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Glu Leu Met Leu
145                 150                 155                 160
cag cgg cac gcc gtc cag gac gcg gag ccg aac gcc cgc acc gag gac      828
Gln Arg His Ala Val Gln Asp Ala Glu Pro Asn Ala Arg Thr Glu Asp
                165                 170                 175
cgt ctc gcg gag atc gag cgc aac atc cgc cgc cgc atg acc atc ctg      876
Arg Leu Ala Glu Ile Glu Arg Asn Ile Arg Arg Arg Met Thr Ile Leu
            180                 185                 190
tgg cag acc gcg ctc atc cgg cag gcc cgc ccc cgc atc gag gac gag      924
Trp Gln Thr Ala Leu Ile Arg Gln Ala Arg Pro Arg Ile Glu Asp Glu
        195                 200                 205
atc gag gtc ggc ctg cgc tac tac acg ctc tcc ctg ctc cgg gag atc      972
Ile Glu Val Gly Leu Arg Tyr Tyr Thr Leu Ser Leu Leu Arg Glu Ile
    210                 215                 220
ccg gcg ctc aac cgg cac gtc gtc gac acg ctc acg gag cgt ttc ggc     1020
Pro Ala Leu Asn Arg His Val Val Asp Thr Leu Thr Glu Arg Phe Gly
225                 230                 235                 240
gcc gac ctg cgc aac agc gcc ggt cag gcc atc gtc cgc ccg ggc tcc     1068
Ala Asp Leu Arg Asn Ser Ala Gly Gln Ala Ile Val Arg Pro Gly Ser
                245                 250                 255
tgg atc ggc ggc gac cac gac ggc aac ccc ttc gtc acc gcc gac aca     1116
Trp Ile Gly Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Asp Thr
            260                 265                 270
ctg gac tac gct tcc cga cgc gcc gcc cag acc gtc ctc aag tac tac     1164
Leu Asp Tyr Ala Ser Arg Arg Ala Ala Gln Thr Val Leu Lys Tyr Tyr
        275                 280                 285
gtc acg cag ctc cac gcc ctc gag cac gag ctg agc ctc tcc gac cgc     1212
Val Thr Gln Leu His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg
    290                 295                 300
atg acc tcc gtc acc gtg gag ctc gtc gcc ctc gcc ggg cgg gga aag     1260
Met Thr Ser Val Thr Val Glu Leu Val Ala Leu Ala Gly Arg Gly Lys
305                 310                 315                 320
aac gac gtc ccc tcg cgt gtc gac gag ccc tac cgc cgc gcc gtc cac     1308
Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val His
                325                 330                 335
ggc gtc cgg ggc cgc atc ctc gcc acg acc gcg gcg ctc atc ggg gag     1356
Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu
            340                 345                 350
gac gcc gtc gag ggc gtc tgg cac cgc gag cat gag ccc tac ggc tcc     1404
Asp Ala Val Glu Gly Val Trp His Arg Glu His Glu Pro Tyr Gly Ser
        355                 360                 365
ccg cag gag ttc gag gcg gac ctc agg gtc atc gac acc tcg ctg cgt     1452
Pro Gln Glu Phe Glu Ala Asp Leu Arg Val Ile Asp Thr Ser Leu Arg
    370                 375                 380
gcc tcc cac gac gag atc atc gcc gac gac cgt ctc agc tcc atc cgg     1500
Ala Ser His Asp Glu Ile Ile Ala Asp Asp Arg Leu Ser Ser Ile Arg
385                 390                 395                 400
gcg gcc gtc gcc tcc ttc ggg ttc cac ctg tac tcg atc gac ctg cga     1548
Ala Ala Val Ala Ser Phe Gly Phe His Leu Tyr Ser Ile Asp Leu Arg
                405                 410                 415
cag aac tcc gag tcc ttc gag aac gtc ctc acc gag gtc ttc gcc acc     1596
Gln Asn Ser Glu Ser Phe Glu Asn Val Leu Thr Glu Val Phe Ala Thr
            420                 425                 430
gcg cac gtc cac ccc aac tac gac acg ctg cgg gag gag gtg aag atc     1644
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Ala His Val His Pro Asn Tyr Asp Thr Leu Arg Glu Glu Val Lys Ile
        435                 440                 445
gag ctg ctc acc cgc gaa ctg cag acc ccg cgc ccc ctc gtc ccg cgc      1692
Glu Leu Leu Thr Arg Glu Leu Gln Thr Pro Arg Pro Leu Val Pro Arg
    450                 455                 460
ggc tac cgg ggc ttc tcc gag ccg acc cag cgg gag ctc gac ctc atc      1740
Gly Tyr Arg Gly Phe Ser Glu Pro Thr Gln Arg Glu Leu Asp Leu Ile
465                 470                 475                 480
tcc cag gcc gcg gac tcc gtc gcc cgc ttc ggc gag cag atg atc ccg      1788
Ser Gln Ala Ala Asp Ser Val Ala Arg Phe Gly Glu Gln Met Ile Pro
                485                 490                 495
cac cag atc atc tcc atg gcg cag tcg gtc agc gac atc ctc gag ccg      1836
His Gln Ile Ile Ser Met Ala Gln Ser Val Ser Asp Ile Leu Glu Pro
            500                 505                 510
atg gtg ctg ctc aag gag gtc ggc ctc atc cag gcc aac ggc cag ggc      1884
Met Val Leu Leu Lys Glu Val Gly Leu Ile Gln Ala Asn Gly Gln Gly
        515                 520                 525
ccg acc ggc agc gtc gac atc atc ccg ctg ttc gag acg atc gac gac      1932
Pro Thr Gly Ser Val Asp Ile Ile Pro Leu Phe Glu Thr Ile Asp Asp
    530                 535                 540
ctc cag gcc ggc gcc ggc atc ctc cgt gag ctg tgg gac ctg ccg atc      1980
Leu Gln Ala Gly Ala Gly Ile Leu Arg Glu Leu Trp Asp Leu Pro Ile
545                 550                 555                 560
tac cgg gcg tac ctc gcc cag cgc ggc gac atc cag gag gtc atg ctc      2028
Tyr Arg Ala Tyr Leu Ala Gln Arg Gly Asp Ile Gln Glu Val Met Leu
                565                 570                 575
ggc tac tcg gac tcc aac aag gac ggc ggc tac ttc gcc gcc aac tgg      2076
Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp
            580                 585                 590
gcg ctc tac gac gcc gag acc gac ctg gtg aag gtc ggc cgc gag tac      2124
Ala Leu Tyr Asp Ala Glu Thr Asp Leu Val Lys Val Gly Arg Glu Tyr
        595                 600                 605
ggt gtg cgc ctg cga ctc ttc cac ggc cgc ggc ggc acc gtc ggc cgt      2172
Gly Val Arg Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg
    610                 615                 620
ggt ggc ggc ccc tcc tac gac gcg ctc ctc gcc cag ccg cag ggg gcg      2220
Gly Gly Gly Pro Ser Tyr Asp Ala Leu Leu Ala Gln Pro Gln Gly Ala
625                 630                 635                 640
gtc gac ggt tcc gtg cgc atc acc gag cag ggc gag atc atc tcg gcc      2268
Val Asp Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala
                645                 650                 655
aag tac ggc tcc ccg cgt acg gcc cgc cgc aac ctg gag gca ctg gtc      2316
Lys Tyr Gly Ser Pro Arg Thr Ala Arg Arg Asn Leu Glu Ala Leu Val
            660                 665                 670
tcc gcg acg ctc gag gcc agc ctg ctc acc gtc gac gac ctc gcc gac      2364
Ser Ala Thr Leu Glu Ala Ser Leu Leu Thr Val Asp Asp Leu Ala Asp
        675                 680                 685
cgg gcc cgc gcg acg cag ata atg agc gaa ctc gcg cag atc tcc cgc      2412
Arg Ala Arg Ala Thr Gln Ile Met Ser Glu Leu Ala Gln Ile Ser Arg
    690                 695                 700
cgc aag tac tcc gag ctc gtc cac gag gac ccg ggg ttc atc ccg tac      2460
Arg Lys Tyr Ser Glu Leu Val His Glu Asp Pro Gly Phe Ile Pro Tyr
705                 710                 715                 720
ttc acc cag tcg acc ccg ctc gac gag atc ggc tcc ctc aac atc ggc      2508
Phe Thr Gln Ser Thr Pro Leu Asp Glu Ile Gly Ser Leu Asn Ile Gly
                725                 730                 735
tcc cgc ccg acc gcc cgc aag cag acc aag ggc gtc gac gat ctc cgc      2556
Ser Arg Pro Thr Ala Arg Lys Gln Thr Lys Gly Val Asp Asp Leu Arg
            740                 745                 750
gcc atc ccg tgg gtg ctc gcc tgg tcc cag tcg cgt gtg ctg ctg ccg      2604
Ala Ile Pro Trp Val Leu Ala Trp Ser Gln Ser Arg Val Leu Leu Pro
        755                 760                 765
ggc tgg ttc ggc gtc ggc acg gcc ctg gcc gag tgg atc ggg gag ggg      2652
Gly Trp Phe Gly Val Gly Thr Ala Leu Ala Glu Trp Ile Gly Glu Gly
    770                 775                 780
gag gac agg gac gag cgc atc gcc gag ctg cgg gag ctc tac gag tcc      2700
Glu Asp Arg Asp Glu Arg Ile Ala Glu Leu Arg Glu Leu Tyr Glu Ser
785                 790                 795                 800
tgg ccc ttc ttc acc tcg atc atg tcc aac atg gcg cag gtc atg tcg      2748
Trp Pro Phe Phe Thr Ser Ile Met Ser Asn Met Ala Gln Val Met Ser
                805                 810                 815
aag gcg ggc atg gat ctc gcg gag ctc tac gcc cgg ctc atc gac gac      2796
Lys Ala Gly Met Asp Leu Ala Glu Leu Tyr Ala Arg Leu Ile Asp Asp
            820                 825                 830
cgg gag gtc gcc gag cgc gtc cac ggt gtc atc acg gag gag ttc gag      2844
Arg Glu Val Ala Glu Arg Val His Gly Val Ile Thr Glu Glu Phe Glu
        835                 840                 845
ctc acc cgc gag atg ttc agc acc gtc acc ggc agc gcc gag ctg ctc      2892
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Leu Thr Arg Glu Met Phe Ser Thr Val Thr Gly Ser Ala Glu Leu Leu
    850                 855                 860
gcc gac aac ccg gcg ctg gcc cgt tcg gtg cgc agg cgc ttc ccg tac      2940
Ala Asp Asn Pro Ala Leu Ala Arg Ser Val Arg Arg Arg Phe Pro Tyr
865                 870                 875                 880
ctg ctg ccg ctc aac atc atc cag ctg gag ctg ctg cgc cgc cac cgt      2988
Leu Leu Pro Leu Asn Ile Ile Gln Leu Glu Leu Leu Arg Arg His Arg
                885                 890                 895
gcc ggc gac tcc cga cgc gcc gtg tcc cgc ggc atc cag ctg acg atg      3036
Ala Gly Asp Ser Arg Arg Ala Val Ser Arg Gly Ile Gln Leu Thr Met
            900                 905                 910
aac gga ctc gcc acc gca ctg cgc aac tcc ggg tag acctggtgta          3082
Asn Gly Leu Ala Thr Ala Leu Arg Asn Ser Gly
        915                 920
gactgagccg gagtttgtgc cgcccgattc ccgcaaagga ccttcatgac cctcgcactc    3142
cagatcatcc tcgtgctcac cgccgtgctc atgacggtgt tcgttctgct gcacaagggt    3202
aagggcggcg gcctgtccag cctcttcggt ggcggcatgc agtcgaacct ctcgggttcg    3262
acggtcgtcg agaagaacct cgaccgctac acgatcctca tggccgtcat ctggatcgcc    3322
tgcatcgtgg cgctgaacct catccaggct ttcgccggct aggttcaatg               3372
<210>  138
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<213>  Corynebacterium humireducens
<400>  138
Met Thr Val Arg Asp His Leu Gln Glu Asp Ile Arg Tyr Leu Gly Arg
1               5                   10                  15
Ile Leu Gly Gln Val Ile Ala Glu Gln Glu Gly Glu Asp Val Phe Asn
            20                  25                  30
Leu Val Glu His Ala Arg Gln Gln Ala Phe Glu Val Ala Lys Gly Asn
        35                  40                  45
Ala Ser Leu Glu Val Leu Val Asp Leu Phe Arg Asn Ile Glu Pro Glu
    50                  55                  60
Arg Ala Thr Pro Val Ile Arg Ala Phe Ser His Phe Ala Leu Met Ala
65                  70                  75                  80
Asn Leu Ala Glu Asp Ile His Asp Asp Phe His Arg Glu Arg Ile Leu
                85                  90                  95
Asp Glu Gly Gly Ala Pro Asp Ser Thr Leu Asn Ala Thr Trp Glu Lys
            100                 105                 110
Phe Arg Glu Ala Gly Val Ser Ala Ala Asp Ile Glu Arg Ser Leu Ser
        115                 120                 125
Ala Gly Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg
    130                 135                 140
Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Glu Leu Met Leu
145                 150                 155                 160
Gln Arg His Ala Val Gln Asp Ala Glu Pro Asn Ala Arg Thr Glu Asp
                165                 170                 175
Arg Leu Ala Glu Ile Glu Arg Asn Ile Arg Arg Arg Met Thr Ile Leu
            180                 185                 190
Trp Gln Thr Ala Leu Ile Arg Gln Ala Arg Pro Arg Ile Glu Asp Glu
        195                 200                 205
Ile Glu Val Gly Leu Arg Tyr Tyr Thr Leu Ser Leu Leu Arg Glu Ile
    210                 215                 220
Pro Ala Leu Asn Arg His Val Val Asp Thr Leu Thr Glu Arg Phe Gly
225                 230                 235                 240
Ala Asp Leu Arg Asn Ser Ala Gly Gln Ala Ile Val Arg Pro Gly Ser
                245                 250                 255
Trp Ile Gly Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Asp Thr
            260                 265                 270


Leu Asp Tyr Ala Ser Arg Arg Ala Ala Gln Thr Val Leu Lys Tyr Tyr
        275                 280                 285
Val Thr Gln Leu His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg
    290                 295                 300
Met Thr Ser Val Thr Val Glu Leu Val Ala Leu Ala Gly Arg Gly Lys
305                 310                 315                 320
Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val His
                325                 330                 335
Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu
            340                 345                 350
Asp Ala Val Glu Gly Val Trp His Arg Glu His Glu Pro Tyr Gly Ser
        355                 360                 365
Pro Gln Glu Phe Glu Ala Asp Leu Arg Val Ile Asp Thr Ser Leu Arg
    370                 375                 380
Ala Ser His Asp Glu Ile Ile Ala Asp Asp Arg Leu Ser Ser Ile Arg
385                 390                 395                 400
Ala Ala Val Ala Ser Phe Gly Phe His Leu Tyr Ser Ile Asp Leu Arg
                405                 410                 415
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Gln Asn Ser Glu Ser Phe Glu Asn Val Leu Thr Glu Val Phe Ala Thr
            420                 425                 430
Ala His Val His Pro Asn Tyr Asp Thr Leu Arg Glu Glu Val Lys Ile
        435                 440                 445
Glu Leu Leu Thr Arg Glu Leu Gln Thr Pro Arg Pro Leu Val Pro Arg
    450                 455                 460
Gly Tyr Arg Gly Phe Ser Glu Pro Thr Gln Arg Glu Leu Asp Leu Ile
465                 470                 475                 480
Ser Gln Ala Ala Asp Ser Val Ala Arg Phe Gly Glu Gln Met Ile Pro
                485                 490                 495
His Gln Ile Ile Ser Met Ala Gln Ser Val Ser Asp Ile Leu Glu Pro
            500                 505                 510
Met Val Leu Leu Lys Glu Val Gly Leu Ile Gln Ala Asn Gly Gln Gly
        515                 520                 525
Pro Thr Gly Ser Val Asp Ile Ile Pro Leu Phe Glu Thr Ile Asp Asp
    530                 535                 540
Leu Gln Ala Gly Ala Gly Ile Leu Arg Glu Leu Trp Asp Leu Pro Ile
545                 550                 555                 560
Tyr Arg Ala Tyr Leu Ala Gln Arg Gly Asp Ile Gln Glu Val Met Leu
                565                 570                 575
Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp
            580                 585                 590
Ala Leu Tyr Asp Ala Glu Thr Asp Leu Val Lys Val Gly Arg Glu Tyr
        595                 600                 605
Gly Val Arg Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg
    610                 615                 620
Gly Gly Gly Pro Ser Tyr Asp Ala Leu Leu Ala Gln Pro Gln Gly Ala
625                 630                 635                 640
Val Asp Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala
                645                 650                 655
Lys Tyr Gly Ser Pro Arg Thr Ala Arg Arg Asn Leu Glu Ala Leu Val
            660                 665                 670
Ser Ala Thr Leu Glu Ala Ser Leu Leu Thr Val Asp Asp Leu Ala Asp
        675                 680                 685
Arg Ala Arg Ala Thr Gln Ile Met Ser Glu Leu Ala Gln Ile Ser Arg
    690                 695                 700
Arg Lys Tyr Ser Glu Leu Val His Glu Asp Pro Gly Phe Ile Pro Tyr
705                 710                 715                 720
Phe Thr Gln Ser Thr Pro Leu Asp Glu Ile Gly Ser Leu Asn Ile Gly
                725                 730                 735
Ser Arg Pro Thr Ala Arg Lys Gln Thr Lys Gly Val Asp Asp Leu Arg
            740                 745                 750
Ala Ile Pro Trp Val Leu Ala Trp Ser Gln Ser Arg Val Leu Leu Pro
        755                 760                 765
Gly Trp Phe Gly Val Gly Thr Ala Leu Ala Glu Trp Ile Gly Glu Gly
    770                 775                 780
Glu Asp Arg Asp Glu Arg Ile Ala Glu Leu Arg Glu Leu Tyr Glu Ser
785                 790                 795                 800
Trp Pro Phe Phe Thr Ser Ile Met Ser Asn Met Ala Gln Val Met Ser
                805                 810                 815
Lys Ala Gly Met Asp Leu Ala Glu Leu Tyr Ala Arg Leu Ile Asp Asp
            820                 825                 830
Arg Glu Val Ala Glu Arg Val His Gly Val Ile Thr Glu Glu Phe Glu
        835                 840                 845
Leu Thr Arg Glu Met Phe Ser Thr Val Thr Gly Ser Ala Glu Leu Leu
    850                 855                 860
Ala Asp Asn Pro Ala Leu Ala Arg Ser Val Arg Arg Arg Phe Pro Tyr
865                 870                 875                 880
Leu Leu Pro Leu Asn Ile Ile Gln Leu Glu Leu Leu Arg Arg His Arg
                885                 890                 895


Ala Gly Asp Ser Arg Arg Ala Val Ser Arg Gly Ile Gln Leu Thr Met
            900                 905                 910
Asn Gly Leu Ala Thr Ala Leu Arg Asn Ser Gly
        915                 920
<210>  139
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gtgaagagga tcgagttgtc caccccgacc atcagcagcc ccagggagat gatggcgagg     180
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aaggcccacc gctgggccgg ggtggagtcg acgttgtcga ggtgcgtcac gcagcggaac      240
tgtaccgacc gttcgttaca gtttcaacgc ggggcatgaa tcctccgtac gctcgggacc      300
atg gca cgc acc tac gca cag cag ctc gtc gac gcc ctc gag agg cag         348
Met Ala Arg Thr Tyr Ala Gln Gln Leu Val Asp Ala Leu Glu Arg Gln
1               5                  10                  15
ggc gtg gaa cgg atc tac gga gtc gtc ggg gac agc ctc aac ccc atc         396
Gly Val Glu Arg Ile Tyr Gly Val Val Gly Asp Ser Leu Asn Pro Ile
            20                  25                  30
gtc gac gcc gtc cgc acc tcc ccg atc gag tgg atc cac gtc cgc aac         444
Val Asp Ala Val Arg Thr Ser Pro Ile Glu Trp Ile His Val Arg Asn
        35                  40                  45
gag gag gcc gcc gcc ttc gcc gcc ggc gcc gag tcc ctc ctc acc ggc         492
Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Leu Thr Gly
    50                  55                  60
cgc ctc gcc gtg tgc gcg ggc tcc tgc ggc ccc ggc aac ctc cac ctc         540
Arg Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His Leu
65                  70                  75                  80
atc cag ggt ctc tac gac gcc cac cgc aac ggc gcc cac gtc ctc gcc         588
Ile Gln Gly Leu Tyr Asp Ala His Arg Asn Gly Ala His Val Leu Ala
                85                  90                  95
ctg gcc tcc cac atc ccc agc aac cag atc ggt acc tca tac ttc cag         636
Leu Ala Ser His Ile Pro Ser Asn Gln Ile Gly Thr Ser Tyr Phe Gln
            100                 105                 110
gag acc cac ccc gaa cag ctc ttc gcg gaa tgt tcc ggt tac tgc gag         684
Glu Thr His Pro Glu Gln Leu Phe Ala Glu Cys Ser Gly Tyr Cys Glu
        115                 120                 125
atg gtc aac tcc gcc gac cag ggc gcc cgc gtc ctg cac cac gcg atc         732
Met Val Asn Ser Ala Asp Gln Gly Ala Arg Val Leu His His Ala Ile
    130                 135                 140
cag tcg acg atg gcc ggg cag ggc gtg tcc gtg ctg gtc atc ccg ggg         780
Gln Ser Thr Met Ala Gly Gln Gly Val Ser Val Leu Val Ile Pro Gly
145                 150                 155                 160
gac atc gcc acg cag gac gcc ggc gac gac cgg ttc ctg cag tcc acc         828
Asp Ile Ala Thr Gln Asp Ala Gly Asp Asp Arg Phe Leu Gln Ser Thr
                165                 170                 175
gtc gcc acc ggc cgc ccc gtg ctc cac ccc gac gcc cgc gag gcc gcc         876
Val Ala Thr Gly Arg Pro Val Leu His Pro Asp Ala Arg Glu Ala Ala
            180                 185                 190
gcc ctg gtc gcg gcc atc aac gcc gcc gac acg gtg acc ctg ttc tgc         924
Ala Leu Val Ala Ala Ile Asn Ala Ala Asp Thr Val Thr Leu Phe Cys
        195                 200                 205
ggc gca ggc gta cgc gac gcc cgc gag cag gtc ctc gcc ctg gcg gag         972
Gly Ala Gly Val Arg Asp Ala Arg Glu Gln Val Leu Ala Leu Ala Glu
    210                 215                 220
aag atc aag gcc ccc atc ggc cac gcc ctc ggc ggc aag atg cac atc        1020
Lys Ile Lys Ala Pro Ile Gly His Ala Leu Gly Gly Lys Met His Ile
225                 230                 235                 240
cag cac gac aac ccc ttc gac gtc ggc atg tcc ggg ctc ctc ggc tac        1068
Gln His Asp Asn Pro Phe Asp Val Gly Met Ser Gly Leu Leu Gly Tyr
                245                 250                 255
ggc gcc tgc cac gac gca ctg cac gac gcc gac ctg ctc atc ctc ctg        1116
Gly Ala Cys His Asp Ala Leu His Asp Ala Asp Leu Leu Ile Leu Leu
            260                 265                 270
ggc acc gac ttc ccc tac acc gag ttc ctg ccc acc ggg aac gtc gcg        1164
Gly Thr Asp Phe Pro Tyr Thr Glu Phe Leu Pro Thr Gly Asn Val Ala
        275                 280                 285
cag gtc gac agc gac gcc gcg cac atc ggc cgc cgc acc acg gtg cac        1212
Gln Val Asp Ser Asp Ala Ala His Ile Gly Arg Arg Thr Thr Val His
    290                 295                 300
cac ccg gtg gtc ggc gac gtc ggc gcc acc ctc gac acc atc ctc ccg        1260
His Pro Val Val Gly Asp Val Gly Ala Thr Leu Asp Thr Ile Leu Pro
305                 310                 315                 320
cac ctg gag gag aag acc gac cgc agc ttc ctc gac ggg atg ctc cgc        1308
His Leu Glu Glu Lys Thr Asp Arg Ser Phe Leu Asp Gly Met Leu Arg
                325                 330                 335
aag cac gcc cgg acg ctg gag aag gtc gtg gag gtg tac acg cgg gac        1356
Lys His Ala Arg Thr Leu Glu Lys Val Val Glu Val Tyr Thr Arg Asp
            340                 345                 350
gtc ggg aag cac acc ccc atc cac ccg gag tac ctc gcc gcc gtc ctc        1404
Val Gly Lys His Thr Pro Ile His Pro Glu Tyr Leu Ala Ala Val Leu
        355                 360                 365
gac gag ctc gcc gcc gac gac gcc gtg ttc acc gtc gac acc ggc atg        1452
Asp Glu Leu Ala Ala Asp Asp Ala Val Phe Thr Val Asp Thr Gly Met
    370                 375                 380
tgc aac gtg tgg gcc gcg cgc tac ctc acc ccc aac gga cga cgc gcg        1500
Cys Asn Val Trp Ala Ala Arg Tyr Leu Thr Pro Asn Gly Arg Arg Ala
385                 390                 395                 400
cag atc ggc tcc ctc cgc cac ggc acg atg gcc aac gcg ctg ccg cac        1548
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Gln Ile Gly Ser Leu Arg His Gly Thr Met Ala Asn Ala Leu Pro His
                405                 410                 415
gcc atc ggc gcg cag ttc gcc gac cgg aac cgt cag gtc atc agc ctc      1596
Ala Ile Gly Ala Gln Phe Ala Asp Arg Asn Arg Gln Val Ile Ser Leu
            420                 425                 430
aac ggc gac ggc ggc ctc gcc atg ctc ctc ggc gaa ctg ctc acc gtg      1644
Asn Gly Asp Gly Gly Leu Ala Met Leu Leu Gly Glu Leu Leu Thr Val
        435                 440                 445
gaa ctc cac gac ctg ccc gtg aag atg gtc gtg ttc aac aac tcc tcg      1692
Glu Leu His Asp Leu Pro Val Lys Met Val Val Phe Asn Asn Ser Ser
    450                 455                 460
ctc ggc atg gtc aaa ctc gag atg ctc gtc gag ggc atg ccc cag cac      1740
Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Met Pro Gln His
465                 470                 475                 480
ggc acc gac cac ggg cag gtc gac ttc gcg gcg atc gcg gcc gcc gcg      1788
Gly Thr Asp His Gly Gln Val Asp Phe Ala Ala Ile Ala Ala Ala Ala
                485                 490                 495
ggc atc cac tcc gtg ctc atc gac gac ccc gcc acc ctc cgc gag cag      1836
Gly Ile His Ser Val Leu Ile Asp Asp Pro Ala Thr Leu Arg Glu Gln
            500                 505                 510
ctc gcc gcg gcg ctc gcc cac ccc ggg ccc gtg ctc atc gac gtc cgc      1884
Leu Ala Ala Ala Leu Ala His Pro Gly Pro Val Leu Ile Asp Val Arg
        515                 520                 525
acc gac ccc gac gcc ctc tcc ctc ccg ccg gag atc acc tgg gag atg      1932
Thr Asp Pro Asp Ala Leu Ser Leu Pro Pro Glu Ile Thr Trp Glu Met
    530                 535                 540
ctc atc ggc ttc tcc cgg gcc gcg acc cgt acc gtc ctc ggc ggc ggc      1980
Leu Ile Gly Phe Ser Arg Ala Ala Thr Arg Thr Val Leu Gly Gly Gly
545                 550                 555                 560
gtc ggc gag atg gtg cac ctc gcg cgc acg aac ctg cgc aac atc ggc      2028
Val Gly Glu Met Val His Leu Ala Arg Thr Asn Leu Arg Asn Ile Gly
                565                 570                 575
gcg gcc ggg gcg gtc tag tctgggcgtc atgaccccga ccgtccggat             2076
Ala Ala Gly Ala Val
            580
cgacctcgcc cgcctcgacg cgaacatcgc cgcgcaaccc gggcggctgc gaccgcacgt     2136
gaagacccac aagatcctgg agatcgcccg ccggcagctc gcggcgggtg cccacggcct     2196
cacggtcgcg acggtggggg aggcggaggt cttcgccgag gtctgcgacg acatcttcat     2256
cgcctacccc gtctgggccg acaagaggct gcgcgacctg gccgggaggg tgcggctgag     2316
cgtcggctgc gactcgctgg ccgccgccga                                     2346
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Val Asp Ala Val Arg Thr Ser Pro Ile Glu Trp Ile His Val Arg Asn
        35                  40                  45
Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Leu Thr Gly
    50                  55                  60
Arg Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His Leu
65                  70                  75                  80
Ile Gln Gly Leu Tyr Asp Ala His Arg Asn Gly Ala His Val Leu Ala
                85                  90                  95
Leu Ala Ser His Ile Pro Ser Asn Gln Ile Gly Thr Ser Tyr Phe Gln
            100                 105                 110
Glu Thr His Pro Glu Gln Leu Phe Ala Glu Cys Ser Gly Tyr Cys Glu
        115                 120                 125
Met Val Asn Ser Ala Asp Gln Gly Ala Arg Val Leu His His Ala Ile
    130                 135                 140
Gln Ser Thr Met Ala Gly Gln Gly Val Ser Val Leu Val Ile Pro Gly
145                 150                 155                 160
Asp Ile Ala Thr Gln Asp Ala Gly Asp Asp Arg Phe Leu Gln Ser Thr
                165                 170                 175
Val Ala Thr Gly Arg Pro Val Leu His Pro Asp Ala Arg Glu Ala Ala
            180                 185                 190
Ala Leu Val Ala Ala Ile Asn Ala Ala Asp Thr Val Thr Leu Phe Cys
        195                 200                 205
Gly Ala Gly Val Arg Asp Ala Arg Glu Gln Val Leu Ala Leu Ala Glu
    210                 215                 220
Lys Ile Lys Ala Pro Ile Gly His Ala Leu Gly Gly Lys Met His Ile
225                 230                 235                 240
Gln His Asp Asn Pro Phe Asp Val Gly Met Ser Gly Leu Leu Gly Tyr
                245                 250                 255
Gly Ala Cys His Asp Ala Leu His Asp Ala Asp Leu Leu Ile Leu Leu
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            260                 265                 270
Gly Thr Asp Phe Pro Tyr Thr Glu Phe Leu Pro Thr Gly Asn Val Ala
        275                 280                 285
Gln Val Asp Ser Asp Ala Ala His Ile Gly Arg Arg Thr Thr Val His
    290                 295                 300
His Pro Val Val Gly Asp Val Gly Ala Thr Leu Asp Thr Ile Leu Pro
305                 310                 315                 320
His Leu Glu Glu Lys Thr Asp Arg Ser Phe Leu Asp Gly Met Leu Arg
                325                 330                 335
Lys His Ala Arg Thr Leu Glu Lys Val Val Glu Val Tyr Thr Arg Asp
            340                 345                 350
Val Gly Lys His Thr Pro Ile His Pro Glu Tyr Leu Ala Ala Val Leu
        355                 360                 365
Asp Glu Leu Ala Ala Asp Asp Ala Val Phe Thr Val Asp Thr Gly Met
    370                 375                 380
Cys Asn Val Trp Ala Ala Arg Tyr Leu Thr Pro Asn Gly Arg Arg Ala
385                 390                 395                 400
Gln Ile Gly Ser Leu Arg His Gly Thr Met Ala Asn Ala Leu Pro His
                405                 410                 415
Ala Ile Gly Ala Gln Phe Ala Asp Arg Asn Arg Gln Val Ile Ser Leu
            420                 425                 430
Asn Gly Asp Gly Gly Leu Ala Met Leu Leu Gly Glu Leu Leu Thr Val
        435                 440                 445
Glu Leu His Asp Leu Pro Val Lys Met Val Val Phe Asn Asn Ser Ser
    450                 455                 460
Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Met Pro Gln His
465                 470                 475                 480
Gly Thr Asp His Gly Gln Val Asp Phe Ala Ala Ile Ala Ala Ala Ala
                485                 490                 495
Gly Ile His Ser Val Leu Ile Asp Asp Pro Ala Thr Leu Arg Glu Gln
            500                 505                 510
Leu Ala Ala Ala Leu Ala His Pro Gly Pro Val Leu Ile Asp Val Arg
        515                 520                 525
Thr Asp Pro Asp Ala Leu Ser Leu Pro Pro Glu Ile Thr Trp Glu Met
    530                 535                 540
Leu Ile Gly Phe Ser Arg Ala Ala Thr Arg Thr Val Leu Gly Gly Gly
545                 550                 555                 560
Val Gly Glu Met Val His Leu Ala Arg Thr Asn Leu Arg Asn Ile Gly
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gcatcgcacc gggtggactg ttcgccctct acgtcgccgg ttacacgctg ggccgtttct      120
ggatcgagct catgcgcgac gattccgcca cgatgatcct cggccagcgg gtcaacacct      180
gggtctccgc cgtggtgttc ctcgtctcga tcgcggtatt cgtgtggttg cagcgacgtc      240
agcgggctgt tgtccgagaa acagagtagg ttggtagccg tgtctagacg aaccaagatt      300
gtg tgc acc ctc ggt cct gcc gtc gcc tcc aag gac gcg atc acg cgt          348
Val Cys Thr Leu Gly Pro Ala Val Ala Ser Lys Asp Ala Ile Thr Arg
1               5                   10                  15
ctg gtg gag gac ggc atg gac gtc gcc cgc ctg aac ttc tcc cac ggt        396
Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn Phe Ser His Gly
            20                  25                  30

gat cac ccc gat cac gag cag aac tac aag tgg gtc cgg gaa gcc acc        444
Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val Arg Glu Ala Thr
        35                  40                  45
gat gag acc ggc cgt gcc gtc ggc atc ctc gct gac ctc cag ggc ccg        492
Asp Glu Thr Gly Arg Ala Val Gly Ile Leu Ala Asp Leu Gln Gly Pro
    50                  55                  60
aag atc cgc ctc ggt cgc ttc atc gac ggt gcc acc gtc tgg gag acc        540
Lys Ile Arg Leu Gly Arg Phe Ile Asp Gly Ala Thr Val Trp Glu Thr
65                  70                  75                  80
ggt gag gtc atc cgc atc acc gtg gac gat gtc gag ggc acg cac gac        588
Gly Glu Val Ile Arg Ile Thr Val Asp Asp Val Glu Gly Thr His Asp
                85                  90                  95
cgc gtg tcc acc acc tac aag aac ctc gcg cag gac gcc aag ccc ggc        636
Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Gln Asp Ala Lys Pro Gly
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           100                 105                 110
gac cgt ctg ctc gtc gac gac ggc aag gtc ggc ctg acc tgc ctc gag        684
Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu Thr Cys Leu Glu
        115                 120                 125
gtc gac ggc aac gac gtc gtc tgc gag gtc acc gag ggc ggc ccc gtc        732
Val Asp Gly Asn Asp Val Val Cys Glu Val Thr Glu Gly Gly Pro Val
    130                 135                 140
tcc aac aac aag ggc gtc tcc ctc ccg ggc atg gac atc tct gtg ccg        780
Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp Ile Ser Val Pro
145                 150                 155                 160
gcg ctg tcg gag aag gac atc gcc gac ctc gag ttc gcc ctc aag ctg        828
Ala Leu Ser Glu Lys Asp Ile Ala Asp Leu Glu Phe Ala Leu Lys Leu
                165                 170                 175
ggc gtc gac ttc atc gcc ctg tcc ttc gtc cgc tcc ccg gcg gac gtc        876
Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser Pro Ala Asp Val
            180                 185                 190
gac ctc gtc cac gag gtc atg gac cgc gtc ggc cgc cac gtg ccg gtc        924
Asp Leu Val His Glu Val Met Asp Arg Val Gly Arg His Val Pro Val
        195                 200                 205
atc gcg aag ctg gag aag ccg gag gcc gtc cac gcc ctc gag tcc atc        972
Ile Ala Lys Leu Glu Lys Pro Glu Ala Val His Ala Leu Glu Ser Ile
    210                 215                 220
gtc ctc gcc ttc gac gcc atc atg gtc gcc cgc ggt gac ctc ggc gtc       1020
Val Leu Ala Phe Asp Ala Ile Met Val Ala Arg Gly Asp Leu Gly Val
225                 230                 235                 240
gag gtg ccg ctg gag cag gtc ccg ctg gtg cag aag cgg gcc atc cag       1068
Glu Val Pro Leu Glu Gln Val Pro Leu Val Gln Lys Arg Ala Ile Gln
                245                 250                 255
atc gcc cgc gag aac gcg aag ccg gtc att gtc gcc acg cag atg ctc       1116
Ile Ala Arg Glu Asn Ala Lys Pro Val Ile Val Ala Thr Gln Met Leu
            260                 265                 270
gac tcc atg atc gag aac tcc acc ccg acc cgc gcc gag gcc tcc gac       1164
Asp Ser Met Ile Glu Asn Ser Thr Pro Thr Arg Ala Glu Ala Ser Asp
        275                 280                 285
gtc gcc aac gcc gtc ctc gac ggc gcc gac gcg gtc atg ctc tcc ggt       1212
Val Ala Asn Ala Val Leu Asp Gly Ala Asp Ala Val Met Leu Ser Gly
    290                 295                 300
gag acc tcc atc ggt gtg gac ccg cac aac gtc gtg cgc acc atg gcc       1260
Glu Thr Ser Ile Gly Val Asp Pro His Asn Val Val Arg Thr Met Ala
305                 310                 315                 320
cgc atc gtc acc cag gcc gag acc gac ggc cac gtg ccg ccg ctg agc       1308
Arg Ile Val Thr Gln Ala Glu Thr Asp Gly His Val Pro Pro Leu Ser
                325                 330                 335
cat gtc ccg cgc acc aag cgg ggc gtc atc tcc tac tcg gcc cgt gac       1356
His Val Pro Arg Thr Lys Arg Gly Val Ile Ser Tyr Ser Ala Arg Asp
            340                 345                 350
atc gcc gag cgt ctc aac gcc cgc gcc ctg gtc tgc ttc acc acc tcc       1404
Ile Ala Glu Arg Leu Asn Ala Arg Ala Leu Val Cys Phe Thr Thr Ser
        355                 360                 365
ggt gac acc gcc cgc cgt gtc gcc cgc ctg cac tcg cac ctg ccg ctg       1452
Gly Asp Thr Ala Arg Arg Val Ala Arg Leu His Ser His Leu Pro Leu
    370                 375                 380
ctg gtg ttc acc ccg cac ccg gcg gtc cgt tcg cag ctg gcc ctc acc       1500
Leu Val Phe Thr Pro His Pro Ala Val Arg Ser Gln Leu Ala Leu Thr
385                 390                 395                 400
tgg ggc gcc gag acc ttc ctc tgc gcc cag gcc ctg tcc acc gac gac       1548
Trp Gly Ala Glu Thr Phe Leu Cys Ala Gln Ala Leu Ser Thr Asp Asp
                405                 410                 415
atg atg gcc gag ctg gac cgt tcc ctg ctc gcc atg gac gac tac cac       1596
Met Met Ala Glu Leu Asp Arg Ser Leu Leu Ala Met Asp Asp Tyr His
            420                 425                 430
cgc gac gac atg atg gtc gtc gtc gcc ggc acc ccg ccc ggg gtc tcc       1644
Arg Asp Asp Met Met Val Val Val Ala Gly Thr Pro Pro Gly Val Ser
        435                 440                 445
ggc aac acg aac atg atc cac gtc cac ctg ctg ggc gag gac acg agt       1692
Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly Glu Asp Thr Ser
    450                 455                 460
tcc ccg acc ggc agg tag ccggagaaca gaaaaaggag cggcggagag              1740
Ser Pro Thr Gly Arg
465
gatcatcctc tccgccgctc ctgtcgtgtg cggctacttc accggggtcg gctccagctt      1800
ccacacctca cgcgcgtagt cgttgatggt gcggtcggag gagaaacggc ccgaggcgca      1860
gatgttcgcc cagcacatac gcgcccagtg caggcggtcg gcgtagtcgg cggccatgcg      1920
gtcgcgggtc tcgcggtagt cggcgaagtc accgaggacg tagtagacgt ccggggtctc      1980
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<213> Corynebacterium humireducens
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Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val Arg Glu Ala Thr
35 40 45
Asp Glu Thr Gly Arg Ala Val Gly Ile Leu Ala Asp Leu Gln Gly Pro
50 55 60
Lys Ile Arg Leu Gly Arg Phe Ile Asp Gly Ala Thr Val Trp Glu Thr
65 70 75 80
Gly Glu Val Ile Arg Ile Thr Val Asp Asp Val Glu Gly Thr His Asp
85 90 95
Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Gln Asp Ala Lys Pro Gly
100 105 110
Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu Thr Cys Leu Glu
115 120 125
Val Asp Gly Asn Asp Val Val Cys Glu Val Thr Glu Gly Gly Pro Val
130 135 140
Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp Ile Ser Val Pro
145 150 155 160
Ala Leu Ser Glu Lys Asp Ile Ala Asp Leu Glu Phe Ala Leu Lys Leu
165 170 175
Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser Pro Ala Asp Val
180 185 190
Asp Leu Val His Glu Val Met Asp Arg Val Gly Arg His Val Pro Val
195 200 205
Ile Ala Lys Leu Glu Lys Pro Glu Ala Val His Ala Leu Glu Ser Ile
210 215 220
Val Leu Ala Phe Asp Ala Ile Met Val Ala Arg Gly Asp Leu Gly Val
225 230 235 240
Glu Val Pro Leu Glu Gln Val Pro Leu Val Gln Lys Arg Ala Ile Gln
245 250 255
Ile Ala Arg Glu Asn Ala Lys Pro Val Ile Val Ala Thr Gln Met Leu
260 265 270
Asp Ser Met Ile Glu Asn Ser Thr Pro Thr Arg Ala Glu Ala Ser Asp
275 280 285
Val Ala Asn Ala Val Leu Asp Gly Ala Asp Ala Val Met Leu Ser Gly
290 295 300
Glu Thr Ser Ile Gly Val Asp Pro His Asn Val Val Arg Thr Met Ala
305 310 315 320
Arg Ile Val Thr Gln Ala Glu Thr Asp Gly His Val Pro Pro Leu Ser
325 330 335
His Val Pro Arg Thr Lys Arg Gly Val Ile Ser Tyr Ser Ala Arg Asp
340 345 350
Ile Ala Glu Arg Leu Asn Ala Arg Ala Leu Val Cys Phe Thr Thr Ser
355 360 365
Gly Asp Thr Ala Arg Arg Val Ala Arg Leu His Ser His Leu Pro Leu
370 375 380
Leu Val Phe Thr Pro His Pro Ala Val Arg Ser Gln Leu Ala Leu Thr
385 390 395 400
Trp Gly Ala Glu Thr Phe Leu Cys Ala Gln Ala Leu Ser Thr Asp Asp
405 410 415
Met Met Ala Glu Leu Asp Arg Ser Leu Leu Ala Met Asp Asp Tyr His
420 425 430
Arg Asp Asp Met Met Val Val Val Ala Gly Thr Pro Pro Gly Val Ser
435 440 445
Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly Glu Asp Thr Ser
450 455 460
Ser Pro Thr Gly Arg
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gagctgaagc tcaacgagca cgaggcggag cgcttcgccc actcggctga cacgctgcgc 180
gcgatcaagg aggagttctt ccccgccgac tgacggcttc cccgagatgc cgaacctccc 240
gaacacaggc acaatatggg ggtatcaccc attttgtcgt gcgcgtacgg gaggacagcc 300
gtg gat gcc agg ctg cag gaa ctg atc acc gag gtc gac ggt ctc atc 348
Val Asp Ala Arg Leu Gln Glu Leu Ile Thr Glu Val Asp Gly Leu Ile

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1               5                  10                  15
gac tgc ctc aag gag gtc gag gag cag gtg gcc ccc gcg atc ggg cgg        396
Asp Cys Leu Lys Glu Val Glu Glu Gln Val Ala Pro Ala Ile Gly Arg
            20                  25                  30
gtc gcc gag aac cac cgc cac ggc gcg gtg aac ctc gtc cac tac gcc        444
Val Ala Glu Asn His Arg His Gly Ala Val Asn Leu Val His Tyr Ala
        35                  40                  45
gag ctg cgg cag cac gac gtc cgc gcg gtc cag ggc ggc ctg gcc tcc        492
Glu Leu Arg Gln His Asp Val Arg Ala Val Gln Gly Gly Leu Ala Ser
    50                  55                  60
atc ggc gcc acc cgc ctg tcg acg gcg gag ccg gcc gtc ctc gcc cgt        540
Ile Gly Ala Thr Arg Leu Ser Thr Ala Glu Pro Ala Val Leu Ala Arg
65                  70                  75                  80
ctc cac gcg gcg cgg aac gtg ctc tcc gcc tac aac ggt gag cag ctc        588
Leu His Ala Ala Arg Asn Val Leu Ser Ala Tyr Asn Gly Glu Gln Leu
                85                  90                  95
aag tac acc ggc agc gag gtc cgt gac gcc ttc gcc acc gcc gac gac        636
Lys Tyr Thr Gly Ser Glu Val Arg Asp Ala Phe Ala Thr Ala Asp Asp
            100                 105                 110
atc ctc gag gac cac gcc ctg cag ctc ctc ggc tac tcc tcc gag gag        684
Ile Leu Glu Asp His Ala Leu Gln Leu Leu Gly Tyr Ser Ser Glu Glu
        115                 120                 125
acg cac tcc cgc atc atg gtg acc ctg ccg acg gag gca ggc gag gac        732
Thr His Ser Arg Ile Met Val Thr Leu Pro Thr Glu Ala Gly Glu Asp
    130                 135                 140
ctc gac ctg gtc cgc ggt ttc gtc gag gcc ggc atg gag ctg gcc cgc        780
Leu Asp Leu Val Arg Gly Phe Val Glu Ala Gly Met Glu Leu Ala Arg
145                 150                 155                 160
atc aac tgc gcc cac gac ggc ccc gag gtg tgg agg cgc atg atc gac        828
Ile Asn Cys Ala His Asp Gly Pro Glu Val Trp Arg Arg Met Ile Asp
                165                 170                 175
aac gtc cac acc gcc gcc cgc gag gcc ggc cgg gag atc agg atc gcc        876
Asn Val His Thr Ala Ala Arg Glu Ala Gly Arg Glu Ile Arg Ile Ala
            180                 185                 190
atg gac ctg gcg ggc ccg aag gtc cgc acc ggg gag atc gag ccg ggc        924
Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Glu Pro Gly
        195                 200                 205
ccg gag gtc ggc cgc gcc cgc gtc acc cgc gag gac acc ggc gtg gtg        972
Pro Glu Val Gly Arg Ala Arg Val Thr Arg Glu Asp Thr Gly Val Val
    210                 215                 220
gtc acc ccg tcg aag atc tgg ctc acc ccc gcc gac ctg gcc gac gac       1020
Val Thr Pro Ser Lys Ile Trp Leu Thr Pro Ala Asp Leu Ala Asp Asp
225                 230                 235                 240
gag gtc ccg ccg gtc ccc gcc gga ctg ccg ggc cgc ccg acg ctg ccg       1068
Glu Val Pro Pro Val Pro Ala Gly Leu Pro Gly Arg Pro Thr Leu Pro
                245                 250                 255
ctg cgc gtc gag cgt gac tgg ctg gag gcc ctg gag atc ggc tcc gag       1116
Leu Arg Val Glu Arg Asp Trp Leu Glu Ala Leu Glu Ile Gly Ser Glu
            260                 265                 270
atc acc ttc cac gac aac cgc gac gcg aag cgc cgg ttc acc gtc acc       1164
Ile Thr Phe His Asp Asn Arg Asp Ala Lys Arg Arg Phe Thr Val Thr
        275                 280                 285
cgc atc gag ggg cag ggg gtg ctg ctg gag ggg cgt cgc aac gcc tac       1212
Arg Ile Glu Gly Gln Gly Val Leu Leu Glu Gly Arg Arg Asn Ala Tyr
    290                 295                 300
gtc tcc aac tcc acc ctc ctc gag acc gac tgg acc aag acc cgc gtc       1260
Val Ser Asn Ser Thr Leu Leu Glu Thr Asp Trp Thr Lys Thr Arg Val
305                 310                 315                 320
tcc ggc gtc ccg ccg acc gag cag cgc ctg cgt ctg agc atc gga gac       1308
Ser Gly Val Pro Pro Thr Glu Gln Arg Leu Arg Leu Ser Ile Gly Asp
                325                 330                 335
acg ctc atc ctc acc gac gac cag acc ccc gcc gtc gtc gcc ccg gac       1356
Thr Leu Ile Leu Thr Asp Asp Gln Thr Pro Ala Val Val Ala Pro Asp
            340                 345                 350
gtc acc ccg cgc atc ggc tgc acg ctg ccg gag gcc gtc gcc gcc atc       1404
Val Thr Pro Arg Ile Gly Cys Thr Leu Pro Glu Ala Val Ala Ala Ile
        355                 360                 365
gag gtc ggg cag aag gtg ctt ttc gac gac ggc tcg atc gcc gcc cgc       1452
Glu Val Gly Gln Lys Val Leu Phe Asp Asp Gly Ser Ile Ala Ala Arg
    370                 375                 380
gcc gtc gac aag cag gtc acg gag cag ggc cac cac gag gtg cgc ctc       1500
Ala Val Asp Lys Gln Val Thr Glu Gln Gly His His Glu Val Arg Leu
385                 390                 395                 400
gag gtg acc tac gcc ggg ccg gag ggc acc aag ctc gcc gcg tac aag       1548
Glu Val Thr Tyr Ala Gly Pro Glu Gly Thr Lys Leu Ala Ala Tyr Lys
                405                 410                 415
ggc atc aac ctg ccg gac acc gtc ctg ccg ctg ccg agc ctc acc gag       1596
Gly Ile Asn Leu Pro Asp Thr Val Leu Pro Leu Pro Ser Leu Thr Glu
```

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           420                 425                 430
gag gac atc gag gcg ttc cgc ttc gtg gcc gag cac ggt gac atc gcg      1644
Glu Asp Ile Glu Ala Phe Arg Phe Val Ala Glu His Gly Asp Ile Ala
       435                 440                 445
aac gtc tcc ttc att cgc gac gcc gac gac gtc aac ttc gtg ctc gac      1692
Asn Val Ser Phe Ile Arg Asp Ala Asp Asp Val Asn Phe Val Leu Asp
   450                 455                 460
acc ctc gag cag atc gcg cag gag tcc gac gac ccg gag cgc gtc cgc      1740
Thr Leu Glu Gln Ile Ala Gln Glu Ser Asp Asp Pro Glu Arg Val Arg
465                 470                 475                 480
aac ctc ggc atc gtg ctc aag atc gag acg atc ccc gcc tac gag ggc      1788
Asn Leu Gly Ile Val Leu Lys Ile Glu Thr Ile Pro Ala Tyr Glu Gly
                485                 490                 495
ctg tgc agc gtc ctg ctc gcc ggc atg cgc cac ccc aac ctc gga gtc      1836
Leu Cys Ser Val Leu Leu Ala Gly Met Arg His Pro Asn Leu Gly Val
           500                 505                 510
atg atc gcc cgc ggc gac ctg gcc gtc gag ctc ggc ttc gag cgc atg      1884
Met Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Glu Arg Met
       515                 520                 525
gcc gag gtc ccg cgc ctc atc gcc cag atg gcg gag gcc gcc cac gtg      1932
Ala Glu Val Pro Arg Leu Ile Ala Gln Met Ala Glu Ala Ala His Val
   530                 535                 540
ccc gtc atc atg gcc acc cag gtg ctc gag aac ctg gcc aag tcc ggc      1980
Pro Val Ile Met Ala Thr Gln Val Leu Glu Asn Leu Ala Lys Ser Gly
545                 550                 555                 560
ctg ccg acc cgc gcc gag atc acc gac gcc gcg tac gcc ctg cgc tcc      2028
Leu Pro Thr Arg Ala Glu Ile Thr Asp Ala Ala Tyr Ala Leu Arg Ser
                565                 570                 575
gag gcc gtg atg ctc aac aag ggc ccg cac atc acc gac gcg atc cgc      2076
Glu Ala Val Met Leu Asn Lys Gly Pro His Ile Thr Asp Ala Ile Arg
           580                 585                 590
atc ctc cac acc ctg tcg acc aag ctc ggc cgt tcc cag cgc aag aac      2124
Ile Leu His Thr Leu Ser Thr Lys Leu Gly Arg Ser Gln Arg Lys Asn
       595                 600                 605
cgc cag atg ctc cgc cag atc tcg agc tgg atg ccc ggg aat gag tag      2172
Arg Gln Met Leu Arg Gln Ile Ser Ser Trp Met Pro Gly Asn Glu
   610                 615                 620
atgaccgccg cacccaggat catcgcccac cgcggttact ccgcgaagta ccccgagttg     2232
acgcccgtcg ccttcgagcg ggcgctggaa ctgcccgtcc acggcatcga gtgcgatgta     2292
cgcctcagcc tcgacgggga ggtggtggtg ttgcatgacc cgctcatcga ccgcgtcgcg     2352
gacggctccg ggcgggtctc ccgcatgacg gtggacgccc tgcgtgacca caactacggc     2412
accgccgagc tgccgcagga catgctcacc ctcccggagc tgctggagat ggtggagccg     2472
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<212>  PRT
<213>  Corynebacterium humireducens
<400>  144
Val Asp Ala Arg Leu Gln Glu Leu Ile Thr Glu Val Asp Gly Leu Ile
1               5                  10                  15
Asp Cys Leu Lys Glu Val Glu Glu Gln Val Ala Pro Ala Ile Gly Arg
           20                  25                  30
Val Ala Glu Asn His Arg His Gly Ala Val Asn Leu Val His Tyr Ala
       35                  40                  45
Glu Leu Arg Gln His Asp Val Arg Ala Val Gln Gly Gly Leu Ala Ser
   50                  55                  60
Ile Gly Ala Thr Arg Leu Ser Thr Ala Glu Pro Ala Val Leu Ala Arg
65                  70                  75                  80
Leu His Ala Ala Arg Asn Val Leu Ser Ala Tyr Asn Gly Glu Gln Leu
                85                  90                  95
Lys Tyr Thr Gly Ser Glu Val Arg Asp Ala Phe Ala Thr Ala Asp Asp
           100                 105                 110
Ile Leu Glu Asp His Ala Leu Gln Leu Leu Gly Tyr Ser Ser Glu Glu
       115                 120                 125
Thr His Ser Arg Ile Met Val Thr Leu Pro Thr Glu Ala Gly Glu Asp
   130                 135                 140
Leu Asp Leu Val Arg Gly Phe Val Glu Ala Gly Met Glu Leu Ala Arg
145                 150                 155                 160
Ile Asn Cys Ala His Asp Gly Pro Glu Val Trp Arg Arg Met Ile Asp
                165                 170                 175
Asn Val His Thr Ala Ala Arg Glu Ala Gly Arg Glu Ile Arg Ile Ala
           180                 185                 190
Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Glu Pro Gly
       195                 200                 205
Pro Glu Val Gly Arg Ala Arg Val Thr Arg Glu Asp Thr Gly Val Val
   210                 215                 220
Val Thr Pro Ser Lys Ile Trp Leu Thr Pro Ala Asp Leu Ala Asp Asp
225                 230                 235                 240
Glu Val Pro Pro Val Pro Ala Gly Leu Pro Gly Arg Pro Thr Leu Pro
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                245                 250                 255
Leu Arg Val Glu Arg Asp Trp Leu Glu Ala Leu Glu Ile Gly Ser Glu
            260                 265                 270
Ile Thr Phe His Asp Asn Arg Asp Ala Lys Arg Arg Phe Thr Val Thr
        275                 280                 285
Arg Ile Glu Gly Gln Gly Val Leu Leu Glu Gly Arg Arg Asn Ala Tyr
    290                 295                 300
Val Ser Asn Ser Thr Leu Leu Glu Thr Asp Trp Thr Lys Thr Arg Val
305                 310                 315                 320
Ser Gly Val Pro Pro Thr Glu Gln Arg Leu Arg Leu Ser Ile Gly Asp
                325                 330                 335
Thr Leu Ile Leu Thr Asp Asp Gln Thr Pro Ala Val Val Ala Pro Asp
            340                 345                 350
Val Thr Pro Arg Ile Gly Cys Thr Leu Pro Glu Ala Val Ala Ala Ile
        355                 360                 365
Glu Val Gly Gln Lys Val Leu Phe Asp Asp Gly Ser Ile Ala Ala Arg
    370                 375                 380
Ala Val Asp Lys Gln Val Thr Glu Gln Gly His His Glu Val Arg Leu
385                 390                 395                 400
Glu Val Thr Tyr Ala Gly Pro Glu Gly Thr Lys Leu Ala Ala Tyr Lys
                405                 410                 415
Gly Ile Asn Leu Pro Asp Thr Val Leu Pro Leu Pro Ser Leu Thr Glu
            420                 425                 430
Glu Asp Ile Glu Ala Phe Arg Phe Val Ala Glu His Gly Asp Ile Ala
        435                 440                 445
Asn Val Ser Phe Ile Arg Asp Ala Asp Asp Val Asn Phe Val Leu Asp
    450                 455                 460
Thr Leu Glu Gln Ile Ala Gln Glu Ser Asp Asp Pro Glu Arg Val Arg
465                 470                 475                 480
Asn Leu Gly Ile Val Leu Lys Ile Glu Thr Ile Pro Ala Tyr Glu Gly
                485                 490                 495
Leu Cys Ser Val Leu Leu Ala Gly Met Arg His Pro Asn Leu Gly Val
            500                 505                 510
Met Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Glu Arg Met
        515                 520                 525
Ala Glu Val Pro Arg Leu Ile Ala Gln Met Ala Glu Ala Ala His Val
    530                 535                 540
Pro Val Ile Met Ala Thr Gln Val Leu Glu Asn Leu Ala Lys Ser Gly
545                 550                 555                 560
Leu Pro Thr Arg Ala Glu Ile Thr Asp Ala Ala Tyr Ala Leu Arg Ser
                565                 570                 575
Glu Ala Val Met Leu Asn Lys Gly Pro His Ile Thr Asp Ala Ile Arg
            580                 585                 590
Ile Leu His Thr Leu Ser Thr Lys Leu Gly Arg Ser Gln Arg Lys Asn
        595                 600                 605
Arg Gln Met Leu Arg Gln Ile Ser Ser Trp Met Pro Gly Asn Glu
    610                 615                 620
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<222>  (301)..(1578)
<223>  gen enolaza
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ggtcccgggc gatctacgcc tacaaccgtt ccgaggccta cctcatcgac gtgcgtgacg     120
cggccgcgtc ctatgccctg aaccagccgg cccggtgacg gccacccctg gttgcccgct     180
gcaatcgtcg ggttgtagcc cctggtggcg gtttttctgg aagaattgtc cccggacgcg     240
tgtcgagagc gcgcgacgat gacgaactcc catctcatat ggctatagga ggccccaaaa     300
gtg gct gac atc att cac gtt ttc gca cga gag atc atg gat tcc cgt       348
Val Ala Asp Ile Ile His Val Phe Ala Arg Glu Ile Met Asp Ser Arg
1               5                   10                  15
ggc aac ccg acc gtc gag gcc ggc gtt gtg ctg gat gac gga acc ctc       396
Gly Asn Pro Thr Val Glu Ala Gly Val Val Leu Asp Asp Gly Thr Leu
            20                  25                  30

gcc acc gcc ggt gtc ccc tcc ggc gcc tcc acc ggt gtc cac gag gca       444
Ala Thr Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
        35                  40                  45
cac gag ctg cgt gac ggc ggc gac cgc tac ctg ggc aag ggt gtc ctg       492
His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
    50                  55                  60
aag gcc gtc gag aac gtc aac gag gag atc gcc gac gag ctg gcc ggc       540
Lys Ala Val Glu Asn Val Asn Glu Glu Ile Ala Asp Glu Leu Ala Gly
65                  70                  75                  80
ttc gag gcc gat gac cag cgc gcc atc gac cag gcc atg atc cag ctg       588
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Phe Glu Ala Asp Asp Gln Arg Ala Ile Asp Gln Ala Met Ile Gln Leu
                85                  90                  95
gac ggc acc gac aac aag gcc cgc ctg ggt gcc aac gcc atc ctg ggt      636
Asp Gly Thr Asp Asn Lys Ala Arg Leu Gly Ala Asn Ala Ile Leu Gly
            100                 105                 110
gtc tcc atg gct gtg gcc cgc gcc gcc gcc gag tcc gcc ggc ctg ccg      684
Val Ser Met Ala Val Ala Arg Ala Ala Ala Glu Ser Ala Gly Leu Pro
        115                 120                 125
ctc tac cgt tac gtc ggt ggc ccg aac gca cac gtg ctg ccg gtc ccg      732
Leu Tyr Arg Tyr Val Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
    130                 135                 140
atg atg aac atc ctc aac ggt ggc gcc cac gcc gac tcc ggc gtc gac      780
Met Met Asn Ile Leu Asn Gly Gly Ala His Ala Asp Ser Gly Val Asp
145                 150                 155                 160
gtc cag gag ttc atg atc gcc ccg atc ggt gcc gag acc ttc tcc gag      828
Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
                165                 170                 175
gct ctg cag gtc ggc gcc gag gtg tac cac acc ctg aag tcc gtc atc      876
Ala Leu Gln Val Gly Ala Glu Val Tyr His Thr Leu Lys Ser Val Ile
            180                 185                 190
cag gag aag ggc ctg tcc acc ggc ctg ggc gac gag ggc ggt ttc gcc      924
Gln Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
        195                 200                 205
ccg tcc gtc gag tcc acc cgt gcg gcc ctg gac ctc atc gtc gag gcc      972
Pro Ser Val Glu Ser Thr Arg Ala Ala Leu Asp Leu Ile Val Glu Ala
    210                 215                 220
gtc gag aag gcc ggc tac aag ctg ggc gac gat gtc gcc ctg gcc ctg     1020
Val Glu Lys Ala Gly Tyr Lys Leu Gly Asp Asp Val Ala Leu Ala Leu
225                 230                 235                 240
gac gtc gcc tcc tcc gag ttc ttc aag gac ggc aag tac cac ttc gag     1068
Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Lys Tyr His Phe Glu
                245                 250                 255
ggc aag gag ctc tcc gcc gag gag atg tcc aag gtc tac gag gag ctc     1116
Gly Lys Glu Leu Ser Ala Glu Glu Met Ser Lys Val Tyr Glu Glu Leu
            260                 265                 270
atc aac gag tac ccg atc gtc tcc atc gag gat ccg ctg cag gag gac     1164
Ile Asn Glu Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
        275                 280                 285
gac tgg gac ggc tac gtc gcc ctg acc gcc gcc atc ggt gac aag gtc     1212
Asp Trp Asp Gly Tyr Val Ala Leu Thr Ala Ala Ile Gly Asp Lys Val
    290                 295                 300
cag ctg gtc ggc gac gac ttc ttc gtc acc aac ccg gcc cgc ctg aag     1260
Gln Leu Val Gly Asp Asp Phe Phe Val Thr Asn Pro Ala Arg Leu Lys
305                 310                 315                 320
gag ggc atc gcc aag aag gcc gcc aac tcc atc ctg gtg aag gtc aac     1308
Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
                325                 330                 335
cag atc ggt acc ctc acc gag acc ttc gac gcc gtc gag atg gcc cac     1356
Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Glu Met Ala His
            340                 345                 350
cgt gcg ggc tac acc tcg atg atg tcc cac cgt tcc ggt gag acc gag     1404
Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
        355                 360                 365
gac acc acc atc gcc gac ctg gct gtc gca ctg aac tgc ggc cag atc     1452
Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
    370                 375                 380
aag acc ggt gcc ccg gcc cgc tcc gag cgc gtc gcc aag tac aac cag     1500
Lys Thr Gly Ala Pro Ala Arg Ser Glu Arg Val Ala Lys Tyr Asn Gln
385                 390                 395                 400
ctg ctg cgc atc gag cag gag ctc ggc gac gcc gcc gtc tac gcc ggc     1548
Leu Leu Arg Ile Glu Gln Glu Leu Gly Asp Ala Ala Val Tyr Ala Gly
                405                 410                 415
cgc tcc gcc ttc ccg cgc ttc cag aag taa ctgacagcgc tttccgacgc       1598
Arg Ser Ala Phe Pro Arg Phe Gln Lys
            420                 425
ccccgtgcac cccggtgcac gggggcgtcc ccgtatccgt gggggaggac accatggcat   1658
tcttcggcag acgtagggca cggccccggc tggagcccga cttcgtgcac acctggaccg   1718
gtgagcagct ggtccggatc gcggagggcg tcgacctggg caccctccgg gcggtgtacg   1778
ggcgtctcga cgccacctca cggatccact tcctcttcga cttcggtgcc ctcttctccg   1838
acgggtacct cttcgagctc tgggagcggc gtctcctgga                         1878
<210>  146
<211>  425
<212>  PRT
<213>  Corynebacterium humireducens
<400>  146
Val Ala Asp Ile Ile His Val Phe Ala Arg Glu Ile Met Asp Ser Arg
1               5                   10                  15
Gly Asn Pro Thr Val Glu Ala Gly Val Val Leu Asp Asp Gly Thr Leu
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            20                  25                  30
Ala Thr Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
        35                  40                  45
His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
    50                  55                  60
Lys Ala Val Glu Asn Val Asn Glu Glu Ile Ala Asp Glu Leu Ala Gly
65                  70                  75                  80
Phe Glu Ala Asp Asp Gln Arg Ala Ile Asp Gln Ala Met Ile Gln Leu
                85                  90                  95
Asp Gly Thr Asp Asn Lys Ala Arg Leu Gly Ala Asn Ala Ile Leu Gly
            100                 105                 110
Val Ser Met Ala Val Ala Arg Ala Ala Ala Glu Ser Ala Gly Leu Pro
        115                 120                 125
Leu Tyr Arg Tyr Val Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
    130                 135                 140
Met Met Asn Ile Leu Asn Gly Gly Ala His Ala Asp Ser Gly Val Asp
145                 150                 155                 160
Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
                165                 170                 175
Ala Leu Gln Val Gly Ala Glu Val Tyr His Thr Leu Lys Ser Val Ile
            180                 185                 190
Gln Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
        195                 200                 205
Pro Ser Val Glu Ser Thr Arg Ala Ala Leu Asp Leu Ile Val Glu Ala
    210                 215                 220
Val Glu Lys Ala Gly Tyr Lys Leu Gly Asp Asp Val Ala Leu Ala Leu
225                 230                 235                 240
Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Lys Tyr His Phe Glu
                245                 250                 255
Gly Lys Glu Leu Ser Ala Glu Glu Met Ser Lys Val Tyr Glu Glu Leu
            260                 265                 270
Ile Asn Glu Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
        275                 280                 285
Asp Trp Asp Gly Tyr Val Ala Leu Thr Ala Ala Ile Gly Asp Lys Val
    290                 295                 300
Gln Leu Val Gly Asp Asp Phe Phe Val Thr Asn Pro Ala Arg Leu Lys
305                 310                 315                 320
Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
                325                 330                 335
Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Glu Met Ala His
            340                 345                 350
Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
        355                 360                 365
Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
    370                 375                 380
Lys Thr Gly Ala Pro Ala Arg Ser Glu Arg Val Ala Lys Tyr Asn Gln
385                 390                 395                 400
Leu Leu Arg Ile Glu Gln Glu Leu Gly Asp Ala Ala Val Tyr Ala Gly
                405                 410                 415
Arg Ser Ala Phe Pro Arg Phe Gln Lys
            420                 425
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<223>  gen gpmA
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ccgacgccct ggagaacctc ctcgacgacg acgacacccg cctgcggatg gcgaccgacg      120
ccgtccagca cgccgcgaac ttctcgtggt cgaactccgc cgcccagctg gcggcggtgt      180
acgccgaggc cctgagcctg gaggtcgaca actgcccgca acgccgcgaa cgggccgaag      240
ggctctaaac gggggtatt aatccgcacg ctaccggcgg aatcgtggca tattggagac      300
atg acc aac gga aag ctc att ctt ctt cgc cac ggg cag agc cag tgg        348
Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Gln Trp
1               5                   10                  15
aac aaa tcg aac cag ttc acc ggc tgg gtg gac gtt gac ctg acc gag        396
Asn Lys Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asp Leu Thr Glu
            20                  25                  30
cag ggc gtc gcc gag gct gtc cgc ggc ggc gag atg ctc aag gag gct        444
Gln Gly Val Ala Glu Ala Val Arg Gly Gly Glu Met Leu Lys Glu Ala
        35                  40                  45
ggt ctc ctg ccg gac atc gtc tac acc tcc ctg ctg cgt cgt gcc atc        492
Gly Leu Leu Pro Asp Ile Val Tyr Thr Ser Leu Leu Arg Arg Ala Ile
    50                  55                  60
cgc acc gcg aac atc gcg ctc aac gcc gcc gac cgt cac tgg atc ccg        540
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Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp Ile Pro
65                  70                  75                  80
gtc gtc cgc gac tgg cgt ctc aac gag cgc cac tac ggt gcg ctg cag        588
Val Val Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Gln
                85                  90                  95
ggc ctg gac aag gcc gag acc aag gac aag tac ggc gac gag cag ttc        636
Gly Leu Asp Lys Ala Glu Thr Lys Asp Lys Tyr Gly Asp Glu Gln Phe
            100                 105                 110
atg gcg tgg cgt cgt tcc tac gac acc ccg ccg ccg gag ctg gcc gac        684
Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu Ala Asp
        115                 120                 125
gac gcc gag tac tcc cag tcc gac gat gtg cgc tac gcc gcc ctg gag        732
Asp Ala Glu Tyr Ser Gln Ser Asp Asp Val Arg Tyr Ala Ala Leu Glu
    130                 135                 140
aac gca ccg cgt acc gag tgc ctc ctg gac gtc gtc aag cgt ttc atc        780
Asn Ala Pro Arg Thr Glu Cys Leu Leu Asp Val Val Lys Arg Phe Ile
145                 150                 155                 160
ccg tac tac cag gag gag atc gag ccg cgc gtc aag cgt ggc gag acc        828
Pro Tyr Tyr Gln Glu Glu Ile Glu Pro Arg Val Lys Arg Gly Glu Thr
                165                 170                 175
gtc ctc gtc gcc gcg cac ggc aac tcc ctg cgc gcg ctg gtc aag cac        876
Val Leu Val Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val Lys His
            180                 185                 190
ctg gac aac atc tcg gac gag gac atc gcg gcc ctc aac atc ccg acc        924
Leu Asp Asn Ile Ser Asp Glu Asp Ile Ala Ala Leu Asn Ile Pro Thr
        195                 200                 205
ggc atc ccg ctg gtc tac gag ctg gat gct gac ggc aag gtc gtc aac        972
Gly Ile Pro Leu Val Tyr Glu Leu Asp Ala Asp Gly Lys Val Val Asn
    210                 215                 220
ccg ggc ggc acc tac ctc gac ccc gag gcg gcc gcc gcc ggt gct gcc       1020
Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly Ala Ala
225                 230                 235                 240
gct gtc gcg gca cag ggt ggc aag tag cctgtagggc gtgtccgccg              1067
Ala Val Ala Ala Gln Gly Gly Lys
                245
ttctcgcgtt cctgttgggc gtcgccgtca ccggcgtcgc ctttccggcg ttgaactggg     1127
cacgtaagcg gatagtccgc caccgttcct cggccacgct cgaggacaac caggtcacca     1187
ccgtcggcca ggtcctgcac ctggccatcc agggttcccc cacgggcgtc accgtcgtcg     1247
accgcggcgg tgaggtgatc ctgtcgaacg cccgcgccca cgagatggcc ctcgtccacg     1307
accgcaccct caacgagcag gtgtggcagg tggcgggggа                           1347
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<212>  PRT
<213>  Corynebacterium humireducens
<400>  148
Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Gln Trp
1               5                   10                  15
Asn Lys Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asp Leu Thr Glu
            20                  25                  30
Gln Gly Val Ala Glu Ala Val Arg Gly Gly Glu Met Leu Lys Glu Ala
        35                  40                  45
Gly Leu Leu Pro Asp Ile Val Tyr Thr Ser Leu Leu Arg Arg Ala Ile
    50                  55                  60
Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp Ile Pro
65                  70                  75                  80
Val Val Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Gln
                85                  90                  95
Gly Leu Asp Lys Ala Glu Thr Lys Asp Lys Tyr Gly Asp Glu Gln Phe
            100                 105                 110
Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu Ala Asp
        115                 120                 125
Asp Ala Glu Tyr Ser Gln Ser Asp Asp Val Arg Tyr Ala Ala Leu Glu
    130                 135                 140
Asn Ala Pro Arg Thr Glu Cys Leu Leu Asp Val Val Lys Arg Phe Ile
145                 150                 155                 160
Pro Tyr Tyr Gln Glu Glu Ile Glu Pro Arg Val Lys Arg Gly Glu Thr
                165                 170                 175
Val Leu Val Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val Lys His
            180                 185                 190
Leu Asp Asn Ile Ser Asp Glu Asp Ile Ala Ala Leu Asn Ile Pro Thr
        195                 200                 205


Gly Ile Pro Leu Val Tyr Glu Leu Asp Ala Asp Gly Lys Val Val Asn
    210                 215                 220
Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly Ala Ala
225                 230                 235                 240
Ala Val Ala Ala Gln Gly Gly Lys
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245

<210> 149
<211> 1818
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1518)
<223> gen pgk
<400> 149

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ggtcgtctcc tggtacgaca acgagtgggg ctacacctgc cagctcctgc gcctgaccga      120
gctcgtcgcc tccaagctct aggaccgcga ccccgcactt ccccggcctc cggctgagac      180
cgggggagtg cgcccctgtg gcccggggtg tgcctcggca cacgtcgggc ctcagggcta      240
tccacccccc cagatcagcc gccccttttct catctgaaga caaaagtcaa ggagacagcc     300
atg acc gtg aag act ctg cag gac ctg ctc gac gag ggc gtc gac ggc        348
Met Thr Val Lys Thr Leu Gln Asp Leu Leu Asp Glu Gly Val Asp Gly
1               5                  10                  15
cgc cac atc ctc gtc cgc tcc gac ttc aac gtc ccg ctc aac gac gcc        396
Arg His Ile Leu Val Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Ala
            20                  25                  30
ggt gag atc acc gac gcg ggc cgc atc acc gcc tcc ctg ccc acc ctc        444
Gly Glu Ile Thr Asp Ala Gly Arg Ile Thr Ala Ser Leu Pro Thr Leu
        35                  40                  45
aag gcg ctc gtc gag ggt ggc gcg aag gtc atc gtc atg gcc cac ctg        492
Lys Ala Leu Val Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu
    50                  55                  60
ggc cgc ccg aag ggc gag gtc aac ccg aag tac tcc ctg gcc ccg gtc        540
Gly Arg Pro Lys Gly Glu Val Asn Pro Lys Tyr Ser Leu Ala Pro Val
65                  70                  75                  80
gcc gag gcc ctc tcc gag gca ctc ggc cag tac gtc gcc ctc gcc ggc        588
Ala Glu Ala Leu Ser Glu Ala Leu Gly Gln Tyr Val Ala Leu Ala Gly
                85                  90                  95
gac gtc acc ggt gag gac gcc cac gag cgc gcc aac ggc ctg acc gag        636
Asp Val Thr Gly Glu Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu
            100                 105                 110
ggc gac gtc ctg ctc ctc gag aac gtg cgt ttc gac gcc cgc gag acc        684
Gly Asp Val Leu Leu Leu Glu Asn Val Arg Phe Asp Ala Arg Glu Thr
        115                 120                 125
tcc aag gac gag gcc gag cgc ggc gcc ttc gcc gac gag ctc gcc gcc        732
Ser Lys Asp Glu Ala Glu Arg Gly Ala Phe Ala Asp Glu Leu Ala Ala
    130                 135                 140
ctg gcc gcc gac aac ggc gcc ttc gtc tcc gac ggt ttc ggt gtc gtc        780
Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val
145                 150                 155                 160
cac cgt gcg cag gcc tcc gtc tac gac gtc gcc aag cgt ctc ccg gcc        828
His Arg Ala Gln Ala Ser Val Tyr Asp Val Ala Lys Arg Leu Pro Ala
                165                 170                 175
tac gcc ggc aac ctg gtg gag aag gag atc tcc gtc ctg gag aag acc        876
Tyr Ala Gly Asn Leu Val Glu Lys Glu Ile Ser Val Leu Glu Lys Thr
            180                 185                 190
gcc acc aac ccg gag tcc ccg tac gtc gtc gtc ctc ggc ggc tcc aag        924
Ala Thr Asn Pro Glu Ser Pro Tyr Val Val Val Leu Gly Gly Ser Lys
        195                 200                 205
gtc tcc gac aag ctg ggc gtc atc gag gct ctg gcc ggc aag gcc gac        972
Val Ser Asp Lys Leu Gly Val Ile Glu Ala Leu Ala Gly Lys Ala Asp
    210                 215                 220
aag atc atc atc ggt ggc ggc atg tgc tac acc ttc ctc aac gcc cag       1020
Lys Ile Ile Ile Gly Gly Gly Met Cys Tyr Thr Phe Leu Asn Ala Gln
225                 230                 235                 240
ggc tac aac acc cag aag tcc ctg ctg cag gag gag atg atc gac acc       1068
Gly Tyr Asn Thr Gln Lys Ser Leu Leu Gln Glu Glu Met Ile Asp Thr
                245                 250                 255
tgc aag gac ctc ctc gag cgt ttc ggc gac aag atc gtc ctc ccg gtg       1116
Cys Lys Asp Leu Leu Glu Arg Phe Gly Asp Lys Ile Val Leu Pro Val
            260                 265                 270
gac ctc gtg gcc gcc gcc gag ttc tcc gcc gac tcc gag cac aag gtc       1164
Asp Leu Val Ala Ala Ala Glu Phe Ser Ala Asp Ser Glu His Lys Val
        275                 280                 285
gtc gcc ctc gac gag atc ccg gag ggc tgg ctg tcc ccg gac atc ggc       1212
Val Ala Leu Asp Glu Ile Pro Glu Gly Trp Leu Ser Pro Asp Ile Gly
    290                 295                 300

ccg gag tcc gtc aag aag ttc gcc gac gtc ctc gcc acc tcc aag acc       1260
Pro Glu Ser Val Lys Lys Phe Ala Asp Val Leu Ala Thr Ser Lys Thr
305                 310                 315                 320
gtc ttc tgg aac ggc ccg atg ggt gtc ttc gag atg gca ccg ttc tcc       1308
Val Phe Trp Asn Gly Pro Met Gly Val Phe Glu Met Ala Pro Phe Ser
```

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                325                 330                 335
aag ggc acc gag ggc gtc gcc aag gcc atc atc gac gcg acc gcg aac      1356
Lys Gly Thr Glu Gly Val Ala Lys Ala Ile Ile Asp Ala Thr Ala Asn
            340                 345                 350
aac ggt tcc ttc tcc gtc gtc ggt ggc ggc gac tcc gca gcc tcc gtc      1404
Asn Gly Ser Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
        355                 360                 365
cgc gtg ctc ggc ctg gac gag gac ggc ttc tcc cac atc tcc acc ggc      1452
Arg Val Leu Gly Leu Asp Glu Asp Gly Phe Ser His Ile Ser Thr Gly
    370                 375                 380
ggc ggc gcc tcc ctc gag ttc ctc gag ggc aag gag ctc ccg ggc gtt      1500
Gly Gly Ala Ser Leu Glu Phe Leu Glu Gly Lys Glu Leu Pro Gly Val
385                 390                 395                 400
tcc gtc ctg gac cgc taa gcacttacca cccactctga aaggagtgcc              1548
Ser Val Leu Asp Arg
                405
ccacccatgg cacgcacccc cctcatcgcc ggcaactgga agatgaacct ggaccaccac     1608
caggccatcg ccaccgtgca gaagctcgac ttcgccctgc cgaaggagta ctacgagaag     1668
gtcgacgtcg ccgtcaccgt cccgttcacc gacctccgtt ccgtgcagac gctcgtcgac     1728
ggggacaagc tcaaggtcac ctacggtgcc caggacgtct cccggcacga gtccggcgcg     1788
tacaccggtg aggtctccgc tcagatgctc                                     1818
<210>  150
<211>  405
<212>  PRT
<213>  Corynebacterium humireducens
<400>  150
Met Thr Val Lys Thr Leu Gln Asp Leu Leu Asp Glu Gly Val Asp Gly
1               5                   10                  15
Arg His Ile Leu Val Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Ala
            20                  25                  30
Gly Glu Ile Thr Asp Ala Gly Arg Ile Thr Ala Ser Leu Pro Thr Leu
        35                  40                  45
Lys Ala Leu Val Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu
    50                  55                  60
Gly Arg Pro Lys Gly Glu Val Asn Pro Lys Tyr Ser Leu Ala Pro Val
65                  70                  75                  80
Ala Glu Ala Leu Ser Glu Ala Leu Gly Gln Tyr Val Ala Leu Ala Gly
                85                  90                  95
Asp Val Thr Gly Glu Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu
            100                 105                 110
Gly Asp Val Leu Leu Leu Glu Asn Val Arg Phe Asp Ala Arg Glu Thr
        115                 120                 125
Ser Lys Asp Glu Ala Glu Arg Gly Ala Phe Ala Asp Glu Leu Ala Ala
    130                 135                 140
Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val
145                 150                 155                 160
His Arg Ala Gln Ala Ser Val Tyr Asp Val Ala Lys Arg Leu Pro Ala
                165                 170                 175
Tyr Ala Gly Asn Leu Val Glu Lys Glu Ile Ser Val Leu Glu Lys Thr
            180                 185                 190
Ala Thr Asn Pro Glu Ser Pro Tyr Val Val Val Leu Gly Gly Ser Lys
        195                 200                 205
Val Ser Asp Lys Leu Gly Val Ile Glu Ala Leu Ala Gly Lys Ala Asp
    210                 215                 220
Lys Ile Ile Ile Gly Gly Gly Met Cys Tyr Thr Phe Leu Asn Ala Gln
225                 230                 235                 240
Gly Tyr Asn Thr Gln Lys Ser Leu Leu Gln Glu Glu Met Ile Asp Thr
                245                 250                 255
Cys Lys Asp Leu Leu Glu Arg Phe Gly Asp Lys Ile Val Leu Pro Val
            260                 265                 270
Asp Leu Val Ala Ala Ala Glu Phe Ser Ala Asp Ser Glu His Lys Val
        275                 280                 285
Val Ala Leu Asp Glu Ile Pro Glu Gly Trp Leu Ser Pro Asp Ile Gly
    290                 295                 300
Pro Glu Ser Val Lys Lys Phe Ala Asp Val Leu Ala Thr Ser Lys Thr
305                 310                 315                 320
Val Phe Trp Asn Gly Pro Met Gly Val Phe Glu Met Ala Pro Phe Ser
                325                 330                 335
Lys Gly Thr Glu Gly Val Ala Lys Ala Ile Ile Asp Ala Thr Ala Asn
            340                 345                 350
Asn Gly Ser Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
        355                 360                 365
Arg Val Leu Gly Leu Asp Glu Asp Gly Phe Ser His Ile Ser Thr Gly
    370                 375                 380
Gly Gly Ala Ser Leu Glu Phe Leu Glu Gly Lys Glu Leu Pro Gly Val
385                 390                 395                 400
Ser Val Leu Asp Arg
                405
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<210> 151
<211> 2058
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1758)
<223> gen glyxeraldehyt_3_phopshatdehydrogenaza 1
<400> 151

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gcggcgggcg ggcgcagcgt ggcgagccgg gccttcagcg gccgcgtcgc ccgcggactg       60
gaaacggact tcacccggaa caacccggac atcccgccga tctaccccta cctcgtgtcg      120
ctgcaggccg cggaacggcg ggaacgcccg cgggaactgg cctactgcct cgtcggggtg      180
ggcgtcgaga agctcggggg tggccccgcg gcggggattc tggctcgact cgcgcctgaa      240
caggcaattt cacgctaaag tcgtggggac gtttcccttt actttcggag gtaaaaagca      300
gtg acc gcc cac gcg cag cct gag cac aac aac tgg aac gag aag atc         348
Val Thr Ala His Ala Gln Pro Glu His Asn Asn Trp Asn Glu Lys Ile
1               5                  10                  15
gcc ctc gct cag gag atg ctg ccg ctg atc ggc cag ctc cac cgc aac         396
Ala Leu Ala Gln Glu Met Leu Pro Leu Ile Gly Gln Leu His Arg Asn
            20                  25                  30
aac gat gtc gtc gtc tcc atc ttc gga cga ctg ctt gtc ggc gcg acg         444
Asn Asp Val Val Val Ser Ile Phe Gly Arg Leu Leu Val Gly Ala Thr
        35                  40                  45
gac atc gac atc atc aag gcg cac cgt tac gcg cgc cgc gtc gcc gac         492
Asp Ile Asp Ile Ile Lys Ala His Arg Tyr Ala Arg Arg Val Ala Asp
    50                  55                  60
cgt gag atg aag ctc gat cag acc ctc ccg gtc ctg cgc gag ctc gtc         540
Arg Glu Met Lys Leu Asp Gln Thr Leu Pro Val Leu Arg Glu Leu Val
65                  70                  75                  80
gac atg gac ctc ggc acc gcc tcc atc gac ctg ggc cgc ctg gcc acc         588
Asp Met Asp Leu Gly Thr Ala Ser Ile Asp Leu Gly Arg Leu Ala Thr
                85                  90                  95
ggc ttc gag aag tcc ggc ggc acc gac ctg cgt gcc tac ctg gac gag         636
Gly Phe Glu Lys Ser Gly Gly Thr Asp Leu Arg Ala Tyr Leu Asp Glu
            100                 105                 110
cag ctc gcc gac atc gtc ggc aag cgc tcc gag acc gag ccg cgc gac         684
Gln Leu Ala Asp Ile Val Gly Lys Arg Ser Glu Thr Glu Pro Arg Asp
        115                 120                 125
gtc gtc ctc tac ggc ttc ggc cgc atc ggc cgc ctc ctg gcc cgc atc         732
Val Val Leu Tyr Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile
    130                 135                 140
ctc atc tcc cgt gag gcc acc tac ggc ggc gtc cgc ctc cgc gcg gtg         780
Leu Ile Ser Arg Glu Ala Thr Tyr Gly Gly Val Arg Leu Arg Ala Val
145                 150                 155                 160
gtg gta cgc aag aac tcc gag gac gac atc gtc aag cgt gcc tcc ctc         828
Val Val Arg Lys Asn Ser Glu Asp Asp Ile Val Lys Arg Ala Ser Leu
                165                 170                 175
ctg cgc cgt gac tcc gtg cac ggc gcc ttc gac ggc acg atc acc gtc         876
Leu Arg Arg Asp Ser Val His Gly Ala Phe Asp Gly Thr Ile Thr Val
            180                 185                 190
gac aag gag aac aac gtc atc tgg gcc aac ggc acc aag atc cag atc         924
Asp Lys Glu Asn Asn Val Ile Trp Ala Asn Gly Thr Lys Ile Gln Ile
        195                 200                 205
atc tac tcc aac tcc ccg gcc gag gtc gac tac acc gcc tac ggc atc         972
Ile Tyr Ser Asn Ser Pro Ala Glu Val Asp Tyr Thr Ala Tyr Gly Ile
    210                 215                 220
aat gac gcc atc gtg gtg gac aac acc ggc atc tgg cgc gac cgc gag        1020
Asn Asp Ala Ile Val Val Asp Asn Thr Gly Ile Trp Arg Asp Arg Glu
225                 230                 235                 240
gga ctg tcc cag cac ctg cag tcc aag ggc gtc tcc cgc gtc gtc ctc        1068
Gly Leu Ser Gln His Leu Gln Ser Lys Gly Val Ser Arg Val Val Leu
                245                 250                 255
acc gcc ccg ggc aag ggc gac ctg ccg aac atc gtc tac ggc atc aac        1116
Thr Ala Pro Gly Lys Gly Asp Leu Pro Asn Ile Val Tyr Gly Ile Asn
            260                 265                 270
gac gac atg atc acc gac gac gag cag atc atc acc gcc gcc tcc tgc        1164
Asp Asp Met Ile Thr Asp Asp Glu Gln Ile Ile Thr Ala Ala Ser Cys
        275                 280                 285
acc acc aac ggc atc acc ccg gtc ctg aag gtc atc aac gac cgc tac        1212
Thr Thr Asn Gly Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr
    290                 295                 300
ggc gtc gag cac ggt cac gtc gag acc gtc cac tcc ttc acc aac gac        1260
Gly Val Glu His Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp
305                 310                 315                 320

cag aac ctc atc gac aac ttc cac aag ggc acc cgc cgt ggc cgt gcc        1308
Gln Asn Leu Ile Asp Asn Phe His Lys Gly Thr Arg Arg Gly Arg Ala
                325                 330                 335
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gcc tcc ctc aac atg gtc ctc acc gag acc ggc gcc gcc aag gcc gtc      1356
Ala Ser Leu Asn Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val
            340                 345                 350
tcc aag gcc ctg ccg gag ttc gag ggc aag ctc acc ggc aac gcc atc      1404
Ser Lys Ala Leu Pro Glu Phe Glu Gly Lys Leu Thr Gly Asn Ala Ile
        355                 360                 365
cgc gtc ccc acc ccg aac gtc tcc atg gcg gtg ctc aac ctc acc ctg      1452
Arg Val Pro Thr Pro Asn Val Ser Met Ala Val Leu Asn Leu Thr Leu
    370                 375                 380
gag aag gag gtc gac cgc gag gag gtc aac aac ttc ctg cgc aag gtc      1500
Glu Lys Glu Val Asp Arg Glu Glu Val Asn Asn Phe Leu Arg Lys Val
385                 390                 395                 400
tcc ctg cac tcc gac ctg cgc cag cag atc tcc tac atc aac tcc ccg      1548
Ser Leu His Ser Asp Leu Arg Gln Gln Ile Ser Tyr Ile Asn Ser Pro
                405                 410                 415
gag gtc gtg tcc acc gac ttc gtc ggc agc acc cac gcc ggc atc gtc      1596
Glu Val Val Ser Thr Asp Phe Val Gly Ser Thr His Ala Gly Ile Val
            420                 425                 430
gac ggc ctg gcc acc atc gcc tcc ggc aag cac ctc gtg ctc tac gtc      1644
Asp Gly Leu Ala Thr Ile Ala Ser Gly Lys His Leu Val Leu Tyr Val
        435                 440                 445
tgg tac gac aac gag ttc ggc tac tcc aac cag gtc atc cgc atc gtc      1692
Trp Tyr Asp Asn Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val
    450                 455                 460
gag gag gtc gcc ggc gcc cgc ccg gag atc tac ccg cgt cgc ctg gag      1740
Glu Glu Val Ala Gly Ala Arg Pro Glu Ile Tyr Pro Arg Arg Leu Glu
465                 470                 475                 480
gcc tct gag ctg aag tag cttttccagg atcagcttca agctgccgca             1788
Ala Ser Glu Leu Lys
                485
gcgacaggcc cggttctcca cgtggagaac cgggcctgtc gcattcagga ggggcggcag     1848
cggcacaggc agatgaagaa tcgtcgtcgg tgtgtccgct cactgcgcct ggtgttaggc     1908
ccgtgctcta cacccgcccg ctgccggtta cggcaatcat ggccaggagc aggtgctgac     1968
cggtctgaca ggcgcctacg ctcacccagt caactgctga ctgggacatt gacttgagga     2028
tgcgtgcttc ccggcgtatg tggtcccttg                                     2058
<210>  152
<211>  485
<212>  PRT
<213>  Corynebacterium humireducens
<400>  152
Val Thr Ala His Ala Gln Pro Glu His Asn Asn Trp Asn Glu Lys Ile
1               5                   10                  15
Ala Leu Ala Gln Glu Met Leu Pro Leu Ile Gly Gln Leu His Arg Asn
            20                  25                  30
Asn Asp Val Val Val Ser Ile Phe Gly Arg Leu Leu Val Gly Ala Thr
        35                  40                  45
Asp Ile Asp Ile Ile Lys Ala His Arg Tyr Ala Arg Arg Val Ala Asp
    50                  55                  60
Arg Glu Met Lys Leu Asp Gln Thr Leu Pro Val Leu Arg Glu Leu Val
65                  70                  75                  80
Asp Met Asp Leu Gly Thr Ala Ser Ile Asp Leu Gly Arg Leu Ala Thr
                85                  90                  95
Gly Phe Glu Lys Ser Gly Gly Thr Asp Leu Arg Ala Tyr Leu Asp Glu
            100                 105                 110
Gln Leu Ala Asp Ile Val Gly Lys Arg Ser Glu Thr Glu Pro Arg Asp
        115                 120                 125
Val Val Leu Tyr Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile
    130                 135                 140
Leu Ile Ser Arg Glu Ala Thr Tyr Gly Gly Val Arg Leu Arg Ala Val
145                 150                 155                 160
Val Val Arg Lys Asn Ser Glu Asp Asp Ile Val Lys Arg Ala Ser Leu
                165                 170                 175
Leu Arg Arg Asp Ser Val His Gly Ala Phe Asp Gly Thr Ile Thr Val
            180                 185                 190
Asp Lys Glu Asn Asn Val Ile Trp Ala Asn Gly Thr Lys Ile Gln Ile
        195                 200                 205
Ile Tyr Ser Asn Ser Pro Ala Glu Val Asp Tyr Thr Ala Tyr Gly Ile
    210                 215                 220
Asn Asp Ala Ile Val Val Asp Asn Thr Gly Ile Trp Arg Asp Arg Glu
225                 230                 235                 240
Gly Leu Ser Gln His Leu Gln Ser Lys Gly Val Ser Arg Val Val Leu
                245                 250                 255
Thr Ala Pro Gly Lys Gly Asp Leu Pro Asn Ile Val Tyr Gly Ile Asn
            260                 265                 270

Asp Asp Met Ile Thr Asp Asp Glu Gln Ile Ile Thr Ala Ala Ser Cys
        275                 280                 285
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Thr Thr Asn Gly Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr
    290                 295                 300
Gly Val Glu His Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp
305                 310                 315                 320
Gln Asn Leu Ile Asp Asn Phe His Lys Gly Thr Arg Arg Gly Arg Ala
                325                 330                 335
Ala Ser Leu Asn Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val
            340                 345                 350
Ser Lys Ala Leu Pro Glu Phe Glu Gly Lys Leu Thr Gly Asn Ala Ile
        355                 360                 365
Arg Val Pro Thr Pro Asn Val Ser Met Ala Val Leu Asn Leu Thr Leu
    370                 375                 380
Glu Lys Glu Val Asp Arg Glu Glu Val Asn Asn Phe Leu Arg Lys Val
385                 390                 395                 400
Ser Leu His Ser Asp Leu Arg Gln Gln Ile Ser Tyr Ile Asn Ser Pro
                405                 410                 415
Glu Val Val Ser Thr Asp Phe Val Gly Ser Thr His Ala Gly Ile Val
            420                 425                 430
Asp Gly Leu Ala Thr Ile Ala Ser Gly Lys His Leu Val Leu Tyr Val
        435                 440                 445
Trp Tyr Asp Asn Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val
    450                 455                 460
Glu Glu Val Ala Gly Ala Arg Pro Glu Ile Tyr Pro Arg Arg Leu Glu
465                 470                 475                 480
Ala Ser Glu Leu Lys
                485
<210>  153
<211>  1605
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1305)
<223>  gen glyxeraldehyt_3_phopshatdehydrogenaza 2
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gctccattcg ggggtgaatc gggcatgtgt gaccgatatt attcgccggt gtccggagga       60
ccgcccggtg cccggccgcc tgcgaccccc cgttgacaac gactttcggg aagtggggcg      120
gaccggaatg tgagggcaaa cataatcgga aatccgcgga tgtctgaaaa tgtctgattc      180
ttcgctgcac agcggggtaa gtgccgctaa actgtcgctt gatgggccgt gaacgccagt      240
cactacgacg gacagtgcgg tcacatccgg acacgtgtac tcaaacccga ggagaaaatt      300
gtg acc atc cgc gtt ggc atc aac ggc ttc ggc cgt atc ggc cgt aac         348
Val Thr Ile Arg Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
1               5                  10                  15
ttc tac cgc gca gtc ctg gag cgc agc gag gcc atc gag atc gtc gcc        396
Phe Tyr Arg Ala Val Leu Glu Arg Ser Glu Ala Ile Glu Ile Val Ala
            20                  25                  30
gtc aac gac ctc acc gac aac aag acg ctg tcg acc ctc ctg aag tac        444
Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Tyr
        35                  40                  45
gac tcc atc ctc ggc aag ctg ccg ggc gag gtc tcg ttc gac gac gac        492
Asp Ser Ile Leu Gly Lys Leu Pro Gly Glu Val Ser Phe Asp Asp Asp
    50                  55                  60
tcc atc acc tac gac ggc aag acc atc gcc gtc tcc gct gag cgc gac        540
Ser Ile Thr Tyr Asp Gly Lys Thr Ile Ala Val Ser Ala Glu Arg Asp
65                  70                  75                  80
ccg aag aac ctg gac tgg gcc gcc cac aac gtg gac atc gtc atc gag        588
Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
                85                  90                  95
tcc acc ggc ttc ttc acc gac gcc gag gca gcc aag gcc cac atc gag        636
Ser Thr Gly Phe Phe Thr Asp Ala Glu Ala Ala Lys Ala His Ile Glu
            100                 105                 110
gcc ggc gcc aag aag gtc atc atc tcc gcc ccg gcc tcc aac gag gac        684
Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
        115                 120                 125
gcg acc ttc gtc tac ggc gtc aac cac cag gac tac gac ccg gag aac        732
Ala Thr Phe Val Tyr Gly Val Asn His Gln Asp Tyr Asp Pro Glu Asn
    130                 135                 140
cac aac gtc atc tcc gcc gca tcc tgc acc acc aac tgc ctg gcc ccg        780
His Asn Val Ile Ser Ala Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
145                 150                 155                 160
atg gcc aag gtc ctc aac gac aag ctc ggc atc gag cgc ggc ctg atg        828
Met Ala Lys Val Leu Asn Asp Lys Leu Gly Ile Glu Arg Gly Leu Met
                165                 170                 175
acc acc atc cac gcc tac acc ggt gac cag cgt ctg cac gac gcc ccg        876
Thr Thr Ile His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
            180                 185                 190
cac aag gac ctg cgc cgc gcc cgc gcc gcc gcc gtc aac atc gtg ccc        924
His Lys Asp Leu Arg Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro
```

```
        195                 200                 205
acc tcc acc ggt gcc gcc aag gcc gtc tcc ctg gtc ctg ccg gag ctg        972
Thr Ser Thr Gly Ala Ala Lys Ala Val Ser Leu Val Leu Pro Glu Leu
    210                 215                 220
aag ggc aag ctg gac ggc tac gca ctg cgc gtc ccg acc atc acc ggt       1020
Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Thr Ile Thr Gly
225                 230                 235                 240
tcc gcc acc gac ctc acc ttc acc gcc tcc cgc gag acc tct gtc gag       1068
Ser Ala Thr Asp Leu Thr Phe Thr Ala Ser Arg Glu Thr Ser Val Glu
                245                 250                 255
gag gtc aac gcc ttc atc aag gag gcc gcg cag ggc gag ttc ggt gag       1116
Glu Val Asn Ala Phe Ile Lys Glu Ala Ala Gln Gly Glu Phe Gly Glu
            260                 265                 270
acc ctg gcc tac acc gag gat ccg atc gtc tcc acc gac atc gtc acc       1164
Thr Leu Ala Tyr Thr Glu Asp Pro Ile Val Ser Thr Asp Ile Val Thr
        275                 280                 285
gat ccg cac ggc tcc atc ttc gac gcc ggc ctg acc aag gtc atc ggc       1212
Asp Pro His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ile Gly
    290                 295                 300
gac cag gtc aag gtc gtc tcc tgg tac gac aac gag tgg ggc tac acc       1260
Asp Gln Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
305                 310                 315                 320
tgc cag ctc ctg cgc ctg acc gag ctc gtc gcc tcc aag ctc tag           1305
Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu
                325                 330
gaccgcgacc ccgcacttcc ccggcctccg gctgagaccg ggggagtgcg cccctgtggc     1365
ccggggtgtg cctcggcaca cgtcgggcct cagggctatc cacccccтca gatcagccgc     1425
ccctttctca tctgaagaca aaagtcaagg agacagccat gaccgtgaag actctgcagg     1485
acctgctcga cgagggcgtc gacggccgcc acatcctcgt ccgctccgac ttcaacgtcc     1545
cgctcaacga cgccggtgag atcaccgacg cgggccgcat caccgcctcc ctgcccaccc     1605
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<211>  334
<212>  PRT
<213>  Corynebacterium humireducens
<400>  154
Val Thr Ile Arg Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
1               5                   10                  15
Phe Tyr Arg Ala Val Leu Glu Arg Ser Glu Ala Ile Glu Ile Val Ala
            20                  25                  30
Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Tyr
        35                  40                  45
Asp Ser Ile Leu Gly Lys Leu Pro Gly Glu Val Ser Phe Asp Asp Asp
    50                  55                  60
Ser Ile Thr Tyr Asp Gly Lys Thr Ile Ala Val Ser Ala Glu Arg Asp
65                  70                  75                  80
Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
                85                  90                  95
Ser Thr Gly Phe Phe Thr Asp Ala Glu Ala Ala Lys Ala His Ile Glu
            100                 105                 110
Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
        115                 120                 125
Ala Thr Phe Val Tyr Gly Val Asn His Gln Asp Tyr Asp Pro Glu Asn
    130                 135                 140
His Asn Val Ile Ser Ala Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
145                 150                 155                 160
Met Ala Lys Val Leu Asn Asp Lys Leu Gly Ile Glu Arg Gly Leu Met
                165                 170                 175
Thr Thr Ile His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
            180                 185                 190
His Lys Asp Leu Arg Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro
        195                 200                 205
Thr Ser Thr Gly Ala Ala Lys Ala Val Ser Leu Val Leu Pro Glu Leu
    210                 215                 220
Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Thr Ile Thr Gly
225                 230                 235                 240
Ser Ala Thr Asp Leu Thr Phe Thr Ala Ser Arg Glu Thr Ser Val Glu
                245                 250                 255
Glu Val Asn Ala Phe Ile Lys Glu Ala Ala Gln Gly Glu Phe Gly Glu
            260                 265                 270
Thr Leu Ala Tyr Thr Glu Asp Pro Ile Val Ser Thr Asp Ile Val Thr
        275                 280                 285
Asp Pro His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ile Gly
    290                 295                 300
Asp Gln Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
305                 310                 315                 320
Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu
                325                 330
<210>  155
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<211> 1380
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1080)
<223> gen tpiA
<400> 155

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aagaccgtct tctggaacgg cccgatgggt gtcttcgaga tggcaccgtt ctccaagggc       60
accgagggcg tcgccaaggc catcatcgac gcgaccgcga acaacggttc cttctccgtc      120
gtcggtggcg gcgactccgc agcctccgtc cgcgtgctcg gcctggacga ggacggcttc      180
tcccacatct ccaccggcgg cggcgcctcc ctcgagttcc tcgagggcaa ggagctcccg      240
ggcgtttccg tcctggaccg ctaagcactt accacccact ctgaaaggag tgccccaccc      300
atg gca cgc acc ccc ctc atc gcc ggc aac tgg aag atg aac ctg gac         348
Met Ala Arg Thr Pro Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp
1               5                  10                  15
cac cac cag gcc atc gcc acc gtg cag aag ctc gac ttc gcc ctg ccg         396
His His Gln Ala Ile Ala Thr Val Gln Lys Leu Asp Phe Ala Leu Pro
            20                  25                  30
aag gag tac tac gag aag gtc gac gtc gcc gtc acc gtc ccg ttc acc         444
Lys Glu Tyr Tyr Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
        35                  40                  45
gac ctc cgt tcc gtg cag acg ctc gtc gac ggg gac aag ctc aag gtc         492
Asp Leu Arg Ser Val Gln Thr Leu Val Asp Gly Asp Lys Leu Lys Val
    50                  55                  60
acc tac ggt gcc cag gac gtc tcc cgg cac gag tcc ggc gcg tac acc         540
Thr Tyr Gly Ala Gln Asp Val Ser Arg His Glu Ser Gly Ala Tyr Thr
65                  70                  75                  80
ggt gag gtc tcc gct cag atg ctc gcc aag ctc ggc tgc acc tgg gtc         588
Gly Glu Val Ser Ala Gln Met Leu Ala Lys Leu Gly Cys Thr Trp Val
                85                  90                  95
gtc gtc ggc cac tcc gag cgc cgc gag tac cac aac gag tcc gac gag         636
Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
            100                 105                 110
ctg gtc gcc gcg aag gcc gct gcc gcc ctc cgc cac ggc atg agc ccg         684
Leu Val Ala Ala Lys Ala Ala Ala Ala Leu Arg His Gly Met Ser Pro
        115                 120                 125
atc gtg tgc gtc ggc gag ccg ctg gag atc cgc gag gcc ggc acc cac         732
Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
    130                 135                 140
gtc gac tac gtc gtc gag cag acc cgt gcc tcc ctg gcc ggc ctg tcc         780
Val Asp Tyr Val Val Glu Gln Thr Arg Ala Ser Leu Ala Gly Leu Ser
145                 150                 155                 160
gcc gag gac ctg tcc aac acc gtc atc gcc tac gag ccc gtg tgg gcc         828
Ala Glu Asp Leu Ser Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
                165                 170                 175
atc ggc acc ggc aag gtc gcc tcc gcg gcc gat gcc cag gag gtc tgt         876
Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
            180                 185                 190
gcg gcg atc cgc ggt ctc gtc cgc gag ctg gcc ggt gac gag gtc gcc         924
Ala Ala Ile Arg Gly Leu Val Arg Glu Leu Ala Gly Asp Glu Val Ala
        195                 200                 205
gac ggc atc cgc atc ctc tac ggc ggt tcc gtc aag acc gac tcg gtc         972
Asp Gly Ile Arg Ile Leu Tyr Gly Gly Ser Val Lys Thr Asp Ser Val
    210                 215                 220
gcc gag atc gtc ggt cag ccc gac gtc gac ggt ggt ctc gtc ggt ggc        1020
Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
225                 230                 235                 240
gcc tcg ctc gac ggc gag gag ttc gcc aag ctg gcg gcc gcc gcg gcg        1068
Ala Ser Leu Asp Gly Glu Glu Phe Ala Lys Leu Ala Ala Ala Ala Ala
                245                 250                 255
tcc gtc gtc tag catcacctca tccaccggcc ccgggcactg aacattcagt            1120
Ser Val Val

gcccggggcc ggtgtccttt ctccggggaa tatggtgcgc aatccccacg cacggccgtc      1180
atatgcgtca tgatggggag gcgaaccgca tccccgcctt cttcgagtac gaacagggag      1240
acactcaatg accgtccgcg atcatctgca ggaagacatc cgctacctcg gccgtatcct      1300
cggccaggtc atcgcggaac aggagggcga ggacgtgttc aacctcgtcg agcacgcccg      1360
ccagcaggcc ttcgaggtgg                                                  1380
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<210> 156
<211> 259
<212> PRT
<213> Corynebacterium humireducens
<400> 156

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Met Ala Arg Thr Pro Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp
1               5                  10                  15
```

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His His Gln Ala Ile Ala Thr Val Gln Lys Leu Asp Phe Ala Leu Pro
            20                  25                  30
Lys Glu Tyr Tyr Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
        35                  40                  45
Asp Leu Arg Ser Val Gln Thr Leu Val Asp Gly Asp Lys Leu Lys Val
    50                  55                  60
Thr Tyr Gly Ala Gln Asp Val Ser Arg His Glu Ser Gly Ala Tyr Thr
65                  70                  75                  80
Gly Glu Val Ser Ala Gln Met Leu Ala Lys Leu Gly Cys Thr Trp Val
                85                  90                  95
Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
            100                 105                 110
Leu Val Ala Ala Lys Ala Ala Ala Ala Leu Arg His Gly Met Ser Pro
        115                 120                 125
Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
    130                 135                 140
Val Asp Tyr Val Val Glu Gln Thr Arg Ala Ser Leu Ala Gly Leu Ser
145                 150                 155                 160
Ala Glu Asp Leu Ser Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
                165                 170                 175
Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
            180                 185                 190
Ala Ala Ile Arg Gly Leu Val Arg Glu Leu Ala Gly Asp Glu Val Ala
        195                 200                 205
Asp Gly Ile Arg Ile Leu Tyr Gly Gly Ser Val Lys Thr Asp Ser Val
    210                 215                 220
Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
225                 230                 235                 240
Ala Ser Leu Asp Gly Glu Glu Phe Ala Lys Leu Ala Ala Ala Ala Ala
                245                 250                 255
Ser Val Val
<210>  157
<211>  1632
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1332)
<223>  gen frutcosebisphosphataldolaza
<400>  157
ccgactggac cgccgacgcc cgcctgccgc acaacttcgg cctggcgccg tcgtcactgc       60
cggaggccct cggcgtcctg cgtatcgacg aacgcgatct ctccgtccag ctctccggct      120
ggatgctgct ggaggccgcc gcccgggtgt ccacctacgc ggagacccag cggtcctgat      180
ccccgcgcgc ggggcggggg gggaggtgac gcgggttttc cgccctctgt tgcgagcgcg      240
ggaggccaaa gggaggcata ctggtatacg gacctgtttg ctaacccgga ggatcaccct      300
atg cct atc gcg act ccc gaa atc tac aac gag atg ctc gac agg gcc         348
Met Pro Ile Ala Thr Pro Glu Ile Tyr Asn Glu Met Leu Asp Arg Ala
1               5                   10                  15
aag gag ggc ggc tac gcc ttc ccg gcc atc aac tgc acc tcc tcg gag         396
Lys Glu Gly Gly Tyr Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu
            20                  25                  30
acc atc aac gcc gct ctc cgc ggc ttc gcc gag gcc gag tcc gac ggc         444
Thr Ile Asn Ala Ala Leu Arg Gly Phe Ala Glu Ala Glu Ser Asp Gly
        35                  40                  45
atc atc cag ttc tcc acc ggt ggc gcc gaa ttc ggc tcc ggt ctg tcc         492
Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ser
    50                  55                  60
gtg aag aac aag gtc gcc ggc gcc gtc gcc ctg gcc tcc ttc gcg cat         540
Val Lys Asn Lys Val Ala Gly Ala Val Ala Leu Ala Ser Phe Ala His
65                  70                  75                  80
gag gcc gcc aag cac tac ggc gtc aac gtc gcc ctg cac acc gac cac         588
Glu Ala Ala Lys His Tyr Gly Val Asn Val Ala Leu His Thr Asp His
                85                  90                  95
tgc cag aag gag gtg ctc gac gag ttc gtg cgc ccg ctg ctg gcc atc         636
Cys Gln Lys Glu Val Leu Asp Glu Phe Val Arg Pro Leu Leu Ala Ile
            100                 105                 110
tcc cag gag cgc gtc gac gcc ggt gag ctc ccg ctc ttc cag tcc cac         684
Ser Gln Glu Arg Val Asp Ala Gly Glu Leu Pro Leu Phe Gln Ser His
        115                 120                 125
atg tgg gac ggt tcc gct gtc ccg atc gac gag aac ctg gag atc gcg         732
Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
    130                 135                 140
aag gag ctg ctg gag aag tcc cgc aag gcg aac att atc ctc gag atc         780
Lys Glu Leu Leu Glu Lys Ser Arg Lys Ala Asn Ile Ile Leu Glu Ile
145                 150                 155                 160
gag atc ggt gtc gtc ggc ggc gag gag gac ggt gtc gag gcc aag gcc         828
Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
                165                 170                 175
```

```
ggc gcc aac ctc tac acc acc gag gag gac ttc gag aag acc atc gac        876
Gly Ala Asn Leu Tyr Thr Thr Glu Glu Asp Phe Glu Lys Thr Ile Asp
            180                 185                 190
gcc atc ggc acc ggt gag aac ggc cgc tac ctg ctg gcc gcg acc ttc        924
Ala Ile Gly Thr Gly Glu Asn Gly Arg Tyr Leu Leu Ala Ala Thr Phe
        195                 200                 205
ggc aac gtc cac ggc gtg tac aag ccg ggc aac gtg aag ctg cgt ccg        972
Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
    210                 215                 220
gag gtc ctg ctc gag ggc cag aag gtg gcc cgc cgc aag ctg ggt ctg       1020
Glu Val Leu Leu Glu Gly Gln Lys Val Ala Arg Arg Lys Leu Gly Leu
225                 230                 235                 240
ggc gac gac gcc ctg ccg ttc gac ttc gtc ttc cac ggt ggc tcc ggc       1068
Gly Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
                245                 250                 255
tcc gag aag gag aag atc gag gag gcg ctg cgt tac ggc acc atc aag       1116
Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Arg Tyr Gly Thr Ile Lys
            260                 265                 270
atg aac gtc gac acg gac acc cag tac gcg ttc acc cgt ccg atc gtc       1164
Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
        275                 280                 285
acg cac atg ttc cag aac tac gac ggc gtc ctc aag atc gac ggc gag       1212
Thr His Met Phe Gln Asn Tyr Asp Gly Val Leu Lys Ile Asp Gly Glu
    290                 295                 300
gtg ggc aac aag aag gcc tac gac ccg cgt tcc tac ctg aag aag gcc       1260
Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Leu Lys Lys Ala
305                 310                 315                 320
gag cag tcg atg gct gag cgc gtc atc gag gcc tgc cag gac ctg cac       1308
Glu Gln Ser Met Ala Glu Arg Val Ile Glu Ala Cys Gln Asp Leu His
                325                 330                 335
tcc gtg ggc aag acc gtc aag tag tcttctccac ccgaggaaag ccccgccctg       1362
Ser Val Gly Lys Thr Val Lys
            340
tgcggggctt tctgcgctta gtatcggtgc atggccaaac tgagaatcgg caccctggaa      1422
cgtctccgcc agctcgaggg ctcgttggag tcccgggcgc tgcgcgtgcg gaagcgcttc      1482
ttccggatcg tgcaggtcgc ggtggccgcg ggggtgtcgt tctgggtggc gcagtccctc      1542
atcgggcatc cggtcccgtt cttcgcgccg atcacggtga tcatcatcct ggggctcacc      1602
ggcggcgacc gcatccggcg ggccctggag                                       1632
<210>  158
<211>  343
<212>  PRT
<213>  Corynebacterium humireducens
<400>  158
Met Pro Ile Ala Thr Pro Glu Ile Tyr Asn Glu Met Leu Asp Arg Ala
1               5                   10                  15
Lys Glu Gly Gly Tyr Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu
            20                  25                  30
Thr Ile Asn Ala Ala Leu Arg Gly Phe Ala Glu Ala Glu Ser Asp Gly
        35                  40                  45
Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ser
    50                  55                  60
Val Lys Asn Lys Val Ala Gly Ala Val Ala Leu Ala Ser Phe Ala His
65                  70                  75                  80
Glu Ala Ala Lys His Tyr Gly Val Asn Val Ala Leu His Thr Asp His
                85                  90                  95
Cys Gln Lys Glu Val Leu Asp Glu Phe Val Arg Pro Leu Leu Ala Ile
            100                 105                 110
Ser Gln Glu Arg Val Asp Ala Gly Glu Leu Pro Leu Phe Gln Ser His
        115                 120                 125
Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
    130                 135                 140
Lys Glu Leu Leu Glu Lys Ser Arg Lys Ala Asn Ile Ile Leu Glu Ile
145                 150                 155                 160
Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
                165                 170                 175
Gly Ala Asn Leu Tyr Thr Thr Glu Glu Asp Phe Glu Lys Thr Ile Asp
            180                 185                 190
Ala Ile Gly Thr Gly Glu Asn Gly Arg Tyr Leu Leu Ala Ala Thr Phe
        195                 200                 205
Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
    210                 215                 220
Glu Val Leu Leu Glu Gly Gln Lys Val Ala Arg Arg Lys Leu Gly Leu
225                 230                 235                 240
Gly Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
                245                 250                 255
Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Arg Tyr Gly Thr Ile Lys
            260                 265                 270
Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
```

```
        275                 280                 285
Thr His Met Phe Gln Asn Tyr Asp Gly Val Leu Lys Ile Asp Gly Glu
    290                 295                 300
Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Leu Lys Lys Ala
305                 310                 315                 320
Glu Gln Ser Met Ala Glu Arg Val Ile Glu Ala Cys Gln Asp Leu His
                325                 330                 335
Ser Val Gly Lys Thr Val Lys
            340
<210>  159
<211>  1566
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1266)
<223>  gen 1-phosphofructokinaza
<400>  159
agaacaccac aaaatccact agttagcaac gatccagaca ggcaaccctt gacaaacgga       60
cacaatcgga caatgatgat gttgtaacac cacattaaat gtgacttaat tcatcatttt      120
cataacgtcc cgcccgggac agccccggag cgccccgatc cccgggtcgc gccccatagg      180
attgatccag ctcaggacct gttcggtcac ccgaccggac accgctccgg gcacgcgtcc      240
cccgccaccc agcggacacg ccgcaacgac acgtttttcc gaacggacag ggagcccgcc      300
gtg att ctc acc ctc acc ccc aac ccc agc atc gac gcg acc atg caa         348
Val Ile Leu Thr Leu Thr Pro Asn Pro Ser Ile Asp Ala Thr Met Gln
1               5                  10                  15
ctg ggg acg cgg ctg cgc cgc ggg ctc gtc cac cgt ccc tcc tcc atc         396
Leu Gly Thr Arg Leu Arg Arg Gly Leu Val His Arg Pro Ser Ser Ile
            20                  25                  30
tcc cag gtg gcc ggc gga aaa ggc gtc aac gtc acg cac gcc ctg acc         444
Ser Gln Val Ala Gly Gly Lys Gly Val Asn Val Thr His Ala Leu Thr
        35                  40                  45
ctc gcg gac aaa ctc agc ctc gcc ctc ttc ccg gcg gac ggc aac gac         492
Leu Ala Asp Lys Leu Ser Leu Ala Leu Phe Pro Ala Asp Gly Asn Asp
    50                  55                  60
ccc ttc gtc gcc ctg gcc cgc cag tcc ggg atc ccc ttc cac gcc atc         540
Pro Phe Val Ala Leu Ala Arg Gln Ser Gly Ile Pro Phe His Ala Ile
65                  70                  75                  80
ccg gtg tcc gag ggc gtc cgc atc aac acc acc ctc act gaa ccg gac         588
Pro Val Ser Glu Gly Val Arg Ile Asn Thr Thr Leu Thr Glu Pro Asp
                85                  90                  95
ggg acc acc acc aag atc aac ggc ctc ggc gcg cag atc gag ccg ccc         636
Gly Thr Thr Thr Lys Ile Asn Gly Leu Gly Ala Gln Ile Glu Pro Pro
            100                 105                 110
acc cgc cgc atc atc gag gag acc gtc gtc cgc ctc gcc gcg aac gcc         684
Thr Arg Arg Ile Ile Glu Glu Thr Val Val Arg Leu Ala Ala Asn Ala
        115                 120                 125
tcc tgg ctg gtc atg gcc ggt tcc ctg ccg ccc ggg gtc ccc acc ggc         732
Ser Trp Leu Val Met Ala Gly Ser Leu Pro Pro Gly Val Pro Thr Gly
    130                 135                 140
tgg tac acg gaa ctc atc acc acc gtc cgc gcg acg cac ccg gac ctg         780
Trp Tyr Thr Glu Leu Ile Thr Thr Val Arg Ala Thr His Pro Asp Leu
145                 150                 155                 160
ccg gtg gcc gtc gac acg tcc gac gcc gcg atg atc gcc ctc ggc gag         828
Pro Val Ala Val Asp Thr Ser Asp Ala Ala Met Ile Ala Leu Gly Glu
                165                 170                 175
ggc ttc gag gtc gcc gcc ccg acc ctc atc aag ccc aac ggc atg gag         876
Gly Phe Glu Val Ala Ala Pro Thr Leu Ile Lys Pro Asn Gly Met Glu
            180                 185                 190
ctc ggg cag ctc gtc gac cgt gac ggc gag cac ctc gag gcg gcc gcc         924
Leu Gly Gln Leu Val Asp Arg Asp Gly Glu His Leu Glu Ala Ala Ala
        195                 200                 205
gcc cgc ggc gac ttc tcc ccg gtc atc gac gcg gcc cgc gtc gtc gtc         972
Ala Arg Gly Asp Phe Ser Pro Val Ile Asp Ala Ala Arg Val Val Val
    210                 215                 220
gac cgc ggc gtc aac gag gtc ctg gtg acg ctc ggc gtc gcc gga gcc        1020
Asp Arg Gly Val Asn Glu Val Leu Val Thr Leu Gly Val Ala Gly Ala
225                 230                 235                 240
gcc ctc gtc acc gcg cag ggc gtc tgg ctc gcc acc cct ccc ccg gtc        1068
Ala Leu Val Thr Ala Gln Gly Val Trp Leu Ala Thr Pro Pro Pro Val
                245                 250                 255
gac gtc atg tcc acc gtc ggc gcg ggc gac agc tcg ctc gcc ggg tac        1116
Asp Val Met Ser Thr Val Gly Ala Gly Asp Ser Ser Leu Ala Gly Tyr
            260                 265                 270
ctc atg gcc cgc gcg gag ggc ggc agt ccc gcc gac tgc ctg gcc cgc        1164
Leu Met Ala Arg Ala Glu Gly Gly Ser Pro Ala Asp Cys Leu Ala Arg
        275                 280                 285
gcc gtc gcc tac ggc acc gcc gcc acc ggc ctg ccc ggc acc acc att        1212
```

```
Ala Val Ala Tyr Gly Thr Ala Ala Thr Gly Leu Pro Gly Thr Thr Ile
    290                 295                 300
cct tcc ccc gca caa ctg aat ctc gag gaa acc cat gtc cgt cat atc      1260
Pro Ser Pro Ala Gln Leu Asn Leu Glu Glu Thr His Val Arg His Ile
305                 310                 315                 320
tcc tga cctggtacac ctggacgccg acctcggcgg cacgaccacc gaggtgatca      1316
Ser
ccgccctggc gggcgtcgtc cacgccgccg gccgcgccag ctccccgcaa ctgctcgccg    1376
acgccgccct cgcccgtgag gcccagaacc ccaccggtgt gcccggccgc gtcgccatcc    1436
cccactgccg ttccgccgcc gtcgaggtcc cgaccctggc cttcgcccga ctgtcgcgcc    1496
ccgtcgactt cggcggtccc gacggcgacg ccgagctcgt cttcctcatc gccgcccccg    1556
agggcggcgg                                                          1566
<210>  160
<211>  321
<212>  PRT
<213>  Corynebacterium humireducens
<400>  160
Val Ile Leu Thr Leu Thr Pro Asn Pro Ser Ile Asp Ala Thr Met Gln
1               5                  10                  15
Leu Gly Thr Arg Leu Arg Arg Gly Leu Val His Arg Pro Ser Ser Ile
            20                  25                  30
Ser Gln Val Ala Gly Gly Lys Gly Val Asn Val Thr His Ala Leu Thr
        35                  40                  45
Leu Ala Asp Lys Leu Ser Leu Ala Leu Phe Pro Ala Asp Gly Asn Asp
    50                  55                  60
Pro Phe Val Ala Leu Ala Arg Gln Ser Gly Ile Pro Phe His Ala Ile
65                  70                  75                  80
Pro Val Ser Glu Gly Val Arg Ile Asn Thr Thr Leu Thr Glu Pro Asp
                85                  90                  95
Gly Thr Thr Thr Lys Ile Asn Gly Leu Gly Ala Gln Ile Glu Pro Pro
            100                 105                 110
Thr Arg Arg Ile Ile Glu Glu Thr Val Val Arg Leu Ala Ala Asn Ala
        115                 120                 125
Ser Trp Leu Val Met Ala Gly Ser Leu Pro Pro Gly Val Pro Thr Gly
    130                 135                 140
Trp Tyr Thr Glu Leu Ile Thr Thr Val Arg Ala Thr His Pro Asp Leu
145                 150                 155                 160
Pro Val Ala Val Asp Thr Ser Asp Ala Ala Met Ile Ala Leu Gly Glu
                165                 170                 175
Gly Phe Glu Val Ala Ala Pro Thr Leu Ile Lys Pro Asn Gly Met Glu
            180                 185                 190
Leu Gly Gln Leu Val Asp Arg Asp Gly Glu His Leu Glu Ala Ala Ala
        195                 200                 205
Ala Arg Gly Asp Phe Ser Pro Val Ile Asp Ala Ala Arg Val Val Val
    210                 215                 220
Asp Arg Gly Val Asn Glu Val Leu Val Thr Leu Gly Val Ala Gly Ala
225                 230                 235                 240
Ala Leu Val Thr Ala Gln Gly Val Trp Leu Ala Thr Pro Pro Pro Val
                245                 250                 255
Asp Val Met Ser Thr Val Gly Ala Gly Asp Ser Ser Leu Ala Gly Tyr
            260                 265                 270
Leu Met Ala Arg Ala Glu Gly Gly Ser Pro Ala Asp Cys Leu Ala Arg
        275                 280                 285
Ala Val Ala Tyr Gly Thr Ala Ala Thr Gly Leu Pro Gly Thr Thr Ile
    290                 295                 300
Pro Ser Pro Ala Gln Leu Asn Leu Glu Glu Thr His Val Arg His Ile
305                 310                 315                 320
Ser
<210>  161
<211>  1632
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1332)
<223>  gen 6-phosphofructokinaza
<400>  161
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cggcggccgg cgtgtacaac acggggcgcc agaccggtgc ggtcctcggc gcggccgggg     120
tgggggcggc gatgcaggtc ggtgcggcca cggccgggtt cgtgccgggt ctcgctctgt     180
cgctgctgct ccccgtggcc gtcctcggtc tggggctggt ggcggtcgcc ttcttcgaga     240
ccccgccaca cgccgaacca cagggtgccg aacagcgggc cggggactaa agtggtctcc     300
atg cga ctt gcc acc ctc acc tcc ggc ggc gac tgc ccc ggc ctc aac       348
Met Arg Leu Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn
1               5                  10                  15
gcc gtc atc cgc ggc atc gtc cgt acc gcc agc tcc gag ttc ggt tcc       396
Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Ser Glu Phe Gly Ser
            20                  25                  30
```

```
acc gtc gtg gga tac cag gac ggc tgg cag ggc ctg ctg gag gac cgc        444
Thr Val Val Gly Tyr Gln Asp Gly Trp Gln Gly Leu Leu Glu Asp Arg
        35                  40                  45
cgc gtc gac ctc tac gac gac gag cac atc gac cgc atc ctc ctg cgc        492
Arg Val Asp Leu Tyr Asp Asp Glu His Ile Asp Arg Ile Leu Leu Arg
    50                  55                  60
ggt ggc acg atc ctg ggc acc ggt cgt ctg cac ccg gac aag ttc aag        540
Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys
65                  70                  75                  80
gcg ggg ctc gac cag atc aag cag aac ctg gat gac gcg ggc atc gac        588
Ala Gly Leu Asp Gln Ile Lys Gln Asn Leu Asp Asp Ala Gly Ile Asp
                85                  90                  95
gcc ctc atc ccg atc ggc ggc gag ggc acc ctc aag ggc gcg aag tgg        636
Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp
            100                 105                 110
ctg tcc gac aac ggc atc ccg gtc gtc ggc gtg ccg aag acc atc gac        684
Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp
        115                 120                 125
aac gac gtc tac ggc acc gac tac acc ttc ggc ttc gac acc gcc gtc        732
Asn Asp Val Tyr Gly Thr Asp Tyr Thr Phe Gly Phe Asp Thr Ala Val
    130                 135                 140
gcc gtg gcc acc gac gcc gtc gac cgt ctg cac acc acc gcc gag tcc        780
Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser
145                 150                 155                 160
cac aac cgc atc ctc atc gtc gag gtc atg ggc cgt cac gtc ggc tgg        828
His Asn Arg Ile Leu Ile Val Glu Val Met Gly Arg His Val Gly Trp
                165                 170                 175
atc gcg ctg cac gcg ggc atg gcc ggc ggc gcg cac tac acc gtg atc        876
Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile
            180                 185                 190
ccg gag gtg ccc ttc gac atc tcc gag atc tgc aag aag atg gag cgc        924
Pro Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Lys Met Glu Arg
        195                 200                 205
cgc ttc cag atg ggc gag aag tac ggc atc atc gtc gtc gcc gag ggc        972
Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly
    210                 215                 220
gcc gcg ccc aag gag ggc acg atg gag ctc aag tcc ggt ggc gtc gac       1020
Ala Ala Pro Lys Glu Gly Thr Met Glu Leu Lys Ser Gly Gly Val Asp
225                 230                 235                 240
cag ttc ggc cac gag atc ttc acc ggc atc ggc cag cag atc gcc gac       1068
Gln Phe Gly His Glu Ile Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp
                245                 250                 255
gag atc cac gcc cgc ctc ggc cat gac gtc cgc acc tcc gtc ctg ggc       1116
Glu Ile His Ala Arg Leu Gly His Asp Val Arg Thr Ser Val Leu Gly
            260                 265                 270
cac atc cag cgc ggt ggc acc ccg acc gcc ttc gac cgc gtc ctg gcc       1164
His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala
        275                 280                 285
acc cgt tac ggc gtc cgc gcg acc cgc tcc gcc cac cgc ggc gag ttc       1212
Thr Arg Tyr Gly Val Arg Ala Thr Arg Ser Ala His Arg Gly Glu Phe
    290                 295                 300
ggc acc tgc gtg gcg ctc aag ggt gag cgg atc gag aac atc acg ctg       1260
Gly Thr Cys Val Ala Leu Lys Gly Glu Arg Ile Glu Asn Ile Thr Leu
305                 310                 315                 320
gag aag gcc gtg ggc acc ctc aag acc gtg ccg atg gac cgc tgg ctc       1308
Glu Lys Ala Val Gly Thr Leu Lys Thr Val Pro Met Asp Arg Trp Leu
                325                 330                 335
acc gcc cag gcc atg ttc ggc tag gtgcgcgacc tccatctgga cacctgccgg       1362
Thr Ala Gln Ala Met Phe Gly
            340
ctgctcgtcg tcggcatcaa cccgggtctg gtgtcggagc gcgtcgacgc gcccttcgcc      1422
cgcccgggca accgtttctg gccggcgctc cacgccgccg gcatcacgga gacgcttgtc      1482
gacgcccgcg acggcctcac cgccgcccac cacgcggagc tgctgcggcg gggcctcggc      1542
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ctggcgggtg gggcggtgct ggcggagaag                                       1632
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<213>  Corynebacterium humireducens
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Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Ser Glu Phe Gly Ser
            20                  25                  30
Thr Val Val Gly Tyr Gln Asp Gly Trp Gln Gly Leu Leu Glu Asp Arg
        35                  40                  45
Arg Val Asp Leu Tyr Asp Asp Glu His Ile Asp Arg Ile Leu Leu Arg
    50                  55                  60
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Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys
65 70 75 80
Ala Gly Leu Asp Gln Ile Lys Gln Asn Leu Asp Asp Ala Gly Ile Asp
85 90 95
Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp
100 105 110
Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp
115 120 125
Asn Asp Val Tyr Gly Thr Asp Tyr Thr Phe Gly Phe Asp Thr Ala Val
130 135 140
Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser
145 150 155 160
His Asn Arg Ile Leu Ile Val Glu Val Met Gly Arg His Val Gly Trp
165 170 175
Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile
180 185 190
Pro Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Lys Met Glu Arg
195 200 205
Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly
210 215 220
Ala Ala Pro Lys Glu Gly Thr Met Glu Leu Lys Ser Gly Gly Val Asp
225 230 235 240
Gln Phe Gly His Glu Ile Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp
245 250 255
Glu Ile His Ala Arg Leu Gly His Asp Val Arg Thr Ser Val Leu Gly
260 265 270
His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala
275 280 285
Thr Arg Tyr Gly Val Arg Ala Thr Arg Ser Ala His Arg Gly Glu Phe
290 295 300
Gly Thr Cys Val Ala Leu Lys Gly Glu Arg Ile Glu Asn Ile Thr Leu
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Glu Lys Ala Val Gly Thr Leu Lys Thr Val Pro Met Asp Arg Trp Leu
325 330 335
Thr Ala Gln Ala Met Phe Gly
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<222> (301)..(1632)
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cggacgaaga ggccgccccg atccacaccg cccgcctggc gctggctgcg gccacccgcc 240
agaccctggc caacgcgctc ggcctggtcg gtgtcaccgc cccggagagg atgtaagcgc 300
atg acc tcg gat ttc aac gat ctg ccg gcc cac gtc tgg ccg cgc aac 348
Met Thr Ser Asp Phe Asn Asp Leu Pro Ala His Val Trp Pro Arg Asn
1 5 10 15
gcc gcg cgc cag gag gac ggc gtg gtc acc gtc gcg ggt gtc ccg ctg 396
Ala Ala Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
20 25 30
ccg gag atc gcc gag gag ttc ggt acc ccg gtc ttc gtc gtc gac gag 444
Pro Glu Ile Ala Glu Glu Phe Gly Thr Pro Val Phe Val Val Asp Glu
35 40 45
gac gac ttc cgt tcc cgc tgc cag gac atg gcc cgc gcc ttc ggc ggc 492
Asp Asp Phe Arg Ser Arg Cys Gln Asp Met Ala Arg Ala Phe Gly Gly
50 55 60
ccg gag cac gtc cac tac gcc tcc aag gcg ttc ctc acc cgc acc gtc 540
Pro Glu His Val His Tyr Ala Ser Lys Ala Phe Leu Thr Arg Thr Val
65 70 75 80
gcc cgc tgg gtc gac gag gag ggg ctg tcg ctc gac gtc gcc tcg ctc 588
Ala Arg Trp Val Asp Glu Glu Gly Leu Ser Leu Asp Val Ala Ser Leu
85 90 95
aac gag ctg cgg atc gcg ctg gcc gcc gag ttc ccc gcc gcc cgc atc 636
Asn Glu Leu Arg Ile Ala Leu Ala Ala Glu Phe Pro Ala Ala Arg Ile
100 105 110
acc gcg cac ggc aac aac aag ggc ccg tcc ttc ctg cgg gcg tgc gtc 684
Thr Ala His Gly Asn Asn Lys Gly Pro Ser Phe Leu Arg Ala Cys Val
115 120 125
acc gag ggc gtc ggc cac gtc gtc ctc gac tcc gag cag gag ctc gag 732
Thr Glu Gly Val Gly His Val Val Leu Asp Ser Glu Gln Glu Leu Glu
130 135 140
ctt ctc gac gcc atc gcc gcc ggc gcc ggc gtc atc cag aag gtg atg 780

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Leu Leu Asp Ala Ile Ala Ala Gly Ala Gly Val Ile Gln Lys Val Met
145                 150                 155                 160
atc cgc gtc aag ccg ggc atc gag gcg cac acc cac gag gcc atc gcc        828
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Ala Ile Ala
                165                 170                 175
acg tcc cac gag gac cag aag ttc ggc ttc tcc ctg gcc tcc ggc tcg        876
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
            180                 185                 190
gcg ttc cgc gcc gcg gag gcc gcc gtc cgc gcc gag aac ctc gag ctc        924
Ala Phe Arg Ala Ala Glu Ala Ala Val Arg Ala Glu Asn Leu Glu Leu
        195                 200                 205
gtg ggc ctg cac tgc cac gtc ggc tcc cag gtc ttc gac gcc cgg ggc        972
Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Arg Gly
    210                 215                 220
ttc acg atg gcc gcc gac cgc gtg ctg ggc ctc tac tcg cag atc cac       1020
Phe Thr Met Ala Ala Asp Arg Val Leu Gly Leu Tyr Ser Gln Ile His
225                 230                 235                 240
cgc gaa ctc ggc gtg cag ctg ccc gag ctc gat ctc ggc ggc ggc tac       1068
Arg Glu Leu Gly Val Gln Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
                245                 250                 255
ggc atc gcc tac acc gag gac gag cag ccc ctc aac gtc gac gag gtc       1116
Gly Ile Ala Tyr Thr Glu Asp Glu Gln Pro Leu Asn Val Asp Glu Val
            260                 265                 270
gcc cac gac ctg ctc acc gcc gtg gcc aag acc gcc gcg gag ctg ggc       1164
Ala His Asp Leu Leu Thr Ala Val Ala Lys Thr Ala Ala Glu Leu Gly
        275                 280                 285
atc gac gcc ccc gcc gtc ctc gtc gag ccg ggc cgc gcc atc gcc ggc       1212
Ile Asp Ala Pro Ala Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
    290                 295                 300
ccc ggc acg gtg acg gtc tac gag gtc ggc acc gtc aag gac gtc acc       1260
Pro Gly Thr Val Thr Val Tyr Glu Val Gly Thr Val Lys Asp Val Thr
305                 310                 315                 320
gtc tcc gag gac gag aag cga cgc tac ctc tcc gtc gac ggc ggc atg       1308
Val Ser Glu Asp Glu Lys Arg Arg Tyr Leu Ser Val Asp Gly Gly Met
                325                 330                 335
tcc gac aac atc cgc ccg gcc ctc tac gac gcg ctt tac gac gcc cgc       1356
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Asp Ala Leu Tyr Asp Ala Arg
            340                 345                 350
gtg gtc aac cgt ttc acc gag ggc gag gag atc tcc tcc cgc ctc gtc       1404
Val Val Asn Arg Phe Thr Glu Gly Glu Glu Ile Ser Ser Arg Leu Val
        355                 360                 365
ggt tcc cac tgc gag tcc ggc gac att ctc gtc cgc gac gcg cgc tac       1452
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Val Arg Asp Ala Arg Tyr
    370                 375                 380
ccc gac gac atc gtg gtc ggg gac ctc atg gcc gtc gcc gcg acc ggc       1500
Pro Asp Asp Ile Val Val Gly Asp Leu Met Ala Val Ala Ala Thr Gly
385                 390                 395                 400
gcc tac gcc tac gcc atg tcc tcg cgc tac aac gcc ttc ggc cgt ccg       1548
Ala Tyr Ala Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Gly Arg Pro
                405                 410                 415
ccg gtc gtc gcg gtg cgt gcc ggc aag acg aag ctc atg ctg cgc cgc       1596
Pro Val Val Ala Val Arg Ala Gly Lys Thr Lys Leu Met Leu Arg Arg
            420                 425                 430
gag acc gtc gag gac att ctc gcg ctg gag acg tag aaccgacgcc            1642
Glu Thr Val Glu Asp Ile Leu Ala Leu Glu Thr
        435                 440
cgggcagggc gtcagtggaa gaggcccttg aggctgccgg cgtcctccag cagcgccacg     1702
acgagcgagg tgtggatgga accgagcggc acgcccctgg cgggcgtcgg cgcggtcgac     1762
gggtccgggg tggaggaacg ggtcggcgtc gtggacgact cttcgcggtc gacggtgccg     1822
gaggctcccg tggcgcacat gcgcagctcc gcccggtagg cgtccgcctc cgcctgggct     1882
cccggggtgc gctcccaggc ccgcagccag gcctcgtcgg cggccacgga                1932
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<213>  Corynebacterium humireducens
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1                 5                  10                  15
Ala Ala Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
            20                  25                  30
Pro Glu Ile Ala Glu Glu Phe Gly Thr Pro Val Phe Val Val Asp Glu
        35                  40                  45
Asp Asp Phe Arg Ser Arg Cys Gln Asp Met Ala Arg Ala Phe Gly Gly
    50                  55                  60
Pro Glu His Val His Tyr Ala Ser Lys Ala Phe Leu Thr Arg Thr Val
65                  70                  75                  80
Ala Arg Trp Val Asp Glu Glu Gly Leu Ser Leu Asp Val Ala Ser Leu
                85                  90                  95
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Asn Glu Leu Arg Ile Ala Leu Ala Ala Glu Phe Pro Ala Ala Arg Ile
            100                 105                 110
Thr Ala His Gly Asn Asn Lys Gly Pro Ser Phe Leu Arg Ala Cys Val
        115                 120                 125
Thr Glu Gly Val Gly His Val Val Leu Asp Ser Glu Gln Glu Leu Glu
    130                 135                 140
Leu Leu Asp Ala Ile Ala Ala Gly Ala Gly Val Ile Gln Lys Val Met
145                 150                 155                 160
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Ala Ile Ala
                165                 170                 175
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
            180                 185                 190
Ala Phe Arg Ala Ala Glu Ala Ala Val Arg Ala Glu Asn Leu Glu Leu
        195                 200                 205
Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Arg Gly
    210                 215                 220
Phe Thr Met Ala Ala Asp Arg Val Leu Gly Leu Tyr Ser Gln Ile His
225                 230                 235                 240
Arg Glu Leu Gly Val Gln Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
                245                 250                 255
Gly Ile Ala Tyr Thr Glu Asp Glu Gln Pro Leu Asn Val Asp Glu Val
            260                 265                 270
Ala His Asp Leu Leu Thr Ala Val Ala Lys Thr Ala Ala Glu Leu Gly
        275                 280                 285
Ile Asp Ala Pro Ala Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
    290                 295                 300
Pro Gly Thr Val Thr Val Tyr Glu Val Gly Thr Val Lys Asp Val Thr
305                 310                 315                 320
Val Ser Glu Asp Glu Lys Arg Arg Tyr Leu Ser Val Asp Gly Gly Met
                325                 330                 335
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Asp Ala Leu Tyr Asp Ala Arg
            340                 345                 350
Val Val Asn Arg Phe Thr Glu Gly Glu Glu Ile Ser Ser Arg Leu Val
        355                 360                 365
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Val Arg Asp Ala Arg Tyr
    370                 375                 380
Pro Asp Asp Ile Val Val Gly Asp Leu Met Ala Val Ala Ala Thr Gly
385                 390                 395                 400
Ala Tyr Ala Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Gly Arg Pro
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Pro Val Val Ala Val Arg Ala Gly Lys Thr Lys Leu Met Leu Arg Arg
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Glu Thr Val Glu Asp Ile Leu Ala Leu Glu Thr
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gcgcaacgag gccggcgagc tggtctccgc cggtggccgc gtgctcaaca tcgtgggcgt      180
cggcaagacc ctcgaggagg cgcgtgacga cgcctacgcc accatcgagc agatccagct      240
cgagggttcc ttctaccgcg gcgacatcgc actgccggcc gtggagggac ggatctccct      300
gtg acc ggt cgg cag ctc gtc agc gac cgc ggc cag gtc cag ccc ttc         348
Val Thr Gly Arg Gln Leu Val Ser Asp Arg Gly Gln Val Gln Pro Phe
1               5                   10                  15
cgc gtc atg cag atg ctc gac atc gtg cac cga cgc gcc cgc gag ggg         396
Arg Val Met Gln Met Leu Asp Ile Val His Arg Arg Ala Arg Glu Gly
            20                  25                  30
aag cac acc atc atg ctg tgc gcc ggg cag ccc tcc acg ggt gcc ccg         444
Lys His Thr Ile Met Leu Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro
        35                  40                  45
gcc ccg gtc ctg acc gcg gcg gag gag tcc ctc cac gcc tcg ccc ctc         492
Ala Pro Val Leu Thr Ala Ala Glu Glu Ser Leu His Ala Ser Pro Leu
    50                  55                  60
ggg tac acc gag gtg gtc ggt gac cgc gac ctc cgg gag atc gtc gcg         540
Gly Tyr Thr Glu Val Val Gly Asp Arg Asp Leu Arg Glu Ile Val Ala
65                  70                  75                  80
gcc tgg cac tcc gac acc tac ggc gtg cac acc agc gcg gac aac gtg         588
Ala Trp His Ser Asp Thr Tyr Gly Val His Thr Ser Ala Asp Asn Val
                85                  90                  95
gtg atc acc acc ggc tcc tcc ggt ggc ttc gtc gcg tcc ttc ctg gcc         636
Val Ile Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Leu Ala
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            100                 105                 110
gtg ctc gac cac ggc gac gcc gtc gcc ctg tcc tgc ccc ggt tac ccg      684
Val Leu Asp His Gly Asp Ala Val Ala Leu Ser Cys Pro Gly Tyr Pro
        115                 120                 125
gcg tac cgc aac atc ctg gag tcc ctc ggg gcg cgg gtg gtc aac ctc      732
Ala Tyr Arg Asn Ile Leu Glu Ser Leu Gly Ala Arg Val Val Asn Leu
    130                 135                 140
gtg tgc gac gag tcg acc cgc ttc cag ccg acg gcc gcg atg ctc gag      780
Val Cys Asp Glu Ser Thr Arg Phe Gln Pro Thr Ala Ala Met Leu Glu
145                 150                 155                 160
gca ctg ccg gag gct gac agg ccg cgg gcg gtg atc gtc acc tcc ccg      828
Ala Leu Pro Glu Ala Asp Arg Pro Arg Ala Val Ile Val Thr Ser Pro
                165                 170                 175
ggc aac ccc tcc ggc acg acc atc gac ccc gcg gag ctc gag cgc atc      876
Gly Asn Pro Ser Gly Thr Thr Ile Asp Pro Ala Glu Leu Glu Arg Ile
            180                 185                 190
gcc cgc tgg tgc gag gac aac gac gcc gtg ctc atc tcc gac gag gac      924
Ala Arg Trp Cys Glu Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp
        195                 200                 205
tac cac ggc atg tcc ttc ggc cgc ccc ctg gcc acc gca cgc cag ttc      972
Tyr His Gly Met Ser Phe Gly Arg Pro Leu Ala Thr Ala Arg Gln Phe
    210                 215                 220
tcc gac cgg gcg atc gtc gtg ggc acg ctg tcg aag tac tac tcc atg     1020
Ser Asp Arg Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Tyr Ser Met
225                 230                 235                 240
acc ggc tgg cgc gtc ggc tgg ctc atc ctc ccc gac gag ctg gtc acc     1068
Thr Gly Trp Arg Val Gly Trp Leu Ile Leu Pro Asp Glu Leu Val Thr
                245                 250                 255
ccc gtg gag aac ctg cag gcc tcg ctg gcg ctc tgc ccg ccg gcg atc     1116
Pro Val Glu Asn Leu Gln Ala Ser Leu Ala Leu Cys Pro Pro Ala Ile
            260                 265                 270
tcg cag gtc gcc ggg cgt gcc gcc ttc acc ccg gag gcg cgc gcc gaa     1164
Ser Gln Val Ala Gly Arg Ala Ala Phe Thr Pro Glu Ala Arg Ala Glu
        275                 280                 285
ctc gac tcc cac gtc gag cgc tac cgc gcc gcc cgc gcg gtg ctg ctc     1212
Leu Asp Ser His Val Glu Arg Tyr Arg Ala Ala Arg Ala Val Leu Leu
    290                 295                 300
gag gag ctg ccg gcg gcc ggt ttc acc acc atg gcg gaa ccc gac ggc     1260
Glu Glu Leu Pro Ala Ala Gly Phe Thr Thr Met Ala Glu Pro Asp Gly
305                 310                 315                 320
ggg ctc tac ctg tgg ctc gac gtc tcc cac gtc acc gac gac tcc gag     1308
Gly Leu Tyr Leu Trp Leu Asp Val Ser His Val Thr Asp Asp Ser Glu
                325                 330                 335
gcc tgg tgc cac gag ctc gtc gag gag atc ggc gtg gcc ttc gcg ccg     1356
Ala Trp Cys His Glu Leu Val Glu Glu Ile Gly Val Ala Phe Ala Pro
            340                 345                 350
ggc gtc gac ttc gac ccg atc aac ggt cac aag tgg gtc cgc ctc acg     1404
Gly Val Asp Phe Asp Pro Ile Asn Gly His Lys Trp Val Arg Leu Thr
        355                 360                 365
ctg tgc gcc ccg gag gag gag acc cgc gag gcg atc cgg cgc ctc ggc     1452
Leu Cys Ala Pro Glu Glu Glu Thr Arg Glu Ala Ile Arg Arg Leu Gly
    370                 375                 380
gag tac gtg cgt cgc tga ccgcgcggcg acctgcggcg cgggggaaac             1500
Glu Tyr Val Arg Arg
385
ggcccggatc cggggactcc cgggccaccc ccgccgctgg tcatgcgata atcgggggcg    1560
tggctgagaa gaagaagatc gcgaacgtcc tgtccaaccg ctacgcctcc gcggagctga    1620
gcaacctgtg gagcccggag tacaagatca tcctggagcg tcagctctgg atcgccgtga    1680
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ccgtcatcga ccgggtcgac ctcgagtcga                                     1770
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Arg Val Met Gln Met Leu Asp Ile Val His Arg Arg Ala Arg Glu Gly
            20                  25                  30
Lys His Thr Ile Met Leu Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro
        35                  40                  45
Ala Pro Val Leu Thr Ala Ala Glu Glu Ser Leu His Ala Ser Pro Leu
    50                  55                  60
Gly Tyr Thr Glu Val Val Gly Asp Arg Asp Leu Arg Glu Ile Val Ala
65                  70                  75                  80
Ala Trp His Ser Asp Thr Tyr Gly Val His Thr Ser Ala Asp Asn Val
                85                  90                  95
Val Ile Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Leu Ala
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            100                 105                 110
Val Leu Asp His Gly Asp Ala Val Ala Leu Ser Cys Pro Gly Tyr Pro
        115                 120                 125
Ala Tyr Arg Asn Ile Leu Glu Ser Leu Gly Ala Arg Val Val Asn Leu
    130                 135                 140
Val Cys Asp Glu Ser Thr Arg Phe Gln Pro Thr Ala Ala Met Leu Glu
145                 150                 155                 160
Ala Leu Pro Glu Ala Asp Arg Pro Arg Ala Val Ile Val Thr Ser Pro
                165                 170                 175


Gly Asn Pro Ser Gly Thr Thr Ile Asp Pro Ala Glu Leu Glu Arg Ile
            180                 185                 190
Ala Arg Trp Cys Glu Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp
        195                 200                 205
Tyr His Gly Met Ser Phe Gly Arg Pro Leu Ala Thr Ala Arg Gln Phe
    210                 215                 220
Ser Asp Arg Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Tyr Ser Met
225                 230                 235                 240
Thr Gly Trp Arg Val Gly Trp Leu Ile Leu Pro Asp Glu Leu Val Thr
                245                 250                 255
Pro Val Glu Asn Leu Gln Ala Ser Leu Ala Leu Cys Pro Pro Ala Ile
            260                 265                 270
Ser Gln Val Ala Gly Arg Ala Ala Phe Thr Pro Glu Ala Arg Ala Glu
        275                 280                 285
Leu Asp Ser His Val Glu Arg Tyr Arg Ala Ala Arg Ala Val Leu Leu
    290                 295                 300
Glu Glu Leu Pro Ala Ala Gly Phe Thr Thr Met Ala Glu Pro Asp Gly
305                 310                 315                 320
Gly Leu Tyr Leu Trp Leu Asp Val Ser His Val Thr Asp Asp Ser Glu
                325                 330                 335
Ala Trp Cys His Glu Leu Val Glu Glu Ile Gly Val Ala Phe Ala Pro
            340                 345                 350
Gly Val Asp Phe Asp Pro Ile Asn Gly His Lys Trp Val Arg Leu Thr
        355                 360                 365
Leu Cys Ala Pro Glu Glu Glu Thr Arg Glu Ala Ile Arg Arg Leu Gly
    370                 375                 380
Glu Tyr Val Arg Arg
385
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ccccgtatga tgcgccagtt ctgcggcggt gatgcgtgca ttgttctgga tcagtgacag      180
aatcatgcgg tcaatgtcgt ccatacgccg gattctgtca cacgtgcagt cccggcgtcc      240
cccggtgaat gaaaagttca ggagtatcgg ccgcggcgcc gggcgggcac gataccgggc      300
atg gac atc acg gac ctc ctg agc ttc tgg gcg gtc agc ctc ctg ctg        348
Met Asp Ile Thr Asp Leu Leu Ser Phe Trp Ala Val Ser Leu Leu Leu
1               5                   10                  15
atc gtc acc ccg ggc ccc gac tgg gcg ttc gtg ctc ggg cac gct ttc        396
Ile Val Thr Pro Gly Pro Asp Trp Ala Phe Val Leu Gly His Ala Phe
            20                  25                  30
cga cgc cgc ccc ctc gcc ccg ccc ctt ctc ggc atc ggc ctg ggc tac        444
Arg Arg Arg Pro Leu Ala Pro Pro Leu Leu Gly Ile Gly Leu Gly Tyr
        35                  40                  45
ctc ggc ctg acc acc gtg gtg gcc ggc ggc ctc ggg gcg ctc gtg gcc        492
Leu Gly Leu Thr Thr Val Val Ala Gly Gly Leu Gly Ala Leu Val Ala
    50                  55                  60
cgt cac ccc gcg ctg ctc acg ctc gtc acc gtc gcc ggt gtc ctg gtg        540
Arg His Pro Ala Leu Leu Thr Leu Val Thr Val Ala Gly Val Leu Val
65                  70                  75                  80
ctc ctg cgt ctc ggc tgg cag atg atg cgc gcg gcg ctg gcc ggg ccc        588
Leu Leu Arg Leu Gly Trp Gln Met Met Arg Ala Ala Leu Ala Gly Pro
                85                  90                  95
gtc acg gtg gag gtg gac acc gcg gac ccg gct gtc ccg gag ggg ccg        636
Val Thr Val Glu Val Asp Thr Ala Asp Pro Ala Val Pro Glu Gly Pro
            100                 105                 110
gcc ggc ggg gga gtg gcg acg ctg acg cgc ccg cag gtg ggc gtc gag        684
Ala Gly Gly Gly Val Ala Thr Leu Thr Arg Pro Gln Val Gly Val Glu
        115                 120                 125
aag cac gcg gtg gtc acc ggg gcc gcg gtg agt ggc ctc aac ccc aag        732
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Lys His Ala Val Val Thr Gly Ala Ala Val Ser Gly Leu Asn Pro Lys
    130                 135                 140
ggg ctc atg ctg ttc atc gcg ctg ctg ccc cag ttc gtg ggc gcg gag        780
Gly Leu Met Leu Phe Ile Ala Leu Leu Pro Gln Phe Val Gly Ala Glu
145                 150                 155                 160
gcg acg tgg ccg gtg tgg acg cag atg ttc gtc ctc gga ctg gtg ttc        828
Ala Thr Trp Pro Val Trp Thr Gln Met Phe Val Leu Gly Leu Val Phe
                165                 170                 175
atc gcc tcg gcg acc gtg ttc tac gcg ctg ctc ggc gtt ttc gcc ggg        876
Ile Ala Ser Ala Thr Val Phe Tyr Ala Leu Leu Gly Val Phe Ala Gly
            180                 185                 190
cgg gtg ctg gcg ggc tcg gag cgg gcc tcc cgg atc ctc acc ggc gtg        924
Arg Val Leu Ala Gly Ser Glu Arg Ala Ser Arg Ile Leu Thr Gly Val
        195                 200                 205
gcc ggc ggg gcg atg atg tgt gtc gcg gca ggg atg ctc gcg cag cac        972
Ala Gly Gly Ala Met Met Cys Val Ala Ala Gly Met Leu Ala Gln His
    210                 215                 220
ctc ctc tga tgggggtagt tgagtagggg cattcatcgg gtgcgagttc             1021
Leu Leu
225
cgcgcctccc gatgaatgcc cctgctcgga taccctccta ctccacgtgc gccggcgtcg   1081
acggcgacac cagcggcatc ggcgcgtact cggcacgcag ctcgcgcagc ttccgggcgt   1141
gctcggagag gcggacgtcc tcggtggtac gggggacgaa ctggcgggcg ggcagggcgt   1201
tgccgtcggc gtccgtcgcc aggtaggtga cggtggcgtg gatggcggtc tgcaggttct   1261
cgcggccccc gcgcgggttg                                              1281
<210>  168
<211>  226
<212>  PRT
<213>  Corynebacterium humireducens
<400>  168
Met Asp Ile Thr Asp Leu Leu Ser Phe Trp Ala Val Ser Leu Leu Leu
1               5                   10                  15
Ile Val Thr Pro Gly Pro Asp Trp Ala Phe Val Leu Gly His Ala Phe
            20                  25                  30
Arg Arg Arg Pro Leu Ala Pro Pro Leu Leu Gly Ile Gly Leu Gly Tyr
        35                  40                  45
Leu Gly Leu Thr Thr Val Val Ala Gly Gly Leu Gly Ala Leu Val Ala
    50                  55                  60
Arg His Pro Ala Leu Leu Thr Leu Val Thr Val Ala Gly Val Leu Val
65                  70                  75                  80
Leu Leu Arg Leu Gly Trp Gln Met Met Arg Ala Ala Leu Ala Gly Pro
                85                  90                  95
Val Thr Val Glu Val Asp Thr Ala Asp Pro Ala Val Pro Glu Gly Pro
            100                 105                 110
Ala Gly Gly Gly Val Ala Thr Leu Thr Arg Pro Gln Val Gly Val Glu
        115                 120                 125
Lys His Ala Val Val Thr Gly Ala Ala Val Ser Gly Leu Asn Pro Lys
    130                 135                 140
Gly Leu Met Leu Phe Ile Ala Leu Leu Pro Gln Phe Val Gly Ala Glu
145                 150                 155                 160
Ala Thr Trp Pro Val Trp Thr Gln Met Phe Val Leu Gly Leu Val Phe
                165                 170                 175
Ile Ala Ser Ala Thr Val Phe Tyr Ala Leu Leu Gly Val Phe Ala Gly
            180                 185                 190
Arg Val Leu Ala Gly Ser Glu Arg Ala Ser Arg Ile Leu Thr Gly Val
        195                 200                 205
Ala Gly Gly Ala Met Met Cys Val Ala Ala Gly Met Leu Ala Gln His
    210                 215                 220
Leu Leu
225
<210>  169
<211>  1347
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1047)
<223>  gen dapB
<400>  169
ccggtgccga aggagtcgag ccaggtgcgc agggagttgc ggttgactcc gagatcggag     60
gcgatcgcgt tgatcgttgc tccgggagtc gactcgtaca acgccactgc gtcacgcttg    120
aactgctcgg tgtaggtctt gcgtggcatg gtggaaaggt acctcacttc cccagcgaaa    180
tgctggtttc agcgtgtcca ccatcaaggg gtcaggtccg ctggtgatgt tgatgcgcat    240
gcaacgattc tatgcgccta gactggggca ctgaatcttt caggaactca aggaggaacc    300
atg gcg atc aag gtg gga gtg ctc ggc gcg aag ggc cgt gtc ggc tcg      348
Met Ala Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Ser
1               5                   10                  15
gcg gtg tgc gag ggc gtc aac ggg gcg gag ggc ctc gag ctc gtc gcg      396
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```
Ala Val Cys Glu Gly Val Asn Gly Ala Glu Gly Leu Glu Leu Val Ala
            20                  25                  30
cag gtc gat cag gac gat gac ctg cag ctg ctt ctc gac gcc ggg gcg        444
Gln Val Asp Gln Asp Asp Asp Leu Gln Leu Leu Leu Asp Ala Gly Ala
        35                  40                  45
gag gtc gtc gtc gac ttc acc act ccg ggt tcc gtg atg ggc aac ctg        492
Glu Val Val Val Asp Phe Thr Thr Pro Gly Ser Val Met Gly Asn Leu
    50                  55                  60
gag ttc tgc atc gcc aac ggc atc cac gcg gtg gtc ggc acc acc ggc        540
Glu Phe Cys Ile Ala Asn Gly Ile His Ala Val Val Gly Thr Thr Gly
65                  70                  75                  80

ttc gac gag gag cgc ctc gcg cag gtc cgt gag tgg tgt gcc gcc gag        588
Phe Asp Glu Glu Arg Leu Ala Gln Val Arg Glu Trp Cys Ala Ala Glu
                85                  90                  95
ggg gcg ggc aac gtc ctc atc gcc ccg aac ttc gcg atc tct gca gtg        636
Gly Ala Gly Asn Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
            100                 105                 110
ctg gcc atg gag ttc gcg cgg cag gcc gcc cgc ttc ttc gac tcc gcc        684
Leu Ala Met Glu Phe Ala Arg Gln Ala Ala Arg Phe Phe Asp Ser Ala
        115                 120                 125
gag gtc gtc gag tac cac cac ccc tac aag ctg gac gcc ccc tcc ggc        732
Glu Val Val Glu Tyr His His Pro Tyr Lys Leu Asp Ala Pro Ser Gly
    130                 135                 140
acc gcg atc cac acc gcg cag ggc atc gcc gcc gcc cgc cgg gag gcc        780
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Arg Glu Ala
145                 150                 155                 160
ggc ctc ggc ccc atc ccg gat gcc acc gag cag acc ctc gag ggt gcc        828
Gly Leu Gly Pro Ile Pro Asp Ala Thr Glu Gln Thr Leu Glu Gly Ala
                165                 170                 175
cgc ggc gcc gac gtc gac ggc gtg cgt gtc cac ggc gtg cgc atg acc        876
Arg Gly Ala Asp Val Asp Gly Val Arg Val His Gly Val Arg Met Thr
            180                 185                 190
ggc atg gtc gcc cac gag gac atc atc ttc ggt gcc cag ggc cag tcc        924
Gly Met Val Ala His Glu Asp Ile Ile Phe Gly Ala Gln Gly Gln Ser
        195                 200                 205
ctg acc atc cgc cag gac tcc tac gac cgc acc tcc ttc gtg ccg ggc        972
Leu Thr Ile Arg Gln Asp Ser Tyr Asp Arg Thr Ser Phe Val Pro Gly
    210                 215                 220
gtg ctc ctc ggt gtc cgt gag atc gcg aac cac gac ggc ctg acc gtg       1020
Val Leu Leu Gly Val Arg Glu Ile Ala Asn His Asp Gly Leu Thr Val
225                 230                 235                 240
ggg ctc gac agc tac ctg gga ctc tag atggccaagc ccgtcgacct             1067
Gly Leu Asp Ser Tyr Leu Gly Leu
                245

ggacgtccag ctcatcgcgg ccacgcagtt caccccgccc gccggggtcg actgggaggc     1127
cgacgacacc gccaccggcg ccgaggcgct cgtcgagttc gcgggccgcg cctgctacga     1187
gaccttcgac aaacccaacc cgcgcaccgc ggccaacgac gcctacctcc gccacatcat     1247
ggaggtcgga cacaccgcac tgctcgagca cgccaccgcg acgctctaca tccgcggcat     1307
ctcccgctcc gccacccacg agctggtccg ccaccgcaac                           1347
<210>  170
<211>  248
<212>  PRT
<213>  Corynebacterium humireducens
<400>  170
Met Ala Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Ser
1               5                   10                  15
Ala Val Cys Glu Gly Val Asn Gly Ala Glu Gly Leu Glu Leu Val Ala
            20                  25                  30
Gln Val Asp Gln Asp Asp Asp Leu Gln Leu Leu Leu Asp Ala Gly Ala
        35                  40                  45
Glu Val Val Val Asp Phe Thr Thr Pro Gly Ser Val Met Gly Asn Leu
    50                  55                  60
Glu Phe Cys Ile Ala Asn Gly Ile His Ala Val Val Gly Thr Thr Gly
65                  70                  75                  80
Phe Asp Glu Glu Arg Leu Ala Gln Val Arg Glu Trp Cys Ala Ala Glu
                85                  90                  95
Gly Ala Gly Asn Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
            100                 105                 110
Leu Ala Met Glu Phe Ala Arg Gln Ala Ala Arg Phe Phe Asp Ser Ala
        115                 120                 125
Glu Val Val Glu Tyr His His Pro Tyr Lys Leu Asp Ala Pro Ser Gly
    130                 135                 140
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Arg Glu Ala
145                 150                 155                 160
Gly Leu Gly Pro Ile Pro Asp Ala Thr Glu Gln Thr Leu Glu Gly Ala
                165                 170                 175
Arg Gly Ala Asp Val Asp Gly Val Arg Val His Gly Val Arg Met Thr
```

```
            180                 185                 190
Gly Met Val Ala His Glu Asp Ile Ile Phe Gly Ala Gln Gly Gln Ser
        195                 200                 205
Leu Thr Ile Arg Gln Asp Ser Tyr Asp Arg Thr Ser Phe Val Pro Gly
    210                 215                 220
Val Leu Leu Gly Val Arg Glu Ile Ala Asn His Asp Gly Leu Thr Val
225                 230                 235                 240
Gly Leu Asp Ser Tyr Leu Gly Leu
                245
<210>  171
<211>  2145
<212>  AND
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1845)
<223>  gen glucoza-6-phosphat dehydrogenaza

<400>  171
cgaccctcta cgtcaccgag ctggccggcc cggagaccgt caacaccatg ccggagccga      60
ccatcgacgc cgtgctcgag cagggtggcc tccacggcga caccctgagc ggcaccgcgg     120
acgacgcgca ggccgtcttc gagcagctgg tgcaggtcgg catcgacatg gaggacgtct     180
tcgcggtgct ggagcgcgag ggcgtcgaga agttcgtgtc ctcctggtcc gagctgctcg     240
actccatgga gtcccgactg cgctagcagt cccctccccg acaggaaagg acctgagcgc     300
atg ccc ctc ccc gtg acc ggc acc gac gcc tgg atc aac ccg ctg cgg        348
Met Pro Leu Pro Val Thr Gly Thr Asp Ala Trp Ile Asn Pro Leu Arg
1               5                   10                  15
aac acc gtc gac aag cgg ctg ccc cgc atc gcc ggc ccc tcc ggc atg        396
Asn Thr Val Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met
            20                  25                  30
gtg atc ttc ggc gtg acc ggt gac ctg gcc cgc aag aag ctg ctc ccg        444
Val Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro
        35                  40                  45
gcc atc tac gac ctg gcc aac cgt ggc ctc ctg ccg gcc ggt ttc acc        492
Ala Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Ala Gly Phe Thr
    50                  55                  60
ctc atc ggt ttc ggc cgt cgt ccc tgg agc aaa ccc gag ttc gag gag        540
Leu Ile Gly Phe Gly Arg Arg Pro Trp Ser Lys Pro Glu Phe Glu Glu
65                  70                  75                  80
tac gtg cgg gag gcc gtc gag agc ggc gcc cgc acc gag ttc cgc gaa        588
Tyr Val Arg Glu Ala Val Glu Ser Gly Ala Arg Thr Glu Phe Arg Glu
                85                  90                  95
cac gtg tgg gag cgg ctg gcc gag ggc atg cac ttc gtc gag ggc aac        636
His Val Trp Glu Arg Leu Ala Glu Gly Met His Phe Val Glu Gly Asn
            100                 105                 110
ttc gac gac gag ggc ttc gac cgc ctc gcc gcc acc ctc gcc gag atg        684
Phe Asp Asp Glu Gly Phe Asp Arg Leu Ala Ala Thr Leu Ala Glu Met
        115                 120                 125
gac acc tcc cgc ggc acg gcg ggc aac tgg gcc ttc tac ctg tcg gtc        732
Asp Thr Ser Arg Gly Thr Ala Gly Asn Trp Ala Phe Tyr Leu Ser Val
    130                 135                 140
ccg ccg gac ttc ttc acc gcc gtc tgc cac cag ctg gag cgc tcc ggc        780
Pro Pro Asp Phe Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
145                 150                 155                 160
ctg gcg gag gcc ggt gag gag tcg tgg cgt cgc gtg atc atc gag aag        828
Leu Ala Glu Ala Gly Glu Glu Ser Trp Arg Arg Val Ile Ile Glu Lys
                165                 170                 175
ccc ttc ggc cac gac cag gac acg gcc cgg gag ctc aac cgg gtg gtc        876
Pro Phe Gly His Asp Gln Asp Thr Ala Arg Glu Leu Asn Arg Val Val
            180                 185                 190
aac gcc gtc ttc ccg gag gag tcg gtg ttc cgc atc gac cac tac ctg        924
Asn Ala Val Phe Pro Glu Glu Ser Val Phe Arg Ile Asp His Tyr Leu
        195                 200                 205
ggc aag gag acg gtg cag aac atc ctg gcg ctg cgc ttc gcc aac cag        972
Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
    210                 215                 220
ctc ttc gac ccg atc tgg aac gcg cac tac gtc gac cac gtg cag atc       1020
Leu Phe Asp Pro Ile Trp Asn Ala His Tyr Val Asp His Val Gln Ile
225                 230                 235                 240
acc atg gcc gag gac atc ggt ctc ggt ggt cgg gcc ggc tac tac gac       1068
Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
                245                 250                 255
ggc atc ggc gcc gcc cgc gac gtc atg cag aac cac ctc ctc cag ctc       1116
Gly Ile Gly Ala Ala Arg Asp Val Met Gln Asn His Leu Leu Gln Leu
            260                 265                 270
ctg gcg ctg gtg gcc atg gag gag ccc atc gcc ttc gac ccg gct gag       1164
Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ala Phe Asp Pro Ala Glu
        275                 280                 285
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ctg cag gcg gag aag gtc aag gtc ctg cgc gcg acc aac ccc gtc ttc      1212
Leu Gln Ala Glu Lys Val Lys Val Leu Arg Ala Thr Asn Pro Val Phe
    290                 295                 300
ccg ctg aac aag acc acc gcc cgt ggc cag tac gcg gcg ggc tgg cag      1260
Pro Leu Asn Lys Thr Thr Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
305                 310                 315                 320
ggc tcg cac aag gtg cgt ggc ctg cgt gag gag gag ggt ttc gac ccg      1308
Gly Ser His Lys Val Arg Gly Leu Arg Glu Glu Glu Gly Phe Asp Pro
                325                 330                 335
gac tcc acc acg gag acc tac gcc gcc tgc acc ctg gag atc aac tcc      1356
Asp Ser Thr Thr Glu Thr Tyr Ala Ala Cys Thr Leu Glu Ile Asn Ser
            340                 345                 350

cgc cgc tgg gcg ggc gtg ccc ttc tac ctg cgg acc ggc aag cgc ctg      1404
Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
        355                 360                 365
ggg cgc cgc gtc acg gag atc gcc ctc gtg ttc aag gag gcg ccg cac      1452
Gly Arg Arg Val Thr Glu Ile Ala Leu Val Phe Lys Glu Ala Pro His
    370                 375                 380
cag ccc ttc ctc gag ggg cag acg tcc tcg ctg ggg cag aac gcg atc      1500
Gln Pro Phe Leu Glu Gly Gln Thr Ser Ser Leu Gly Gln Asn Ala Ile
385                 390                 395                 400
gtc atc cgc gtc cag ccc gac gag ggc gtg ctc atg cgc ttc ggc tcc      1548
Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Met Arg Phe Gly Ser
                405                 410                 415
aag gtg ccc ggc tcc gcg atg gag gtc cgt gac gtc aac atg gac ttc      1596
Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
            420                 425                 430
tcc tac gcg gag gcc ttc acc gag gcg tcc ccg gag gcc tat gag cgg      1644
Ser Tyr Ala Glu Ala Phe Thr Glu Ala Ser Pro Glu Ala Tyr Glu Arg
        435                 440                 445
ctc atc ctc gat gcg ctt ctc gac gag tcc tcg ctc ttc ccc acc aac      1692
Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
    450                 455                 460
gag gag gtc gag ctc tcc tgg gcg atc ctg gac ccg atc ctc gag ttc      1740
Glu Glu Val Glu Leu Ser Trp Ala Ile Leu Asp Pro Ile Leu Glu Phe
465                 470                 475                 480
tgg gct gag aag ggc cag ccc gag gag tac gag tcc ggc acc tgg ggg      1788
Trp Ala Glu Lys Gly Gln Pro Glu Glu Tyr Glu Ser Gly Thr Trp Gly
                485                 490                 495
ccc gcc tcc gcc gac cgc atg ctg gaa cgg acc ggc cgc gcc tgg cgc      1836
Pro Ala Ser Ala Asp Arg Met Leu Glu Arg Thr Gly Arg Ala Trp Arg
            500                 505                 510
cgc ccc tga cctggaaggg acccgacttg aagatcgaac tgccggacac              1885
Arg Pro

cgacacccgg aacatcgccg ccagcctgct cgaggcccgg gagcacaact cccagaccac     1945
cgggcgggtg ctcaccctca tcgtcgtcgc cgcgctcgac gacgacgtcg accacatcat     2005
ctccgtcacc cgcgacgcct cccacgagca ccccgcccgt gtgctggtgc tgctcaccgg     2065
ccgggaggac gctgactcgc gtctcgacgc cgaggtgcgc gtcggcggtc acgccggcgc     2125
ctcggagatg gtcatcatgc                                                2145
<210>  172
<211>  514
<212>  PRT
<213>  Corynebacterium humireducens
<400>  172
Met Pro Leu Pro Val Thr Gly Thr Asp Ala Trp Ile Asn Pro Leu Arg
1               5                   10                  15
Asn Thr Val Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met
            20                  25                  30
Val Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro
        35                  40                  45
Ala Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Ala Gly Phe Thr
    50                  55                  60
Leu Ile Gly Phe Gly Arg Arg Pro Trp Ser Lys Pro Glu Phe Glu Glu
65                  70                  75                  80
Tyr Val Arg Glu Ala Val Glu Ser Gly Ala Arg Thr Glu Phe Arg Glu
                85                  90                  95
His Val Trp Glu Arg Leu Ala Glu Gly Met His Phe Val Glu Gly Asn
            100                 105                 110
Phe Asp Asp Glu Gly Phe Asp Arg Leu Ala Ala Thr Leu Ala Glu Met
        115                 120                 125
Asp Thr Ser Arg Gly Thr Ala Gly Asn Trp Ala Phe Tyr Leu Ser Val
    130                 135                 140
Pro Pro Asp Phe Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
145                 150                 155                 160
Leu Ala Glu Ala Gly Glu Glu Ser Trp Arg Arg Val Ile Ile Glu Lys
                165                 170                 175
```

```
Pro Phe Gly His Asp Gln Asp Thr Ala Arg Glu Leu Asn Arg Val Val
            180                 185                 190
Asn Ala Val Phe Pro Glu Glu Ser Val Phe Arg Ile Asp His Tyr Leu
        195                 200                 205
Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
    210                 215                 220
Leu Phe Asp Pro Ile Trp Asn Ala His Tyr Val Asp His Val Gln Ile
225                 230                 235                 240
Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
                245                 250                 255
Gly Ile Gly Ala Ala Arg Asp Val Met Gln Asn His Leu Leu Gln Leu
            260                 265                 270
Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ala Phe Asp Pro Ala Glu
        275                 280                 285
Leu Gln Ala Glu Lys Val Lys Val Leu Arg Ala Thr Asn Pro Val Phe
    290                 295                 300
Pro Leu Asn Lys Thr Thr Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
305                 310                 315                 320
Gly Ser His Lys Val Arg Gly Leu Arg Glu Glu Glu Gly Phe Asp Pro
                325                 330                 335
Asp Ser Thr Thr Glu Thr Tyr Ala Ala Cys Thr Leu Glu Ile Asn Ser
            340                 345                 350
Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
        355                 360                 365
Gly Arg Arg Val Thr Glu Ile Ala Leu Val Phe Lys Glu Ala Pro His
    370                 375                 380
Gln Pro Phe Leu Glu Gly Gln Thr Ser Ser Leu Gly Gln Asn Ala Ile
385                 390                 395                 400
Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Met Arg Phe Gly Ser
                405                 410                 415
Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
            420                 425                 430
Ser Tyr Ala Glu Ala Phe Thr Glu Ala Ser Pro Glu Ala Tyr Glu Arg
        435                 440                 445
Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
    450                 455                 460
Glu Glu Val Glu Leu Ser Trp Ala Ile Leu Asp Pro Ile Leu Glu Phe
465                 470                 475                 480
Trp Ala Glu Lys Gly Gln Pro Glu Glu Tyr Glu Ser Gly Thr Trp Gly
                485                 490                 495
Pro Ala Ser Ala Asp Arg Met Leu Glu Arg Thr Gly Arg Ala Trp Arg
            500                 505                 510
Arg Pro
<210>  173
<211>  2055
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1755)
<223>  gen gnd
<400>  173
aaggctgccc acggactcgg ccagcgcgca gaacacgccc ccgttgacca ggccgacggg       60
ctgccggtgc tggtccccca cctcgaggcg ggcgcggacg cggccgtcgg cgatctgcgt      120
gtagacgatc ccgaggtggg cgtcgaggcc gacgttgcgg tcgttgagct gcgcgagctg      180
cgcggcgtcg agggccttgc ctgtcccggc gaggcggaag aggtcggtga aactgtaggt      240
ctcggtcatg agtgccgact ctactgaccc ttcgaaaatg gtgtgtctaa actctgtgcc      300
atg acc tcc cct gag aat ctc gcc cag atc ggc gtc gtc gga ctc gcc        348
Met Thr Ser Pro Glu Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
1               5                   10                  15
gtc atg ggt tcc aac ctg gcc cgc aac ttc gcc cgc aac ggc cac acc        396
Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly His Thr
            20                  25                  30
gtc gcc gtg tac aac cgt tcc ccc gag aag acc cgc gac ctc atc gcc        444
Val Ala Val Tyr Asn Arg Ser Pro Glu Lys Thr Arg Asp Leu Ile Ala
        35                  40                  45
gag cac ggt gac gag ggc acc ttc ctc gcc tcc gag acc gtc gag gac        492
Glu His Gly Asp Glu Gly Thr Phe Leu Ala Ser Glu Thr Val Glu Asp
    50                  55                  60
ttc gtc gcc tcc ctc gag cgc ccg cgt aag gcg atc atc atg gtc cag        540
Phe Val Ala Ser Leu Glu Arg Pro Arg Lys Ala Ile Ile Met Val Gln
65                  70                  75                  80
gcc ggc gcg gcc acc gac gcg gtg atc aac cag ctg gcc gac gcc atg        588
Ala Gly Ala Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
                85                  90                  95
gag gac ggc gac atc atc atc gac ggc ggc aac gcc ctc tac agc gac        636
Glu Asp Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Ser Asp
            100                 105                 110
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```
acc atc cgc cgg gag cgg gag atg gcc gag cgc aac cgt cac ttc gtc        684
Thr Ile Arg Arg Glu Arg Glu Met Ala Glu Arg Asn Arg His Phe Val
        115                 120                 125
ggc gcc ggc atc tcc ggc ggc gag gag ggg gcc ctc aac ggc ccg tcg        732
Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
    130                 135                 140
atc atg ccg ggt ggc ccg aag gag tcc tgg gag acc ctc ggc ccg ctg        780
Ile Met Pro Gly Gly Pro Lys Glu Ser Trp Glu Thr Leu Gly Pro Leu
145                 150                 155                 160
ctg gag tcc gtc gct gcc gtc gtc gac ggc acc ccg tgt gtc acg cac        828
Leu Glu Ser Val Ala Ala Val Val Asp Gly Thr Pro Cys Val Thr His
                165                 170                 175
atc ggc ccg gac ggt gcg ggc cac ttc gtc aag atg gtc cac aac ggc        876
Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
            180                 185                 190

atc gag tac gcc gac atg cag gtc atc ggc gag gcg tac cag ctg ctg        924
Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr Gln Leu Leu
        195                 200                 205
cgc tac ggc gcg ggc atg agc ccg gcc gag atc tcc gag gtc ttc cgc        972
Arg Tyr Gly Ala Gly Met Ser Pro Ala Glu Ile Ser Glu Val Phe Arg
    210                 215                 220
gag tgg aac tcc ggc gac ctc gac tcc tac ctc atc gag atc acc gcc       1020
Glu Trp Asn Ser Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
225                 230                 235                 240
gag gtc ctc gcg cag gtc gac gcc gag acg ggg aag ccg ctc atc gac       1068
Glu Val Leu Ala Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
                245                 250                 255
gtc atc gtc gac gcc ggc cag aag ggc acc ggc cgc tgg acc gtc        1116
Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
            260                 265                 270
aag gcc gcc ctc gac ctg ggc atc ccg gtc acc ggc atc ggc gag gcc       1164
Lys Ala Ala Leu Asp Leu Gly Ile Pro Val Thr Gly Ile Gly Glu Ala
        275                 280                 285
gtc ttc gcc cgc gcc ctg tcc tcc tcc ctc gag cag cgt gcc gcc gcg       1212
Val Phe Ala Arg Ala Leu Ser Ser Ser Leu Glu Gln Arg Ala Ala Ala
    290                 295                 300
cag ggc gtg ctg ccc gcc ggt gag ctc gcc acc ttc gag tcc ctg ggt       1260
Gln Gly Val Leu Pro Ala Gly Glu Leu Ala Thr Phe Glu Ser Leu Gly
305                 310                 315                 320
ctg gac cgc gac gcc ttc atc gag gac gtc cgc cgc gcc ctc tac gcc       1308
Leu Asp Arg Asp Ala Phe Ile Glu Asp Val Arg Arg Ala Leu Tyr Ala
                325                 330                 335
tcc aag ctg gtc gcc tac gcg cag ggc ttc gac gag atc cgg gcc ggc       1356
Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Arg Ala Gly
            340                 345                 350
tcc gcc gag cac gcc tgg gac gtc gac ccc cgc gac ctg gcc acc atc       1404
Ser Ala Glu His Ala Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
        355                 360                 365
tgg cgg ggc ggc tgc atc atc cgc gcc aag ttc ctc aac cgc atc gtc       1452
Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
    370                 375                 380
gag gcc tac gac gcc gac ccg cag ctg ccg tcc ctg ctt ctc gac gcc       1500
Glu Ala Tyr Asp Ala Asp Pro Gln Leu Pro Ser Leu Leu Leu Asp Ala
385                 390                 395                 400
tac ttc ctc gac gag ctg cgc gac ctc atc gac tcc tgg cgt cgc gtc       1548
Tyr Phe Leu Asp Glu Leu Arg Asp Leu Ile Asp Ser Trp Arg Arg Val
                405                 410                 415
atc gtc gcc gcc acc cag ctg ggc ctg ccg gtg ccg gtg ttc gcg tcc       1596
Ile Val Ala Ala Thr Gln Leu Gly Leu Pro Val Pro Val Phe Ala Ser
            420                 425                 430
tcc ctg tcc tac tac gac tcg ctg cgc gcc gag cgt ctg ccg gcc gcc       1644
Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
        435                 440                 445
gtg atc cag ggc cag cgt gac tac ttc ggt gcg cac acc tac ggg cgc       1692
Val Ile Gln Gly Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Gly Arg
    450                 455                 460
gtc gac aag ccg ggt gcc ttc cac acc ctg tgg tcc ggg gac cgc agc       1740
Val Asp Lys Pro Gly Ala Phe His Thr Leu Trp Ser Gly Asp Arg Ser
465                 470                 475                 480
gag atc gag gtg taa tgcccgtgtg ggcgaggatc tcccgtttcc tgccggcggc       1795
Glu Ile Glu Val

ggccatcgtg gtggtgaccg ccagggcagt gcaggaggtc cttgcccacg ggcagtgggc     1855
ggtgtggcgg ctgtcgcggc gggagacccg cctgttcgtc gaggtattcc ggacggtgct     1915
gggcctgttc ctcgtcgtcg gcctcacccg ggtggtcgcc gcgcctccct cccccacgga     1975
actggccgga tgggcgctca ccttggggtt cctgtggatc ctcaccctca cggagacgga     2035
acccggcccc gaccccgagc                                                 2055
```

<210> 174
<211> 484
<212> PRT
<213> Corynebacterium humireducens
<400> 174

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Met Thr Ser Pro Glu Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
1               5                  10                  15
Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly His Thr
            20                  25                  30
Val Ala Val Tyr Asn Arg Ser Pro Glu Lys Thr Arg Asp Leu Ile Ala
        35                  40                  45
Glu His Gly Asp Glu Gly Thr Phe Leu Ala Ser Glu Thr Val Glu Asp
    50                  55                  60
Phe Val Ala Ser Leu Glu Arg Pro Arg Lys Ala Ile Ile Met Val Gln
65                  70                  75                  80

Ala Gly Ala Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
                85                  90                  95
Glu Asp Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Ser Asp
            100                 105                 110
Thr Ile Arg Arg Glu Arg Glu Met Ala Glu Arg Asn Arg His Phe Val
        115                 120                 125
Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
    130                 135                 140
Ile Met Pro Gly Gly Pro Lys Glu Ser Trp Glu Thr Leu Gly Pro Leu
145                 150                 155                 160
Leu Glu Ser Val Ala Ala Val Val Asp Gly Thr Pro Cys Val Thr His
                165                 170                 175
Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
            180                 185                 190
Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr Gln Leu Leu
        195                 200                 205
Arg Tyr Gly Ala Gly Met Ser Pro Ala Glu Ile Ser Glu Val Phe Arg
    210                 215                 220
Glu Trp Asn Ser Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
225                 230                 235                 240
Glu Val Leu Ala Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
                245                 250                 255
Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
            260                 265                 270
Lys Ala Ala Leu Asp Leu Gly Ile Pro Val Thr Gly Ile Gly Glu Ala
        275                 280                 285
Val Phe Ala Arg Ala Leu Ser Ser Ser Leu Glu Gln Arg Ala Ala Ala
    290                 295                 300
Gln Gly Val Leu Pro Ala Gly Glu Leu Ala Thr Phe Glu Ser Leu Gly
305                 310                 315                 320
Leu Asp Arg Asp Ala Phe Ile Glu Asp Val Arg Arg Ala Leu Tyr Ala
                325                 330                 335
Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Arg Ala Gly
            340                 345                 350
Ser Ala Glu His Ala Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
        355                 360                 365
Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
    370                 375                 380
Glu Ala Tyr Asp Ala Asp Pro Gln Leu Pro Ser Leu Leu Leu Asp Ala
385                 390                 395                 400
Tyr Phe Leu Asp Glu Leu Arg Asp Leu Ile Asp Ser Trp Arg Arg Val
                405                 410                 415
Ile Val Ala Ala Thr Gln Leu Gly Leu Pro Val Pro Val Phe Ala Ser
            420                 425                 430
Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
        435                 440                 445
Val Ile Gln Gly Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Gly Arg
    450                 455                 460
Val Asp Lys Pro Gly Ala Phe His Thr Leu Trp Ser Gly Asp Arg Ser
465                 470                 475                 480
Glu Ile Glu Val
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<210> 175
<211> 2103
<212> ADN
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1803)
<223> gen mqo
<400> 175

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cgagaatgtc ctcataccag tcggagaagg cgggaacgct catgatgacc acactagtgg      60
gggtacgggg gcaggggcg ggggagtgag gggcgtcgat aagttcgtgt tttccggacc      120
ttcgtcacac ccccgtgaac ctaaggcgta aggttgatgt ttaccggaca aggggagcgg      180
atctgtgccg aggacgtcag agtccgcacc cggaattgtc ctgcccaccg ggagtagtgc      240
cgacacccgg tgtgggccat gactggccag aaccttcgac gacgaatgag gtaatgcaag      300
gtg tcc acc gaa aac aag aac gct ccc aag gtc act gac gag gtc gat         348
Val Ser Thr Glu Asn Lys Asn Ala Pro Lys Val Thr Asp Glu Val Asp
1               5                  10                  15
gtc gcc ctc gtc ggc gcg ggt gtc atg agc gcc acc ctg ggt gcg atg         396
Val Ala Leu Val Gly Ala Gly Val Met Ser Ala Thr Leu Gly Ala Met
            20                  25                  30
atc cgc gag ctc gag ccg agc tgg tcc cag atg atc ttc gag cgc ctg         444
Ile Arg Glu Leu Glu Pro Ser Trp Ser Gln Met Ile Phe Glu Arg Leu
        35                  40                  45
gac ggc ccc gcc cag gag tcc tcc tcc ccg tgg aac aac gcc ggt acc         492
Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
    50                  55                  60
ggc cac tcc gca ctc tgc gag ctg aac tac acc ccc gag gtc aac ggc         540
Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Asn Gly
65                  70                  75                  80
aag atc gag gtg gcc aag gcc atc ggc atc aac gag aag ttc cag gtc         588
Lys Ile Glu Val Ala Lys Ala Ile Gly Ile Asn Glu Lys Phe Gln Val
                85                  90                  95
tcc cgc cag ttc tgg tcc cac cag atc gac cac ggc gtg ctg gac gac         636
Ser Arg Gln Phe Trp Ser His Gln Ile Asp His Gly Val Leu Asp Asp
            100                 105                 110
ccc aag gag tgg atc aac ccc gtc gcc cac ctg gcc ttc gcc cag ggc         684
Pro Lys Glu Trp Ile Asn Pro Val Ala His Leu Ala Phe Ala Gln Gly
        115                 120                 125
gac gac cag gtc gac tac ctc aag cgc cgc cac gag gcg ctg gcc gac         732
Asp Asp Gln Val Asp Tyr Leu Lys Arg Arg His Glu Ala Leu Ala Asp
    130                 135                 140
aac atc ctc ttc ccg ggc atg gag tgg gtc gag gac gac gcc aag ttc         780
Asn Ile Leu Phe Pro Gly Met Glu Trp Val Glu Asp Asp Ala Lys Phe
145                 150                 155                 160
gcc gag cgc ctc ccg gtc atg tcc gag ggc cgt gac ttc gcc gcc gag         828
Ala Glu Arg Leu Pro Val Met Ser Glu Gly Arg Asp Phe Ala Ala Glu
                165                 170                 175
aag gtc gcc tac tcc ggc acc gac atc ggc acc gac gtc aac ttc ggt         876
Lys Val Ala Tyr Ser Gly Thr Asp Ile Gly Thr Asp Val Asn Phe Gly
            180                 185                 190
gcc ctg acc gag cag ttc ctc act gcc gcc gag gcc tcc ggc acg gag         924
Ala Leu Thr Glu Gln Phe Leu Thr Ala Ala Glu Ala Ser Gly Thr Glu
        195                 200                 205
atc cgc tac ggc cac gag gtc aag aac atc aag aag gac ggt ggc aag         972
Ile Arg Tyr Gly His Glu Val Lys Asn Ile Lys Lys Asp Gly Gly Lys
    210                 215                 220
tgg aag atc acc gtc aag aac gtc cac acg ggt gac acc tcc gtg gtc        1020
Trp Lys Ile Thr Val Lys Asn Val His Thr Gly Asp Thr Ser Val Val
225                 230                 235                 240
aag gcc aag ttc gtg ttc gtc ggc gcc ggc ggc tac gcc ctc gac ctg        1068
Lys Ala Lys Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu
                245                 250                 255
ctg cgc aag gca ggc gtc ccg gag gtc agc ggt tac gcc ggc ttc ccg        1116
Leu Arg Lys Ala Gly Val Pro Glu Val Ser Gly Tyr Ala Gly Phe Pro
            260                 265                 270
gtg tcc ggc ctg tgg ctg cgc tgc acc aac gag gag ctg atc aac cag        1164
Val Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Asn Gln
        275                 280                 285
cac gac gcc aag gtc tac ggc aag gcc aag gtc ggt gcc ccg ccg atg        1212
His Asp Ala Lys Val Tyr Gly Lys Ala Lys Val Gly Ala Pro Pro Met
    290                 295                 300
tcc gtc ccg cac ctt gac acc cgc gtc atc gac ggc aag aag ggc ctc        1260
Ser Val Pro His Leu Asp Thr Arg Val Ile Asp Gly Lys Lys Gly Leu
305                 310                 315                 320
ctg ttc ggc ccc tac ggc ggc tgg agc ccg aag ttc ctc aag gag ggt        1308
Leu Phe Gly Pro Tyr Gly Gly Trp Ser Pro Lys Phe Leu Lys Glu Gly
                325                 330                 335
tcg tac ctc gac ctg ttc aag tcg atc cgc ctg gac aac ctc ccg tcc        1356
Ser Tyr Leu Asp Leu Phe Lys Ser Ile Arg Leu Asp Asn Leu Pro Ser
            340                 345                 350
tac ctc ggt gtc gcc gcc cag gag ttc gcc ctg acc aag tac ctc atc        1404
Tyr Leu Gly Val Ala Ala Gln Glu Phe Ala Leu Thr Lys Tyr Leu Ile
        355                 360                 365
acc gag gtg gcg aag gac ttc gag aag cgc ctc gtc gac ctg cgt gac        1452
Thr Glu Val Ala Lys Asp Phe Glu Lys Arg Leu Val Asp Leu Arg Asp
    370                 375                 380
tac gtc ccg tcc gcc aag gcc gag gac tgg gag acc gtg gtc gcc ggt        1500
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Tyr Val Pro Ser Ala Lys Ala Glu Asp Trp Glu Thr Val Val Ala Gly
385                 390                 395                 400
cag cgc gtc cag gtg atc aag ccg gcc cgc gcg ccg cgc ttc ggc tcc      1548
Gln Arg Val Gln Val Ile Lys Pro Ala Arg Ala Pro Arg Phe Gly Ser
                405                 410                 415
ctc gag ttc ggc acc gcc ctg atc aac agc acc gac ggc tcc atc gcc      1596
Leu Glu Phe Gly Thr Ala Leu Ile Asn Ser Thr Asp Gly Ser Ile Ala
            420                 425                 430
ggc ctg ctg ggt gcc tcc ccg ggt gcc tcc atc gcc ccg gcc gcc atg      1644
Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ala Ala Met
        435                 440                 445
ctc gag ctc gtc gag cgc tgc ttc ggt gac cgc atg atc cag tgg ggc      1692
Leu Glu Leu Val Glu Arg Cys Phe Gly Asp Arg Met Ile Gln Trp Gly
    450                 455                 460
ccg aag ctc aag gag atg atc ccg tcc tac ggc acc aag ctg ggc gac      1740
Pro Lys Leu Lys Glu Met Ile Pro Ser Tyr Gly Thr Lys Leu Gly Asp
465                 470                 475                 480
gac gag aag atg ttc aac gag ctc tgg gac tac acc cag aag acc ctg      1788
Asp Glu Lys Met Phe Asn Glu Leu Trp Asp Tyr Thr Gln Lys Thr Leu
                485                 490                 495
aag ctc gag aag tag ttccactgtg agggccgcga ccaccgggtc gcggccttcg      1843
Lys Leu Glu Lys
            500
ccgattccgt aggctggtgg ccatgcaacg catcgtgccc accatctggt tcaaccggaa     1903
cgccgacgag gccgccgagt tctacgccga cgtcttcccc gacacgcttg tcgacgcccg     1963
cgtcccccac cccgaatccg gcgagaccct caccgtcgac gtgctcatcg acggctaccg     2023
cgtcaccctc ctcaacggtg ggccggagtt cggcccgacc cccgcgatca gcttcttcgt     2083
caacttcgac ccctcccgca                                                2103
<210>  176
<211>  500
<212>  PRT
<213>  Corynebacterium humireducens
<400>  176
Val Ser Thr Glu Asn Lys Asn Ala Pro Lys Val Thr Asp Glu Val Asp
1               5                  10                  15
Val Ala Leu Val Gly Ala Gly Val Met Ser Ala Thr Leu Gly Ala Met
            20                  25                  30
Ile Arg Glu Leu Glu Pro Ser Trp Ser Gln Met Ile Phe Glu Arg Leu
        35                  40                  45
Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
    50                  55                  60
Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Asn Gly
65                  70                  75                  80
Lys Ile Glu Val Ala Lys Ala Ile Gly Ile Asn Glu Lys Phe Gln Val
                85                  90                  95
Ser Arg Gln Phe Trp Ser His Gln Ile Asp His Gly Val Leu Asp Asp
            100                 105                 110
Pro Lys Glu Trp Ile Asn Pro Val Ala His Leu Ala Phe Ala Gln Gly
        115                 120                 125
Asp Asp Gln Val Asp Tyr Leu Lys Arg Arg His Glu Ala Leu Ala Asp
    130                 135                 140
Asn Ile Leu Phe Pro Gly Met Glu Trp Val Glu Asp Asp Ala Lys Phe
145                 150                 155                 160
Ala Glu Arg Leu Pro Val Met Ser Glu Gly Arg Asp Phe Ala Ala Glu
                165                 170                 175
Lys Val Ala Tyr Ser Gly Thr Asp Ile Gly Thr Asp Val Asn Phe Gly
            180                 185                 190
Ala Leu Thr Glu Gln Phe Leu Thr Ala Ala Glu Ala Ser Gly Thr Glu
        195                 200                 205
Ile Arg Tyr Gly His Glu Val Lys Asn Ile Lys Lys Asp Gly Gly Lys
    210                 215                 220
Trp Lys Ile Thr Val Lys Asn Val His Thr Gly Asp Thr Ser Val Val
225                 230                 235                 240
Lys Ala Lys Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu
                245                 250                 255
Leu Arg Lys Ala Gly Val Pro Glu Val Ser Gly Tyr Ala Gly Phe Pro
            260                 265                 270
Val Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Asn Gln
        275                 280                 285
His Asp Ala Lys Val Tyr Gly Lys Ala Lys Val Gly Ala Pro Pro Met
    290                 295                 300
Ser Val Pro His Leu Asp Thr Arg Val Ile Asp Gly Lys Lys Gly Leu
305                 310                 315                 320
Leu Phe Gly Pro Tyr Gly Gly Trp Ser Pro Lys Phe Leu Lys Glu Gly
                325                 330                 335
Ser Tyr Leu Asp Leu Phe Lys Ser Ile Arg Leu Asp Asn Leu Pro Ser
            340                 345                 350
Tyr Leu Gly Val Ala Ala Gln Glu Phe Ala Leu Thr Lys Tyr Leu Ile
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        355                 360                 365
Thr Glu Val Ala Lys Asp Phe Glu Lys Arg Leu Val Asp Leu Arg Asp
    370                 375                 380
Tyr Val Pro Ser Ala Lys Ala Glu Asp Trp Glu Thr Val Val Ala Gly
385                 390                 395                 400
Gln Arg Val Gln Val Ile Lys Pro Ala Arg Ala Pro Arg Phe Gly Ser
                405                 410                 415
Leu Glu Phe Gly Thr Ala Leu Ile Asn Ser Thr Asp Gly Ser Ile Ala
            420                 425                 430
Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ala Ala Met
        435                 440                 445
Leu Glu Leu Val Glu Arg Cys Phe Gly Asp Arg Met Ile Gln Trp Gly
    450                 455                 460
Pro Lys Leu Lys Glu Met Ile Pro Ser Tyr Gly Thr Lys Leu Gly Asp
465                 470                 475                 480
Asp Glu Lys Met Phe Asn Glu Leu Trp Asp Tyr Thr Gln Lys Thr Leu
                485                 490                 495
Lys Leu Glu Lys
            500
<210>  177
<211>  3357
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(3057)
<223>  gen aceE
<400>  177
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cggggtttgc aatctccgcc acacacctcg cggagaggcg ggacaggcct gcgacaaggg      120
gcgatgggac gtcgataagc ggaacgccgg acccgttcat cttcgcaagc tttacaggaa      180
tgcagaacta cgttggccaa tgaaaacacg tatcctggac tggacactcg ggcctgtccg      240
gaccaccttg ccggcgggcc cgttgctcca ccacgacacc cagaaacctg gaggcacatc      300
atg gca gat gac ctg aac gcg aac ggc cgc aag ggc aac tcc cac tac         348
Met Ala Asp Asp Leu Asn Ala Asn Gly Arg Lys Gly Asn Ser His Tyr
1               5                  10                  15
ccg gcg atc cgc gac ggc gtc gcg tcc tac ctc aaa gac acc gac ccg        396
Pro Ala Ile Arg Asp Gly Val Ala Ser Tyr Leu Lys Asp Thr Asp Pro
            20                  25                  30
gag gag acc cag gag tgg atg gac tcc ctc gac ggt ctc ctc gcg gag        444
Glu Glu Thr Gln Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Ala Glu
        35                  40                  45
aag gac ccg gcc cgc gcc cgc tac ctc atg ctc cgc atg ctg gag cgc        492
Lys Asp Pro Ala Arg Ala Arg Tyr Leu Met Leu Arg Met Leu Glu Arg
    50                  55                  60
gcg gcc ctc aag cgt gtc ccg ctg ccg aac ctg acc tcc aca gac ttc        540
Ala Ala Leu Lys Arg Val Pro Leu Pro Asn Leu Thr Ser Thr Asp Phe
65                  70                  75                  80
gtc aac acg atc ccc acc acc atg gag ccg gag ttc ccg ggt gac gag        588
Val Asn Thr Ile Pro Thr Thr Met Glu Pro Glu Phe Pro Gly Asp Glu
                85                  90                  95
gag atg gag aag cgc tac cgc cgc tgg atg cgc tgg aac gcc gcc atc        636
Glu Met Glu Lys Arg Tyr Arg Arg Trp Met Arg Trp Asn Ala Ala Ile
            100                 105                 110
atg gtg cac cgc gcc cag cgc ccc ggc atc ggc gtc ggc ggc cac atc        684
Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile
        115                 120                 125
tcc acc tac gcc tcc gcc gcc ccg ctc tac gag gtc ggc ttc aat cac        732
Ser Thr Tyr Ala Ser Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn His
    130                 135                 140
ttc tgg cgc ggc aag gac cac ccg ggc ggc ggc gac cag atc ttc ttc        780
Phe Trp Arg Gly Lys Asp His Pro Gly Gly Gly Asp Gln Ile Phe Phe
145                 150                 155                 160
cag ggc cac gcc tcc ccc ggc atc tac gcc cgc gcc ttc ctc gag ggg        828
Gln Gly His Ala Ser Pro Gly Ile Tyr Ala Arg Ala Phe Leu Glu Gly
                165                 170                 175
cgc ctg agc gag gac gac ctc gac ggc ttc cgc cag gag gtc tcc cgc        876
Arg Leu Ser Glu Asp Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg
            180                 185                 190
ggt gag ggc aac ggc atc ccg tcc tac ccg cac ccg cac ggc atg cct        924
Gly Glu Gly Asn Gly Ile Pro Ser Tyr Pro His Pro His Gly Met Pro
        195                 200                 205
gat ttc tgg gag ttc ccg acc gtc tcc atg gga ctg ggc ccg atg gac        972
Asp Phe Trp Glu Phe Pro Thr Val Ser Met Gly Leu Gly Pro Met Asp
    210                 215                 220
gcg atc tac cag gca cgt ttc aac cgt tac ctg cac aac cgc ggc atc       1020
Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu His Asn Arg Gly Ile
225                 230                 235                 240
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aag gac acc tcc gac cag cac gtg tgg gcc ttc ctc ggc gac ggc gag      1068
Lys Asp Thr Ser Asp Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu
                245                 250                 255
atg gac gag ccg gag tcc cgc ggc ctc atc cag cac gcc gcg ctg aac      1116
Met Asp Glu Pro Glu Ser Arg Gly Leu Ile Gln His Ala Ala Leu Asn
            260                 265                 270
aac ctg gac aac ctc acc ttc gtg gtc aac tgc aac ctg cag cgt ctc      1164
Asn Leu Asp Asn Leu Thr Phe Val Val Asn Cys Asn Leu Gln Arg Leu
        275                 280                 285
gac ggc ccg gtc cgc ggc aac acg cag atc atc cag gag ctc gag tcc      1212
Asp Gly Pro Val Arg Gly Asn Thr Gln Ile Ile Gln Glu Leu Glu Ser
    290                 295                 300
ttc ttc cgg ggt gcc ggc tgg tcc gtc atc aag gtc atc tgg ggc cgc      1260
Phe Phe Arg Gly Ala Gly Trp Ser Val Ile Lys Val Ile Trp Gly Arg
305                 310                 315                 320
gag tgg gac gcc ctg ctg gag aag gac gag tcc ggc gcg ctg gtc aac      1308
Glu Trp Asp Ala Leu Leu Glu Lys Asp Glu Ser Gly Ala Leu Val Asn
                325                 330                 335
gtc atg aac acc acc ccg gac ggt gac tac cag acc ttc aag gcc aac      1356
Val Met Asn Thr Thr Pro Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn
            340                 345                 350
gac ggc gcc tac gtc cgc gag cac ttc ttc ggc cgc gac gag cgc acc      1404
Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Glu Arg Thr
        355                 360                 365
gcc aaa ctc gtc gag gac atg acc gac gag gag atc tgg gcc ctg ccg      1452
Ala Lys Leu Val Glu Asp Met Thr Asp Glu Glu Ile Trp Ala Leu Pro
    370                 375                 380
cgc ggt ggc cac gac tac cgc aag gtc cac gcc gcc tac aag cgg gcg      1500
Arg Gly Gly His Asp Tyr Arg Lys Val His Ala Ala Tyr Lys Arg Ala
385                 390                 395                 400
ctg gag acc aag gac cgc ccg acc gtc atc ctc gcg ttc acc atc aag      1548
Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala Phe Thr Ile Lys
                405                 410                 415
ggc tac ggc ctg ggc cac aac ttc gag ggc cgc aac gcg acg cac cag      1596
Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln
            420                 425                 430
atg aag aag ctc gcc gcc gag gac ctg aag aac ttc cgc gac aag cag      1644
Met Lys Lys Leu Ala Ala Glu Asp Leu Lys Asn Phe Arg Asp Lys Gln
        435                 440                 445
tcc atc ccg atc ccg gac gag gtc ctc gag gcc gac ccg tac ctg ccg      1692
Ser Ile Pro Ile Pro Asp Glu Val Leu Glu Ala Asp Pro Tyr Leu Pro
    450                 455                 460
ccg tac tac cac ccg ggc gag gac gcc ccg gag atc cag tac atg aag      1740
Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Gln Tyr Met Lys
465                 470                 475                 480
aag cgt cgt cag gag ctg ggc ggt ttc atc ccg gag cgt cgc cag acc      1788
Lys Arg Arg Gln Glu Leu Gly Gly Phe Ile Pro Glu Arg Arg Gln Thr
                485                 490                 495
tac acc ccg ctg cag gtc ccg gac atc gag aag ctg cgc agc gtg cgc      1836
Tyr Thr Pro Leu Gln Val Pro Asp Ile Glu Lys Leu Arg Ser Val Arg
            500                 505                 510
aag ggc tcc ggc aag cag gag gtc gcc tcc acc atg gcg ctc gtg cgt      1884
Lys Gly Ser Gly Lys Gln Glu Val Ala Ser Thr Met Ala Leu Val Arg
        515                 520                 525
gcc ttc aag gag ctc atg cgt gac aag gag ctg ggc cgc cgc gtc gtg      1932
Ala Phe Lys Glu Leu Met Arg Asp Lys Glu Leu Gly Arg Arg Val Val
    530                 535                 540
ccg atc atc ccg gac gag gcc cgc acc ttc ggc ctc gac tcc tgg ttc      1980
Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe
545                 550                 555                 560

ccg acc ctg aag atc tac aac ccg cac ggc cag aac tac gtg ccg gtc      2028
Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val
                565                 570                 575
gac cat gac ctc atg ctg tcc tac cgg gag gcc acc gac ggc cag atc      2076
Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Thr Asp Gly Gln Ile
            580                 585                 590
ctc cac gag ggc atc aac gag gcc ggt tcc gtc gcg tcc ttc atg gcc      2124
Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Met Ala
        595                 600                 605
gcc ggc acc tcc tac gcc acc cac ggc gaa gcg atg atc ccg ctg tac      2172
Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pro Leu Tyr
    610                 615                 620
atc ttc tac tcg atg ttc ggt ttc cag cgc acc ggc gac ggc atc tgg      2220
Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp
625                 630                 635                 640
gcc gcc gcc gac cag atg gcc cgt ggc ttc ctc atc ggc gcc acc gcc      2268
Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Leu Ile Gly Ala Thr Ala
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                645                 650                 655
ggc cgc acc acc ctg acg ggt gag ggc ctg cag cac atg gac ggc cac      2316
Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His
            660                 665                 670
tcg cag atc ctc gcc tcc acg aac ccg ggc gtc gtg tcc tac gac ccg      2364
Ser Gln Ile Leu Ala Ser Thr Asn Pro Gly Val Val Ser Tyr Asp Pro
        675                 680                 685
gcg ttc gcc tac gag atc gcg cac ctg ctc cat gag ggc atc gac cgc      2412
Ala Phe Ala Tyr Glu Ile Ala His Leu Leu His Glu Gly Ile Asp Arg
    690                 695                 700
atg tac ggc ccg ggc cgc ggt gag aac gtc atc tac tac ctc acc gtg      2460
Met Tyr Gly Pro Gly Arg Gly Glu Asn Val Ile Tyr Tyr Leu Thr Val
705                 710                 715                 720
tac aac gag ccg gtc ccg cag ccg gcc gag ccg gag aac ctc gac gtc      2508
Tyr Asn Glu Pro Val Pro Gln Pro Ala Glu Pro Glu Asn Leu Asp Val
                725                 730                 735
gag ggc ctg cac aag ggc atg tac ctg ttc tcc cgc gcg gag gag ctc      2556
Glu Gly Leu His Lys Gly Met Tyr Leu Phe Ser Arg Ala Glu Glu Leu
            740                 745                 750
gag gtc gag gac ggc cac gag gcc tcc atc ctg gcc tcc ggc atc ggc      2604
Glu Val Glu Asp Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly
        755                 760                 765
atg cag tgg gcg ctc aag gcc cag cag atg ctg gcc gag gag tac aac      2652
Met Gln Trp Ala Leu Lys Ala Gln Gln Met Leu Ala Glu Glu Tyr Asn
    770                 775                 780
gtg cgt gcc aac gtc ttc tcc gtc acc tcc tgg gtc gag ctg gcc cgc      2700
Val Arg Ala Asn Val Phe Ser Val Thr Ser Trp Val Glu Leu Ala Arg
785                 790                 795                 800
gag ggt gcg gcg aag aac aag gag cag ctg cgc aac ccg gcc gca gag      2748
Glu Gly Ala Ala Lys Asn Lys Glu Gln Leu Arg Asn Pro Ala Ala Glu
                805                 810                 815
atc gag gag gcc ttc gcc acc agg cag ctg aag cag gtc gac ggc ggc      2796
Ile Glu Glu Ala Phe Ala Thr Arg Gln Leu Lys Gln Val Asp Gly Gly
            820                 825                 830
acc ttc gtg gcc gtc tcc gac ttc gcg acc gac ctg cag gag cag atc      2844
Thr Phe Val Ala Val Ser Asp Phe Ala Thr Asp Leu Gln Glu Gln Ile
        835                 840                 845
cgc gcc tac gtc ccg ggc gag tac atc gtc ctg ggc gcc gac ggc ttc      2892
Arg Ala Tyr Val Pro Gly Glu Tyr Ile Val Leu Gly Ala Asp Gly Phe
    850                 855                 860
ggc ttc tcc gac acc cgt ccg gcc gcc cgc cgc ttc ttc aac atc gac      2940
Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp
865                 870                 875                 880
gcc gag tcc atc gtc gtc gcg gtc ctc atg ggc ctg gcc cgc gag ggc      2988
Ala Glu Ser Ile Val Val Ala Val Leu Met Gly Leu Ala Arg Glu Gly
                885                 890                 895
aag atc gac atc tct gtg gcc cag cag gcc gcc gag aag tac cag ctg      3036
Lys Ile Asp Ile Ser Val Ala Gln Gln Ala Ala Glu Lys Tyr Gln Leu
            900                 905                 910
gac gat ccg acc gct gtg taa ctgatccccc ggtcaaggcc ctgctccggc         3087
Asp Asp Pro Thr Ala Val
        915
agggccttgc tgctttcccg cttgtcgacg cccctctcac tccctgttga ggtaccgcgg     3147
ccaggaggtg tcgcgggtgg ccagcgagat ctccaccgcg gtgtcgagct ccgctgccag     3207
gggctcgggc agcttgtgcc ggagcgcgtc gccgaggcgc gcgatgacct ccaggcgcag     3267
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ggggtcggcg ggcccgccgt acatctcgac                                     3357
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Pro Ala Ile Arg Asp Gly Val Ala Ser Tyr Leu Lys Asp Thr Asp Pro
            20                  25                  30
Glu Glu Thr Gln Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Ala Glu
        35                  40                  45
Lys Asp Pro Ala Arg Ala Arg Tyr Leu Met Leu Arg Met Leu Glu Arg
    50                  55                  60
Ala Ala Leu Lys Arg Val Pro Leu Pro Asn Leu Thr Ser Thr Asp Phe
65                  70                  75                  80
Val Asn Thr Ile Pro Thr Thr Met Glu Pro Glu Phe Pro Gly Asp Glu
                85                  90                  95
Glu Met Glu Lys Arg Tyr Arg Arg Trp Met Arg Trp Asn Ala Ala Ile
            100                 105                 110
Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile
        115                 120                 125
```

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Ser Thr Tyr Ala Ser Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn His
    130                 135                 140
Phe Trp Arg Gly Lys Asp His Pro Gly Gly Gly Asp Gln Ile Phe Phe
145                 150                 155                 160
Gln Gly His Ala Ser Pro Gly Ile Tyr Ala Arg Ala Phe Leu Glu Gly
                165                 170                 175
Arg Leu Ser Glu Asp Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg
            180                 185                 190
Gly Glu Gly Asn Gly Ile Pro Ser Tyr Pro His Pro His Gly Met Pro
        195                 200                 205
Asp Phe Trp Glu Phe Pro Thr Val Ser Met Gly Leu Gly Pro Met Asp
    210                 215                 220
Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu His Asn Arg Gly Ile
225                 230                 235                 240
Lys Asp Thr Ser Asp Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu
                245                 250                 255
Met Asp Glu Pro Glu Ser Arg Gly Leu Ile Gln His Ala Ala Leu Asn
            260                 265                 270
Asn Leu Asp Asn Leu Thr Phe Val Val Asn Cys Asn Leu Gln Arg Leu
        275                 280                 285


Asp Gly Pro Val Arg Gly Asn Thr Gln Ile Ile Gln Glu Leu Glu Ser
    290                 295                 300
Phe Phe Arg Gly Ala Gly Trp Ser Val Ile Lys Val Ile Trp Gly Arg
305                 310                 315                 320
Glu Trp Asp Ala Leu Leu Glu Lys Asp Glu Ser Gly Ala Leu Val Asn
                325                 330                 335
Val Met Asn Thr Thr Pro Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn
            340                 345                 350
Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Glu Arg Thr
        355                 360                 365
Ala Lys Leu Val Glu Asp Met Thr Asp Glu Glu Ile Trp Ala Leu Pro
    370                 375                 380
Arg Gly Gly His Asp Tyr Arg Lys Val His Ala Ala Tyr Lys Arg Ala
385                 390                 395                 400
Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala Phe Thr Ile Lys
                405                 410                 415
Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln
            420                 425                 430
Met Lys Lys Leu Ala Ala Glu Asp Leu Lys Asn Phe Arg Asp Lys Gln
        435                 440                 445
Ser Ile Pro Ile Pro Asp Glu Val Leu Glu Ala Asp Pro Tyr Leu Pro
    450                 455                 460
Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Gln Tyr Met Lys
465                 470                 475                 480
Lys Arg Arg Gln Glu Leu Gly Gly Phe Ile Pro Glu Arg Arg Gln Thr
                485                 490                 495
Tyr Thr Pro Leu Gln Val Pro Asp Ile Glu Lys Leu Arg Ser Val Arg
            500                 505                 510
Lys Gly Ser Gly Lys Gln Glu Val Ala Ser Thr Met Ala Leu Val Arg
        515                 520                 525
Ala Phe Lys Glu Leu Met Arg Asp Lys Glu Leu Gly Arg Arg Val Val
    530                 535                 540
Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe
545                 550                 555                 560
Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val
                565                 570                 575
Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Thr Asp Gly Gln Ile
            580                 585                 590
Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Met Ala
        595                 600                 605
Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pro Leu Tyr
    610                 615                 620
Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp
625                 630                 635                 640
Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Leu Ile Gly Ala Thr Ala
                645                 650                 655
Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His
            660                 665                 670
Ser Gln Ile Leu Ala Ser Thr Asn Pro Gly Val Val Ser Tyr Asp Pro
        675                 680                 685
Ala Phe Ala Tyr Glu Ile Ala His Leu Leu His Glu Gly Ile Asp Arg
    690                 695                 700
Met Tyr Gly Pro Gly Arg Gly Glu Asn Val Ile Tyr Tyr Leu Thr Val
705                 710                 715                 720
Tyr Asn Glu Pro Val Pro Gln Pro Ala Glu Pro Glu Asn Leu Asp Val
                725                 730                 735
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Glu Gly Leu His Lys Gly Met Tyr Leu Phe Ser Arg Ala Glu Glu Leu
            740                 745                 750
Glu Val Glu Asp Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly
        755                 760                 765
Met Gln Trp Ala Leu Lys Ala Gln Gln Met Leu Ala Glu Glu Tyr Asn
    770                 775                 780
Val Arg Ala Asn Val Phe Ser Val Thr Ser Trp Val Glu Leu Ala Arg
785                 790                 795                 800
Glu Gly Ala Ala Lys Asn Lys Glu Gln Leu Arg Asn Pro Ala Ala Glu
                805                 810                 815
Ile Glu Glu Ala Phe Ala Thr Arg Gln Leu Lys Gln Val Asp Gly Gly
            820                 825                 830
Thr Phe Val Ala Val Ser Asp Phe Ala Thr Asp Leu Gln Glu Gln Ile
        835                 840                 845
Arg Ala Tyr Val Pro Gly Glu Tyr Ile Val Leu Gly Ala Asp Gly Phe
    850                 855                 860
Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp
865                 870                 875                 880
Ala Glu Ser Ile Val Val Ala Val Leu Met Gly Leu Ala Arg Glu Gly
                885                 890                 895
Lys Ile Asp Ile Ser Val Ala Gln Gln Ala Ala Glu Lys Tyr Gln Leu
            900                 905                 910
Asp Asp Pro Thr Ala Val
        915
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gcacccagac cgggtgggtc gaccgcatgc agcaccgctc ccgcctctac gaactgctcc      180
gctacaacga gtacaacgcc ttcgaccagg aggttttcac gtactccgcc gacacctacc      240
agcccacctt ccagtagccc accagcaact cctgacattc cttgaaaggg gatgagtacc      300
atg tcc gac aac acc aac atc gag gtc cgc aag ggt ctc tac ggc gtg        348
Met Ser Asp Asn Thr Asn Ile Glu Val Arg Lys Gly Leu Tyr Gly Val
1               5                  10                  15
atc gcc gac tac acc gca gtc tcc aag gtc atg ccg gag acc aac tcc        396
Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
            20                  25                  30
ctg acc tac cgc gga tac gcc gtc cag gac ctc gtc gca gag tgc tcc        444
Leu Thr Tyr Arg Gly Tyr Ala Val Gln Asp Leu Val Ala Glu Cys Ser
        35                  40                  45
ttc gag gag gtc ttc tac ctc ctg tgg aac ggt gag ctg ccg aac gag        492
Phe Glu Glu Val Phe Tyr Leu Leu Trp Asn Gly Glu Leu Pro Asn Glu
    50                  55                  60
gag cag ctg gcg gag ttc aac agg cgc ggc cgt tcc tac cgc aag ctc        540
Glu Gln Leu Ala Glu Phe Asn Arg Arg Gly Arg Ser Tyr Arg Lys Leu
65                  70                  75                  80
gac gcc ggc ctg atc gca ctc atc cac tcc ctg ccg ctc gac tgt cac        588
Asp Ala Gly Leu Ile Ala Leu Ile His Ser Leu Pro Leu Asp Cys His
                85                  90                  95
ccg atg gac gtc atg cgc acc gcc gtg tcc tac atg ggc acc aag gac        636
Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
            100                 105                 110
tcc gag cac ttc acc ccg gac gcc gac cac atc acc cac gtc ggc cac        684
Ser Glu His Phe Thr Pro Asp Ala Asp His Ile Thr His Val Gly His
        115                 120                 125
aac ctc ctc gcc cag ctg ccg atg gtg ctg gcc atg gac atc cgc cgc        732
Asn Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
    130                 135                 140
cgt cag ggc ctc gac atc gtc gcc ccg gac ccg gac aag tcc gtc gcc        780
Arg Gln Gly Leu Asp Ile Val Ala Pro Asp Pro Asp Lys Ser Val Ala
145                 150                 155                 160
cac aac ctg ctg tcg atg gtc ttc ggc aac ggc ccg gag tcc ccg gcg        828
His Asn Leu Leu Ser Met Val Phe Gly Asn Gly Pro Glu Ser Pro Ala
                165                 170                 175
tcc aac ccg gac gac gtg cgt gac ttc gag aag tcg ctc atc ctc tac        876
Ser Asn Pro Asp Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
            180                 185                 190
gcc gag cac tcc ttc aac gcc tcg acc ttc acc tcg cgt gtg atc acc        924
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ser Arg Val Ile Thr
        195                 200                 205
tcg acc cgc tcg gac gtc tac tcc gcg atc acc ggt gcc atc ggc gcc        972
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Ser Thr Arg Ser Asp Val Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala
    210                 215                 220
ctc aag ggc ccg ctg cac ggc ggc gcc aac gag ttc gtc atg cac acc      1020
Leu Lys Gly Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr
225                 230                 235                 240
atg ctg gag atc gac gac ccg gag aag gcc gcc gac tgg gtc aac aac      1068
Met Leu Glu Ile Asp Asp Pro Glu Lys Ala Ala Asp Trp Val Asn Asn
                245                 250                 255
gcc ctg gac aac aag gac ctc atc atg ggc ttc ggt cac cgc gtg tac      1116
Ala Leu Asp Asn Lys Asp Leu Ile Met Gly Phe Gly His Arg Val Tyr
            260                 265                 270
aag aag ggt gac tcg cgt gtc ccg tcc atg gag gcg tcc ttc cgt gac      1164
Lys Lys Gly Asp Ser Arg Val Pro Ser Met Glu Ala Ser Phe Arg Asp
        275                 280                 285
ctc gcc gag cgt cac gac ggc gcc aag tgg gtc gcc atg tac gag aac      1212
Leu Ala Glu Arg His Asp Gly Ala Lys Trp Val Ala Met Tyr Glu Asn
    290                 295                 300
atg cgc gac gcc atg gac gcc cgc acc ggc atc aag ccg aac ctg gac      1260
Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp
305                 310                 315                 320
ttc ccg gcc ggc ccg gcg tac cac ctg ctc ggc ttc ccg gtc gac ttc      1308
Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe Pro Val Asp Phe
                325                 330                 335
ttc acc ccg ctg ttc gtc gtc gcc cgc atc gcc ggc tgg acc gcc cac      1356
Phe Thr Pro Leu Phe Val Val Ala Arg Ile Ala Gly Trp Thr Ala His
            340                 345                 350
atc gtg gag cag tac aac gac aac tcc ctg att cgt ccg ctc tcc gcc      1404
Ile Val Glu Gln Tyr Asn Asp Asn Ser Leu Ile Arg Pro Leu Ser Ala
        355                 360                 365
tac aac ggc ccc gag cag cgc cag gtc acc ccg ctg gcc gcc cgt tag      1452
Tyr Asn Gly Pro Glu Gln Arg Gln Val Thr Pro Leu Ala Ala Arg
    370                 375                 380
ccccacggcc ggcaccggac caccgcgacg cccacggcac tgcccacaca ttggggtggt     1512
gcgcgtgggt ttcgctgttc ggaacacctg tcggcccatt ccgcagggcg ggacagaaac     1572
ggcctttcgg gcgcccgtcc cgcggagtgc ggaaatggac cgcaccgggt ccaccacctg     1632
cagatacccc ctgtgactag gggatactcc cccgaagaca accctctttc ttgcgatact     1692
gtggtgtgcc agagagctca cccgctctca gacacacccc cgacatgacg ttcggaaagg     1752
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1               5                   10                  15
Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
            20                  25                  30
Leu Thr Tyr Arg Gly Tyr Ala Val Gln Asp Leu Val Ala Glu Cys Ser
        35                  40                  45
Phe Glu Glu Val Phe Tyr Leu Leu Trp Asn Gly Glu Leu Pro Asn Glu
    50                  55                  60
Glu Gln Leu Ala Glu Phe Asn Arg Arg Gly Arg Ser Tyr Arg Lys Leu
65                  70                  75                  80
Asp Ala Gly Leu Ile Ala Leu Ile His Ser Leu Pro Leu Asp Cys His
                85                  90                  95
Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
            100                 105                 110
Ser Glu His Phe Thr Pro Asp Ala Asp His Ile Thr His Val Gly His
        115                 120                 125
Asn Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
    130                 135                 140
Arg Gln Gly Leu Asp Ile Val Ala Pro Asp Pro Asp Lys Ser Val Ala
145                 150                 155                 160
His Asn Leu Leu Ser Met Val Phe Gly Asn Gly Pro Glu Ser Pro Ala
                165                 170                 175
Ser Asn Pro Asp Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
            180                 185                 190
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ser Arg Val Ile Thr
        195                 200                 205
Ser Thr Arg Ser Asp Val Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala
    210                 215                 220
Leu Lys Gly Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr
225                 230                 235                 240
Met Leu Glu Ile Asp Asp Pro Glu Lys Ala Ala Asp Trp Val Asn Asn
                245                 250                 255
Ala Leu Asp Asn Lys Asp Leu Ile Met Gly Phe Gly His Arg Val Tyr
            260                 265                 270
Lys Lys Gly Asp Ser Arg Val Pro Ser Met Glu Ala Ser Phe Arg Asp
        275                 280                 285
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Leu Ala Glu Arg His Asp Gly Ala Lys Trp Val Ala Met Tyr Glu Asn
    290                 295                 300
Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp
305                 310                 315                 320
Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe Pro Val Asp Phe
                325                 330                 335
Phe Thr Pro Leu Phe Val Val Ala Arg Ile Ala Gly Trp Thr Ala His
            340                 345                 350
Ile Val Glu Gln Tyr Asn Asp Asn Ser Leu Ile Arg Pro Leu Ser Ala
        355                 360                 365
Tyr Asn Gly Pro Glu Gln Arg Gln Val Thr Pro Leu Ala Ala Arg
    370                 375                 380
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ggtcggtggt ggggcggtgc ggctgagaag atgctggacc acccgatgta gcgacgttct      180
tccagcggaa acagccggat ctccggcgag gttacgccca tccgggggtg gcggctcgga      240

acggtctttg aggctagact cgcaggcgtt gatgcattag accgctcgaa aggatcccgc      300
atg acc cag aac ccc gtg aag atc gcc gtc acc ggt gcc gcc ggc aac         348
Met Thr Gln Asn Pro Val Lys Ile Ala Val Thr Gly Ala Ala Gly Asn
1               5                   10                  15
atc gcc tac tcc ctc ctg tgg cgc atc gcc gca ggt gac gtc tac ggc        396
Ile Ala Tyr Ser Leu Leu Trp Arg Ile Ala Ala Gly Asp Val Tyr Gly
            20                  25                  30
cgc gac acc ccg atc gag ctc acc ctc ctc gag atc ccg gcc gcc gta        444
Arg Asp Thr Pro Ile Glu Leu Thr Leu Leu Glu Ile Pro Ala Ala Val
        35                  40                  45
cgc ggc gcc gag ggc gtg gcc atg gag ctc aac gac tcc gcc ttc ccc        492
Arg Gly Ala Glu Gly Val Ala Met Glu Leu Asn Asp Ser Ala Phe Pro
    50                  55                  60
ctc ctg cgc aac atc acc gtc acc gac agc gcc gac gtc gcc ttc gac        540
Leu Leu Arg Asn Ile Thr Val Thr Asp Ser Ala Asp Val Ala Phe Asp
65                  70                  75                  80
ggc gcc aac gcc gcc ttc ctt gtc ggc gcg aag ccg cgc ggt gca ggc        588
Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Ala Gly
                85                  90                  95
gag gag cgc gcc gac ctg ctg aag aac aac ggc ggc atc ttc ggc ccg        636
Glu Glu Arg Ala Asp Leu Leu Lys Asn Asn Gly Gly Ile Phe Gly Pro
            100                 105                 110
cag ggc agg gcc atc aac gac cgc gcc gcg gac gac gtc cgc gtg ctc        684
Gln Gly Arg Ala Ile Asn Asp Arg Ala Ala Asp Asp Val Arg Val Leu
        115                 120                 125
gtc gtc ggc aac ccg gcc aac acc aac gcc ctg atc gcc cag cgc aac        732
Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Gln Arg Asn
    130                 135                 140
gcc ccg gac gtc ccg gcc gag cgt ttc acc gcg ctg atg cgc ctg gac        780
Ala Pro Asp Val Pro Ala Glu Arg Phe Thr Ala Leu Met Arg Leu Asp
145                 150                 155                 160
cac agc cgt gcg ctg tcc cag ctg gcc gag aag ctc ggc gtg ctc acc        828
His Ser Arg Ala Leu Ser Gln Leu Ala Glu Lys Leu Gly Val Leu Thr
                165                 170                 175
acc gac ttc gag aac gtc gtc gtg tgg ggc aac cac tcc gcg acc cag        876
Thr Asp Phe Glu Asn Val Val Val Trp Gly Asn His Ser Ala Thr Gln
            180                 185                 190
ttc ccg gac gtg acc ttc gcc acc gtc aag ggt gag ccg gtc atc gag        924
Phe Pro Asp Val Thr Phe Ala Thr Val Lys Gly Glu Pro Val Ile Glu
        195                 200                 205
aag atc gac cat gac tgg tac gtc aac gag ttc atc ccg cgc gtc gcg        972
Lys Ile Asp His Asp Trp Tyr Val Asn Glu Phe Ile Pro Arg Val Ala
    210                 215                 220
aag cgt ggc gcc gag atc atc gag gtc cgc ggc aag tcc tcc gcc gcc       1020
Lys Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala
225                 230                 235                 240
tcc gcc gcc tcc gcc gcg gtg gac cac atg cgt gac tgg gtc cag ggc       1068
Ser Ala Ala Ser Ala Ala Val Asp His Met Arg Asp Trp Val Gln Gly
                245                 250                 255
act gag cgg tgg gcc tcc gcc gcc ctg ccg tcc gac ggc tcc tac ggc       1116
Thr Glu Arg Trp Ala Ser Ala Ala Leu Pro Ser Asp Gly Ser Tyr Gly
            260                 265                 270
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atc gac gag ggt ctc gtc gcc ggc ctg ccg acc gtc tcc cgc aac ggc      1164
Ile Asp Glu Gly Leu Val Ala Gly Leu Pro Thr Val Ser Arg Asn Gly
        275                 280                 285
tcc tgg gag atc gtc cag ggc ctc gag ctc aac gac ttc cag cgc gag      1212
Ser Trp Glu Ile Val Gln Gly Leu Glu Leu Asn Asp Phe Gln Arg Glu
    290                 295                 300
atg atc gcc cgg aac gtc gcg gag ctc aag gcc gag cgt gac gca gtc      1260
Met Ile Ala Arg Asn Val Ala Glu Leu Lys Ala Glu Arg Asp Ala Val
305                 310                 315                 320
gct gac ctg ctt cct tag cgcgtcaact cgcatccgcc gccaatcccg             1308
Ala Asp Leu Leu Pro
                325
gtagtgttca ggaacatgcg cttcgggatt gatttcggaa ccacccgtac cgtcattgcg     1368
gcggtcgacc ggggaaacta cccggtcgtc aacgtcacgg acacggacgg cgactcacgg     1428
gagtacatcc cctcggtcgt cgcgctggat ggtgaacggt tggtcggtgg ctgggaggcg     1488
ctggcggtag gtggcccgac cctcacccgc tccttcaagc gtctgctgac ctcccgcacc     1548
gtcaccgcgg agacccccgt ccggctgggc                                      1578
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Met Thr Gln Asn Pro Val Lys Ile Ala Val Thr Gly Ala Ala Gly Asn
1               5                  10                  15


Ile Ala Tyr Ser Leu Leu Trp Arg Ile Ala Ala Gly Asp Val Tyr Gly
            20                  25                  30
Arg Asp Thr Pro Ile Glu Leu Thr Leu Leu Glu Ile Pro Ala Ala Val
        35                  40                  45
Arg Gly Ala Glu Gly Val Ala Met Glu Leu Asn Asp Ser Ala Phe Pro
    50                  55                  60
Leu Leu Arg Asn Ile Thr Val Thr Asp Ser Ala Asp Val Ala Phe Asp
65                  70                  75                  80
Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Ala Gly
                85                  90                  95
Glu Glu Arg Ala Asp Leu Leu Lys Asn Asn Gly Gly Ile Phe Gly Pro
            100                 105                 110
Gln Gly Arg Ala Ile Asn Asp Arg Ala Ala Asp Asp Val Arg Val Leu
        115                 120                 125
Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Gln Arg Asn
    130                 135                 140
Ala Pro Asp Val Pro Ala Glu Arg Phe Thr Ala Leu Met Arg Leu Asp
145                 150                 155                 160
His Ser Arg Ala Leu Ser Gln Leu Ala Glu Lys Leu Gly Val Leu Thr
                165                 170                 175
Thr Asp Phe Glu Asn Val Val Val Trp Gly Asn His Ser Ala Thr Gln
            180                 185                 190
Phe Pro Asp Val Thr Phe Ala Thr Val Lys Gly Glu Pro Val Ile Glu
        195                 200                 205
Lys Ile Asp His Asp Trp Tyr Val Asn Glu Phe Ile Pro Arg Val Ala
    210                 215                 220
Lys Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala
225                 230                 235                 240
Ser Ala Ala Ser Ala Ala Val Asp His Met Arg Asp Trp Val Gln Gly
                245                 250                 255
Thr Glu Arg Trp Ala Ser Ala Ala Leu Pro Ser Asp Gly Ser Tyr Gly
            260                 265                 270
Ile Asp Glu Gly Leu Val Ala Gly Leu Pro Thr Val Ser Arg Asn Gly
        275                 280                 285
Ser Trp Glu Ile Val Gln Gly Leu Glu Leu Asn Asp Phe Gln Arg Glu
    290                 295                 300
Met Ile Ala Arg Asn Val Ala Glu Leu Lys Ala Glu Arg Asp Ala Val
305                 310                 315                 320
Ala Asp Leu Leu Pro
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gtcatggtcg acgagccccg cgccggcgtc gaggcgggag gcggcggtgg ccagtcctcg      180
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gcgccgttgt tccgtgacat cgcgtcctgg ctgctcaacc gggacaacat cccggcgtca      240
ccgcccatgg aggacatgct gatcctccac gcccactaac ccagcccacc acggaggagt      300
atg acc atg gag acc aca gtg acc aca ctg tcc cac ctc gcc cgt atc         348
Met Thr Met Glu Thr Thr Val Thr Thr Leu Ser His Leu Ala Arg Ile
1               5                  10                  15
gcc ggg gga gag ctg acc gga tcc gtg gcc ccg gtc gtc acg tcg gtg         396
Ala Gly Gly Glu Leu Thr Gly Ser Val Ala Pro Val Val Thr Ser Val
            20                  25                  30
gag ctc gac tcc tcc cgc ctc gcg gac gag ggc gcg ctc ttc gcc gcc         444
Glu Leu Asp Ser Ser Arg Leu Ala Asp Glu Gly Ala Leu Phe Ala Ala
        35                  40                  45
gtc ccc ggc acg cgc cgc cac ggt gcg gag ttc gcg cgc ggc acg ccg         492
Val Pro Gly Thr Arg Arg His Gly Ala Glu Phe Ala Arg Gly Thr Pro
    50                  55                  60
gcc gtc gcg atc ctc acc gac gcc gcc gga aag gag ctt ctc gac gcc         540
Ala Val Ala Ile Leu Thr Asp Ala Ala Gly Lys Glu Leu Leu Asp Ala
65                  70                  75                  80
gcc ggc gac acc cgc cct gtc atc ctc gtc gat gac gtc cgc gcg gtc         588
Ala Gly Asp Thr Arg Pro Val Ile Leu Val Asp Asp Val Arg Ala Val
                85                  90                  95
ctc ggg gcc gtg gcc gcg gag atc cac ggc cac ccc tcg gag cgt ctc         636
Leu Gly Ala Val Ala Ala Glu Ile His Gly His Pro Ser Glu Arg Leu
            100                 105                 110
acc ctg ctc ggc atc acc ggc acc tcc ggg aag acg acc acc agc tac         684
Thr Leu Leu Gly Ile Thr Gly Thr Ser Gly Lys Thr Thr Thr Ser Tyr
        115                 120                 125
ctg ctc gag cag ggg ctc atg gcg gcc gac ctg aag gtc ggc ctc atc         732
Leu Leu Glu Gln Gly Leu Met Ala Ala Asp Leu Lys Val Gly Leu Ile
    130                 135                 140
ggc acg acg ggc acg cgc atc aac ggc cgt ccc gtc ccc acc gac ctc         780
Gly Thr Thr Gly Thr Arg Ile Asn Gly Arg Pro Val Pro Thr Asp Leu
145                 150                 155                 160
acg acc ccg gag gcc acg acc ctg cag ccc ctg ttc gtg cgg atg ctc         828
Thr Thr Pro Glu Ala Thr Thr Leu Gln Pro Leu Phe Val Arg Met Leu
                165                 170                 175
gcg gag ggc gtc acg cac gtg gtc atg gag gtc tcc tcc cac gcc ctg         876
Ala Glu Gly Val Thr His Val Val Met Glu Val Ser Ser His Ala Leu
            180                 185                 190
gag ctg ggc cgg gtg gcg ggc acg cgt ttc gac gtc gcc ggg ttc acc         924
Glu Leu Gly Arg Val Ala Gly Thr Arg Phe Asp Val Ala Gly Phe Thr
        195                 200                 205
aac ctc tcc cag gac cac ctc gac ttc cac ccg acg atg gag gag tac         972
Asn Leu Ser Gln Asp His Leu Asp Phe His Pro Thr Met Glu Glu Tyr
    210                 215                 220
ttc gcg gcc aag gcc cgc ttc ttc gac ccg gcg tcg ccg ctg gcc gcg        1020
Phe Ala Ala Lys Ala Arg Phe Phe Asp Pro Ala Ser Pro Leu Ala Ala
225                 230                 235                 240
gag cgg tcc gtc gtc tgc gtc gac gac gag tgg ggg cgg cgg atg gcc        1068
Glu Arg Ser Val Val Cys Val Asp Asp Glu Trp Gly Arg Arg Met Ala
                245                 250                 255
gac ctg gcc tcg gac ccg gtg acc gtc gcg acc cgc ggc gcg gag gcc        1116
Asp Leu Ala Ser Asp Pro Val Thr Val Ala Thr Arg Gly Ala Glu Ala
            260                 265                 270
gac gtc acc gcc gtc cag agc tcg ctc acg ccc acc ggc gcc cag gtc        1164
Asp Val Thr Ala Val Gln Ser Ser Leu Thr Pro Thr Gly Ala Gln Val
        275                 280                 285
atc cgg ctc acc ctg ccg gag ggg gcc gtc gag gcg gag ctg ccg ctg        1212
Ile Arg Leu Thr Leu Pro Glu Gly Ala Val Glu Ala Glu Leu Pro Leu
    290                 295                 300
ccg ggt gac ttc aac atc gcc aac gcc gcc ctg gcc acc gcc atg gcg        1260
Pro Gly Asp Phe Asn Ile Ala Asn Ala Ala Leu Ala Thr Ala Met Ala
305                 310                 315                 320
tgg gcc gtg ggc gtc gac ccg cag gcc ttc acc gcc ggt ttc ctc gac        1308
Trp Ala Val Gly Val Asp Pro Gln Ala Phe Thr Ala Gly Phe Leu Asp
                325                 330                 335
gtc gcg gtc ccc ggg cgc atg gag cgt atc gac gag ggc cag gac ttc        1356
Val Ala Val Pro Gly Arg Met Glu Arg Ile Asp Glu Gly Gln Asp Phe
            340                 345                 350
ctc gcc gtc gtc gac tac gcc cac aag ccg gcc gcc gtc gcc gcc gtc        1404
Leu Ala Val Val Asp Tyr Ala His Lys Pro Ala Ala Val Ala Ala Val
        355                 360                 365
ctc gac acc ctc cgc ggg cag gtc cgc ggc cgc ctc ggc gtg gtc gtc        1452
Leu Asp Thr Leu Arg Gly Gln Val Arg Gly Arg Leu Gly Val Val Val
    370                 375                 380
ggg gcc ggt ggt gac cgc gac gcc acc aag cgt ccc ctc atg ggg gcg        1500
Gly Ala Gly Gly Asp Arg Asp Ala Thr Lys Arg Pro Leu Met Gly Ala
385                 390                 395                 400
gag gcc gcc cac cgc gcc gac ctg gtc atc atc acc gac gac aac ccg        1548
```

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Glu Ala Ala His Arg Ala Asp Leu Val Ile Ile Thr Asp Asp Asn Pro
                405                 410                 415
cgc agc gag gtg ccc gcc acc atc cgg gcg gcc gtg ctg cag ggg gcg      1596
Arg Ser Glu Val Pro Ala Thr Ile Arg Ala Ala Val Leu Gln Gly Ala
            420                 425                 430
gtc gac gcc ggg acg gac gcg gag atc cgc gag atc ggg gac cgc gcc      1644
Val Asp Ala Gly Thr Asp Ala Glu Ile Arg Glu Ile Gly Asp Arg Ala
        435                 440                 445
gcc gcc atc gac gcg ctg atc gag tgg gcc cgc ccg ggg gac ggc gtc      1692
Ala Ala Ile Asp Ala Leu Ile Glu Trp Ala Arg Pro Gly Asp Gly Val
    450                 455                 460
gtc gtc gcc ggc aag ggc cac gag gtc ggc cag ctg gtc aac ggc gtc      1740
Val Val Ala Gly Lys Gly His Glu Val Gly Gln Leu Val Asn Gly Val
465                 470                 475                 480
aac cac cat ttc gac gac cgg gaa gag gtc cgg cgc gca ctc aag gag      1788
Asn His His Phe Asp Asp Arg Glu Glu Val Arg Arg Ala Leu Lys Glu
                485                 490                 495
aag aag cat tga tccccctcac tctcgcggag atcgcggaca tcaccggcgg          1840
Lys Lys His

tgaactctcg cacgtgaccg acccggagac ccgggtgacc gggtccgtcg agttcgactc    1900
ccgccgggtc accccgggcg ggctgttcct cgccctgccg ggggcgcgcg tcgacggaca    1960
cgacttcgcc gccaccgccg tcgagtccgg cgcggtcgcc gtcctggcgg cgcggccggt    2020
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cgcccacgac gaggacggct                                               2100
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            20                  25                  30
Glu Leu Asp Ser Ser Arg Leu Ala Asp Glu Gly Ala Leu Phe Ala Ala
        35                  40                  45
Val Pro Gly Thr Arg Arg His Gly Ala Glu Phe Ala Arg Gly Thr Pro
    50                  55                  60
Ala Val Ala Ile Leu Thr Asp Ala Ala Gly Lys Glu Leu Leu Asp Ala
65                  70                  75                  80
Ala Gly Asp Thr Arg Pro Val Ile Leu Val Asp Asp Val Arg Ala Val
                85                  90                  95
Leu Gly Ala Val Ala Ala Glu Ile His Gly His Pro Ser Glu Arg Leu
            100                 105                 110
Thr Leu Leu Gly Ile Thr Gly Thr Ser Gly Lys Thr Thr Thr Ser Tyr
        115                 120                 125
Leu Leu Glu Gln Gly Leu Met Ala Ala Asp Leu Lys Val Gly Leu Ile
    130                 135                 140
Gly Thr Thr Gly Thr Arg Ile Asn Gly Arg Pro Val Pro Thr Asp Leu
145                 150                 155                 160
Thr Thr Pro Glu Ala Thr Thr Leu Gln Pro Leu Phe Val Arg Met Leu
                165                 170                 175
Ala Glu Gly Val Thr His Val Val Met Glu Val Ser Ser His Ala Leu
            180                 185                 190
Glu Leu Gly Arg Val Ala Gly Thr Arg Phe Asp Val Ala Gly Phe Thr
        195                 200                 205
Asn Leu Ser Gln Asp His Leu Asp Phe His Pro Thr Met Glu Glu Tyr
    210                 215                 220
Phe Ala Ala Lys Ala Arg Phe Phe Asp Pro Ala Ser Pro Leu Ala Ala
225                 230                 235                 240
Glu Arg Ser Val Val Cys Val Asp Asp Glu Trp Gly Arg Arg Met Ala
                245                 250                 255
Asp Leu Ala Ser Asp Pro Val Thr Val Ala Thr Arg Gly Ala Glu Ala
            260                 265                 270
Asp Val Thr Ala Val Gln Ser Ser Leu Thr Pro Thr Gly Ala Gln Val
        275                 280                 285
Ile Arg Leu Thr Leu Pro Glu Gly Ala Val Glu Ala Glu Leu Pro Leu
    290                 295                 300
Pro Gly Asp Phe Asn Ile Ala Asn Ala Ala Leu Ala Thr Ala Met Ala
305                 310                 315                 320
Trp Ala Val Gly Val Asp Pro Gln Ala Phe Thr Ala Gly Phe Leu Asp
                325                 330                 335
Val Ala Val Pro Gly Arg Met Glu Arg Ile Asp Glu Gly Gln Asp Phe
            340                 345                 350
Leu Ala Val Val Asp Tyr Ala His Lys Pro Ala Ala Val Ala Ala Val
        355                 360                 365
Leu Asp Thr Leu Arg Gly Gln Val Arg Gly Arg Leu Gly Val Val Val
    370                 375                 380
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Gly Ala Gly Gly Asp Arg Asp Ala Thr Lys Arg Pro Leu Met Gly Ala
385                 390                 395                 400
Glu Ala Ala His Arg Ala Asp Leu Val Ile Ile Thr Asp Asp Asn Pro
                405                 410                 415
Arg Ser Glu Val Pro Ala Thr Ile Arg Ala Ala Val Leu Gln Gly Ala
            420                 425                 430
Val Asp Ala Gly Thr Asp Ala Glu Ile Arg Glu Ile Gly Asp Arg Ala
        435                 440                 445
Ala Ala Ile Asp Ala Leu Ile Glu Trp Ala Arg Pro Gly Asp Gly Val
    450                 455                 460
Val Val Ala Gly Lys Gly His Glu Val Gly Gln Leu Val Asn Gly Val
465                 470                 475                 480
Asn His His Phe Asp Asp Arg Glu Glu Val Arg Arg Ala Leu Lys Glu
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acgacgcgca ggccgtcttc gagcagctgg tgcaggtcgg catcgacatg gaggacgtct      180
tcgcggtgct ggagcgcgag ggcgtcgaga agttcgtgtc ctcctggtcc gagctgctcg      240
actccatgga gtcccgactg cgctagcagt cccctccccg acaggaaagg acctgagcgc      300
atg ccc ctc ccc gtg acc ggc acc gac gcc tgg atc aac ccg ctg cgg         348
Met Pro Leu Pro Val Thr Gly Thr Asp Ala Trp Ile Asn Pro Leu Arg
1               5                   10                  15
aac acc gtc gac aag cgg ctg ccc cgc atc gcc ggc ccc tcc ggc atg         396
Asn Thr Val Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met
            20                  25                  30
gtg atc ttc ggc gtg acc ggt gac ctg gcc cgc aag aag ctg ctc ccg         444
Val Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro
        35                  40                  45
gcc atc tac gac ctg gcc aac cgt ggc ctc ctg ccg gcc ggt ttc acc         492
Ala Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Ala Gly Phe Thr
    50                  55                  60
ctc atc ggt ttc ggc cgt cgt ccc tgg agc aaa ccc gag ttc gag gag         540
Leu Ile Gly Phe Gly Arg Arg Pro Trp Ser Lys Pro Glu Phe Glu Glu
65                  70                  75                  80
tac gtg cgg gag gcc gtc gag agc ggc gcc cgc acc gag ttc cgc gaa         588
Tyr Val Arg Glu Ala Val Glu Ser Gly Ala Arg Thr Glu Phe Arg Glu
                85                  90                  95
cac gtg tgg gag cgg ctg gcc gag ggc atg cac ttc gtc gag ggc aac         636
His Val Trp Glu Arg Leu Ala Glu Gly Met His Phe Val Glu Gly Asn
            100                 105                 110
ttc gac gac gag ggc ttc gac cgc ctc gcc gcc acc ctc gcc gag atg         684
Phe Asp Asp Glu Gly Phe Asp Arg Leu Ala Ala Thr Leu Ala Glu Met
        115                 120                 125
gac acc tcc cgc ggc acg gcg ggc aac tgg gcc ttc tac ctg tcg gtc         732
Asp Thr Ser Arg Gly Thr Ala Gly Asn Trp Ala Phe Tyr Leu Ser Val
    130                 135                 140
ccg ccg gac ttc ttc acc gcc gtc tgc cac cag ctg gag cgc tcc ggc         780
Pro Pro Asp Phe Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
145                 150                 155                 160
ctg gcg gag gcc ggt gag gag tcg tgg cgt cgc gtg atc atc gag aag         828
Leu Ala Glu Ala Gly Glu Glu Ser Trp Arg Arg Val Ile Ile Glu Lys
                165                 170                 175
ccc ttc ggc cac gac cag gac acg gcc cgg gag ctc aac cgg gtg gtc         876
Pro Phe Gly His Asp Gln Asp Thr Ala Arg Glu Leu Asn Arg Val Val
            180                 185                 190
aac gcc gtc ttc ccg gag gag tcg gtg ttc cgc atc gac cac tac ctg         924
Asn Ala Val Phe Pro Glu Glu Ser Val Phe Arg Ile Asp His Tyr Leu
        195                 200                 205
ggc aag gag acg gtg cag aac atc ctg gcg ctg cgc ttc gcc aac cag         972
Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
    210                 215                 220
ctc ttc gac ccg atc tgg aac gcg cac tac gtc gac cac gtg cag atc        1020
Leu Phe Asp Pro Ile Trp Asn Ala His Tyr Val Asp His Val Gln Ile
225                 230                 235                 240
acc atg gcc gag gac atc ggt ctc ggt ggt cgg gcc ggc tac tac gac        1068
Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
                245                 250                 255
ggc atc ggc gcc gcc cgc gac gtc atg cag aac cac ctc ctc cag ctc        1116
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Gly Ile Gly Ala Ala Arg Asp Val Met Gln Asn His Leu Leu Gln Leu
            260                 265                 270
ctg gcg ctg gtg gcc atg gag gag ccc atc gcc ttc gac ccg gct gag      1164
Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ala Phe Asp Pro Ala Glu
        275                 280                 285
ctg cag gcg gag aag gtc aag gtc ctg cgc gcg acc aac ccc gtc ttc      1212
Leu Gln Ala Glu Lys Val Lys Val Leu Arg Ala Thr Asn Pro Val Phe
    290                 295                 300
ccg ctg aac aag acc acc gcc cgt ggc cag tac gcg gcg ggc tgg cag      1260
Pro Leu Asn Lys Thr Thr Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
305                 310                 315                 320
ggc tcg cac aag gtg cgt ggc ctg cgt gag gag gag ggt ttc gac ccg      1308
Gly Ser His Lys Val Arg Gly Leu Arg Glu Glu Glu Gly Phe Asp Pro
                325                 330                 335
gac tcc acc acg gag acc tac gcc gcc tgc acc ctg gag atc aac tcc      1356
Asp Ser Thr Thr Glu Thr Tyr Ala Ala Cys Thr Leu Glu Ile Asn Ser
            340                 345                 350
cgc cgc tgg gcg ggc gtg ccc ttc tac ctg cgg acc ggc aag cgc ctg      1404
Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
        355                 360                 365
ggg cgc cgc gtc acg gag atc gcc ctc gtg ttc aag gag gcg ccg cac      1452
Gly Arg Arg Val Thr Glu Ile Ala Leu Val Phe Lys Glu Ala Pro His
    370                 375                 380
cag ccc ttc ctc gag ggg cag acg tcc tcg ctg ggg cag aac gcg atc      1500
Gln Pro Phe Leu Glu Gly Gln Thr Ser Ser Leu Gly Gln Asn Ala Ile
385                 390                 395                 400
gtc atc cgc gtc cag ccc gac gag ggc gtg ctc atg cgc ttc ggc tcc      1548
Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Met Arg Phe Gly Ser
                405                 410                 415
aag gtg ccc ggc tcc gcg atg gag gtc cgt gac gtc aac atg gac ttc      1596
Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
            420                 425                 430
tcc tac gcg gag gcc ttc acc gag gcg tcc ccg gag gcc tat gag cgg      1644
Ser Tyr Ala Glu Ala Phe Thr Glu Ala Ser Pro Glu Ala Tyr Glu Arg
        435                 440                 445
ctc atc ctc gat gcg ctt ctc gac gag tcc tcg ctc ttc ccc acc aac      1692
Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
    450                 455                 460
gag gag gtc gag ctc tcc tgg gcg atc ctg gac ccg atc ctc gag ttc      1740
Glu Glu Val Glu Leu Ser Trp Ala Ile Leu Asp Pro Ile Leu Glu Phe
465                 470                 475                 480
tgg gct gag aag ggc cag ccc gag gag tac gag tcc ggc acc tgg ggg      1788
Trp Ala Glu Lys Gly Gln Pro Glu Glu Tyr Glu Ser Gly Thr Trp Gly
                485                 490                 495
ccc gcc tcc gcc gac cgc atg ctg gaa cgg acc ggc cgc gcc tgg cgc      1836
Pro Ala Ser Ala Asp Arg Met Leu Glu Arg Thr Gly Arg Ala Trp Arg
            500                 505                 510
cgc ccc tga cctggaaggg acccgacttg aagatcgaac tgccggacac              1885
Arg Pro

cgacacccgg aacatcgccg ccagcctgct cgaggcccgg gagcacaact cccagaccac     1945
cgggcgggtg ctcaccctca tcgtcgtcgc cgcgctcgac gacgacgtcg accacatcat     2005
ctccgtcacc cgcgacgcct cccacgagca ccccgcccgt gtgctggtgc tgctcaccgg     2065
ccgggaggac gctgactcgc gtctcgacgc cgaggtgcgc gtcggcggtc acgccggcgc     2125
ctcggagatg gtcatcatgc                                                2145
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Asn Thr Val Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met
            20                  25                  30
Val Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro
        35                  40                  45
Ala Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Ala Gly Phe Thr
    50                  55                  60
Leu Ile Gly Phe Gly Arg Arg Pro Trp Ser Lys Pro Glu Phe Glu Glu
65                  70                  75                  80
Tyr Val Arg Glu Ala Val Glu Ser Gly Ala Arg Thr Glu Phe Arg Glu
                85                  90                  95
His Val Trp Glu Arg Leu Ala Glu Gly Met His Phe Val Glu Gly Asn
            100                 105                 110
Phe Asp Asp Glu Gly Phe Asp Arg Leu Ala Ala Thr Leu Ala Glu Met
        115                 120                 125
Asp Thr Ser Arg Gly Thr Ala Gly Asn Trp Ala Phe Tyr Leu Ser Val
    130                 135                 140
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Pro Pro Asp Phe Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
145                 150                 155                 160
Leu Ala Glu Ala Gly Glu Glu Ser Trp Arg Arg Val Ile Ile Glu Lys
                165                 170                 175
Pro Phe Gly His Asp Gln Asp Thr Ala Arg Glu Leu Asn Arg Val Val
            180                 185                 190
Asn Ala Val Phe Pro Glu Glu Ser Val Phe Arg Ile Asp His Tyr Leu
        195                 200                 205
Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
    210                 215                 220
Leu Phe Asp Pro Ile Trp Asn Ala His Tyr Val Asp His Val Gln Ile
225                 230                 235                 240
Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
                245                 250                 255
Gly Ile Gly Ala Ala Arg Asp Val Met Gln Asn His Leu Leu Gln Leu
            260                 265                 270
Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ala Phe Asp Pro Ala Glu
        275                 280                 285
Leu Gln Ala Glu Lys Val Lys Val Leu Arg Ala Thr Asn Pro Val Phe
    290                 295                 300
Pro Leu Asn Lys Thr Thr Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
305                 310                 315                 320
Gly Ser His Lys Val Arg Gly Leu Arg Glu Glu Glu Gly Phe Asp Pro
                325                 330                 335
Asp Ser Thr Thr Glu Thr Tyr Ala Ala Cys Thr Leu Glu Ile Asn Ser
            340                 345                 350
Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
        355                 360                 365
Gly Arg Arg Val Thr Glu Ile Ala Leu Val Phe Lys Glu Ala Pro His
    370                 375                 380
Gln Pro Phe Leu Glu Gly Gln Thr Ser Ser Leu Gly Gln Asn Ala Ile
385                 390                 395                 400
Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Met Arg Phe Gly Ser
                405                 410                 415
Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
            420                 425                 430
Ser Tyr Ala Glu Ala Phe Thr Glu Ala Ser Pro Glu Ala Tyr Glu Arg
        435                 440                 445
Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
    450                 455                 460
Glu Glu Val Glu Leu Ser Trp Ala Ile Leu Asp Pro Ile Leu Glu Phe
465                 470                 475                 480
Trp Ala Glu Lys Gly Gln Pro Glu Glu Tyr Glu Ser Gly Thr Trp Gly
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Pro Ala Ser Ala Asp Arg Met Leu Glu Arg Thr Gly Arg Ala Trp Arg
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ccccaccaac gaggaggtcg agctctcctg ggcgatcctg gacccgatcc tcgagttctg      180
ggctgagaag ggccagcccg aggagtacga gtccggcacc tgggggcccg cctccgccga      240
ccgcatgctg gaacggaccg gccgcgcctg gcgccgcccc tgacctggaa gggacccgac      300
ttg aag atc gaa ctg ccg gac acc gac acc cgg aac atc gcc gcc agc         348
Leu Lys Ile Glu Leu Pro Asp Thr Asp Thr Arg Asn Ile Ala Ala Ser
1               5                   10                  15
ctg ctc gag gcc cgg gag cac aac tcc cag acc acc ggg cgg gtg ctc        396
Leu Leu Glu Ala Arg Glu His Asn Ser Gln Thr Thr Gly Arg Val Leu
            20                  25                  30
acc ctc atc gtc gtc gcc gcg ctc gac gac gac gtc gac cac atc atc        444
Thr Leu Ile Val Val Ala Ala Leu Asp Asp Asp Val Asp His Ile Ile
        35                  40                  45
tcc gtc acc cgc gac gcc tcc cac gag cac ccc gcc cgt gtg ctg gtg        492
Ser Val Thr Arg Asp Ala Ser His Glu His Pro Ala Arg Val Leu Val
    50                  55                  60
ctg ctc acc ggc cgg gag gac gct gac tcg cgt ctc gac gcc gag gtg        540
Leu Leu Thr Gly Arg Glu Asp Ala Asp Ser Arg Leu Asp Ala Glu Val
65                  70                  75                  80
cgc gtc ggc ggt cac gcc ggc gcc tcg gag atg gtc atc atg cgc atc        588
Arg Val Gly Gly His Ala Gly Ala Ser Glu Met Val Ile Met Arg Ile
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                85                  90                  95
acg ggc gag atg gtc aac cac ctc gcc gcg gtg gtc acc ccc ctg ctg        636
Thr Gly Glu Met Val Asn His Leu Ala Ala Val Val Thr Pro Leu Leu
            100                 105                 110
ctg ccg gac acc ccg gtc gtc gcc tgg tgg ccg acc acc gcg ccg gag        684
Leu Pro Asp Thr Pro Val Val Ala Trp Trp Pro Thr Thr Ala Pro Glu
        115                 120                 125
aac ccc tcc ggg cat ccg ctg ggc cag ctg gcg cag cgc cgc atc acc        732
Asn Pro Ser Gly His Pro Leu Gly Gln Leu Ala Gln Arg Arg Ile Thr
    130                 135                 140
aac gcg gac cac ccg gac agt gag tcg gtc ctc cgg ctc cgc cgt gcc        780
Asn Ala Asp His Pro Asp Ser Glu Ser Val Leu Arg Leu Arg Arg Ala
145                 150                 155                 160
acc tac gcc ccc ggt gac tcc gac atg gtg tgg tcg aag atc acc gcc        828
Thr Tyr Ala Pro Gly Asp Ser Asp Met Val Trp Ser Lys Ile Thr Ala
                165                 170                 175
tgg cgc ggt atc gtc gcc tcc tcc ctg gac cgt cac ccg cac gag gac        876
Trp Arg Gly Ile Val Ala Ser Ser Leu Asp Arg His Pro His Glu Asp
            180                 185                 190
gtg gag gcc gcc gtc ctc acc ggc ccg gcg gat gag ccg cag atc gac        924
Val Glu Ala Ala Val Leu Thr Gly Pro Ala Asp Glu Pro Gln Ile Asp
        195                 200                 205
atc gcc gcc ggc tgg ctc gcc gac cgc ctc ggt gtg ccg gtc cgc cgg        972
Ile Ala Ala Gly Trp Leu Ala Asp Arg Leu Gly Val Pro Val Arg Arg
    210                 215                 220
gag gtg tgt gaa ccg ggt aac gac gcc cgg ctc ttc ccc atc cgt cgt       1020
Glu Val Cys Glu Pro Gly Asn Asp Ala Arg Leu Phe Pro Ile Arg Arg
225                 230                 235                 240
ctc aag ttc gaa cgc gcc tcc ggc ccg gtc cgc gtc gag gtg ctc gac       1068
Leu Lys Phe Glu Arg Ala Ser Gly Pro Val Arg Val Glu Val Leu Asp
                245                 250                 255
cac cgg acc gtg ctc gtc gcc ctg cca ggg cgc ccg gag tcg ctc gtc       1116
His Arg Thr Val Leu Val Ala Leu Pro Gly Arg Pro Glu Ser Leu Val
            260                 265                 270
gcc atg aac gag cgt tcc gac gcc gac tgc ctc tcc gag gaa ctg cgt       1164
Ala Met Asn Glu Arg Ser Asp Ala Asp Cys Leu Ser Glu Glu Leu Arg
        275                 280                 285
cac ctc gac ccc gat ctc gcc tac gcc aac gct ctg cgc gga ctc acc       1212
His Leu Asp Pro Asp Leu Ala Tyr Ala Asn Ala Leu Arg Gly Leu Thr
    290                 295                 300
cgt gtg aaa gga atc aat ggt cac cct gcg tcg tcc tga caccctgtcc       1261
Arg Val Lys Gly Ile Asn Gly His Pro Ala Ser Ser
305                 310                 315
accctgctcg accaggccgc cacgtcgctc atcgacgtcg tcgctgccct ccagaccacc     1321
gggggcggtg tccacgccga cggtgtggcc cgcctggtgc tcaccggcgg cggcgccggc     1381
atcggcctgc tggagcgcgt ccgtgagctc gaggacgccg actcccgcat cgactggtcc     1441
cgcgtccacg tcttcttcgg cgacgagcgc aacgtgcccg tctcccacga ggactccaac     1501
gaggggcagg cgcgtaccgc cctgctcagc cacgtcgaca tcccggaggc                1551
<210>  188
<211>  316
<212>  PRT
<213>  Corynebacterium humireducens
<400>  188
Leu Lys Ile Glu Leu Pro Asp Thr Asp Thr Arg Asn Ile Ala Ala Ser
1                   5                  10                  15
Leu Leu Glu Ala Arg Glu His Asn Ser Gln Thr Thr Gly Arg Val Leu
            20                  25                  30
Thr Leu Ile Val Val Ala Ala Leu Asp Asp Asp Val Asp His Ile Ile
        35                  40                  45
Ser Val Thr Arg Asp Ala Ser His Glu His Pro Ala Arg Val Leu Val
    50                  55                  60
Leu Leu Thr Gly Arg Glu Asp Ala Asp Ser Arg Leu Asp Ala Glu Val
65                  70                  75                  80
Arg Val Gly Gly His Ala Gly Ala Ser Glu Met Val Ile Met Arg Ile
                85                  90                  95
Thr Gly Glu Met Val Asn His Leu Ala Ala Val Val Thr Pro Leu Leu
            100                 105                 110
Leu Pro Asp Thr Pro Val Val Ala Trp Trp Pro Thr Thr Ala Pro Glu
        115                 120                 125
Asn Pro Ser Gly His Pro Leu Gly Gln Leu Ala Gln Arg Arg Ile Thr
    130                 135                 140
Asn Ala Asp His Pro Asp Ser Glu Ser Val Leu Arg Leu Arg Arg Ala
145                 150                 155                 160
Thr Tyr Ala Pro Gly Asp Ser Asp Met Val Trp Ser Lys Ile Thr Ala
                165                 170                 175
Trp Arg Gly Ile Val Ala Ser Ser Leu Asp Arg His Pro His Glu Asp
            180                 185                 190
Val Glu Ala Ala Val Leu Thr Gly Pro Ala Asp Glu Pro Gln Ile Asp
```

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        195                 200                 205
Ile Ala Ala Gly Trp Leu Ala Asp Arg Leu Gly Val Pro Val Arg Arg
    210                 215                 220
Glu Val Cys Glu Pro Gly Asn Asp Ala Arg Leu Phe Pro Ile Arg Arg
225                 230                 235                 240
Leu Lys Phe Glu Arg Ala Ser Gly Pro Val Arg Val Glu Val Leu Asp
                245                 250                 255
His Arg Thr Val Leu Val Ala Leu Pro Gly Arg Pro Glu Ser Leu Val
            260                 265                 270
Ala Met Asn Glu Arg Ser Asp Ala Asp Cys Leu Ser Glu Glu Leu Arg
        275                 280                 285
His Leu Asp Pro Asp Leu Ala Tyr Ala Asn Ala Leu Arg Gly Leu Thr
    290                 295                 300
Arg Val Lys Gly Ile Asn Gly His Pro Ala Ser Ser
305                 310                 315
<210>  189
<211>  2283
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1983)
<223>  gen hutU (Urocanat Hydrataza)
<400>  189
gctacctgtc cccggagatc gaggagtcgg tgcagctgct cacctccggg gcgctgctgg        60
aggcggtgga gggggtcgtc ggaaagctgg catgagcggg cgaatctcag atatgagact       120
aaaggggcct ccgggccctc gatcccgact gtgacctgtc ttaccgtcag aagtgtcacc       180
gacaccggcc acaccagccc ggtgctccac acccgacgat gacagccccg ggccacccgg       240
atcgcgggtg ccccggggcc ccggcctgat cggcccccac cgtagaagga gacccacccc       300
atg acc gag tcc ccg cgc acc atc cgt gcc ccg cac ggc acc gag ctc          348
Met Thr Glu Ser Pro Arg Thr Ile Arg Ala Pro His Gly Thr Glu Leu
1               5                   10                  15
agc gcc aag agc tgg caa acc gag gca ccc ctg cgc atg ctc atg aac          396
Ser Ala Lys Ser Trp Gln Thr Glu Ala Pro Leu Arg Met Leu Met Asn
            20                  25                  30
aac ctc gac ccg gag gtc gcc gag cgc ccc gag gac ctc gtc gtc tac          444
Asn Leu Asp Pro Glu Val Ala Glu Arg Pro Glu Asp Leu Val Val Tyr
        35                  40                  45
ggc ggc acc ggc cgc gcg gca cgc agc tgg gag gcc tac gac gcg atc          492
Gly Gly Thr Gly Arg Ala Ala Arg Ser Trp Glu Ala Tyr Asp Ala Ile
    50                  55                  60
atc gag acg ctc agg gac ctc gag gag gac gag acc ctg ctc gtc cag          540
Ile Glu Thr Leu Arg Asp Leu Glu Glu Asp Glu Thr Leu Leu Val Gln
65                  70                  75                  80
tcc ggc aag ccc gtc ggc gtc ttc cgc acc aac gtc tgg gca ccc cgc          588
Ser Gly Lys Pro Val Gly Val Phe Arg Thr Asn Val Trp Ala Pro Arg
                85                  90                  95
gtg ctc atc gcc aac tcc aac ctc gtc ggc gac tgg gcc aac tgg ccc          636
Val Leu Ile Ala Asn Ser Asn Leu Val Gly Asp Trp Ala Asn Trp Pro
            100                 105                 110
gag ttc cgc cgc ctc gag gcc gag ggc ctc atg atg tac ggc cag atg          684
Glu Phe Arg Arg Leu Glu Ala Glu Gly Leu Met Met Tyr Gly Gln Met
        115                 120                 125
acc gcc ggt tcc tgg atc tac atc gcc acc cag ggc atc ctc cag ggc          732
Thr Ala Gly Ser Trp Ile Tyr Ile Ala Thr Gln Gly Ile Leu Gln Gly
    130                 135                 140
acc tac gag acc ttc gcc gcc gtg gcc cgc aag cgt ttc ggc ggc acc          780
Thr Tyr Glu Thr Phe Ala Ala Val Ala Arg Lys Arg Phe Gly Gly Thr
145                 150                 155                 160
ctc gcc ggc acc ctc acc ctc acc ggc ggc tgc ggc ggc atg ggc ggg          828
Leu Ala Gly Thr Leu Thr Leu Thr Gly Gly Cys Gly Gly Met Gly Gly
                165                 170                 175
gcc cag ccg ctg tcc gtc acc ctc aac ggc ggt gtc tgc ctc atc gtc          876
Ala Gln Pro Leu Ser Val Thr Leu Asn Gly Gly Val Cys Leu Ile Val
            180                 185                 190
gac gtc gac gag tcc cgg ctc agg cgt cgg cag gcc aag cgc tac ctc          924
Asp Val Asp Glu Ser Arg Leu Arg Arg Arg Gln Ala Lys Arg Tyr Leu
        195                 200                 205
gat gag gtc gcc acc gat ctc gac gac gcc gtc gcc cgc gtc agc gcc          972
Asp Glu Val Ala Thr Asp Leu Asp Asp Ala Val Ala Arg Val Ser Ala
    210                 215                 220
gcc aag gag gag aag cgt gcc ctg tcc gtc ggc cta gtg ggc aat gcc         1020
Ala Lys Glu Glu Lys Arg Ala Leu Ser Val Gly Leu Val Gly Asn Ala
225                 230                 235                 240

gcc gag gtg ttc ccc gag ctg ctg cgc cgc cac cgc gcc ggg gag atc         1068
Ala Glu Val Phe Pro Glu Leu Leu Arg Arg His Arg Ala Gly Glu Ile
                245                 250                 255
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acc gtc gac gtg gtc acc gac cag acc tcc gcc cac gac ccg ctc agc      1116
Thr Val Asp Val Val Thr Asp Gln Thr Ser Ala His Asp Pro Leu Ser
            260                 265                 270
tac ctg ccc acc gag atc acc gtc gag gac tgg cag cgc gag gcc gcc      1164
Tyr Leu Pro Thr Glu Ile Thr Val Glu Asp Trp Gln Arg Glu Ala Ala
        275                 280                 285
gag gac ccc atc acc ttc acc aag aag gca cgc gag tcc atg gcc gtg      1212
Glu Asp Pro Ile Thr Phe Thr Lys Lys Ala Arg Glu Ser Met Ala Val
    290                 295                 300
cag gtc cag gcc atg gtc gag ttc cag gac gag ggc gcc gag gtc ttc      1260
Gln Val Gln Ala Met Val Glu Phe Gln Asp Glu Gly Ala Glu Val Phe
305                 310                 315                 320
gac tac ggc aac tcc atc cgc gat gag gcc cgc cac gcc ggc tac tcc      1308
Asp Tyr Gly Asn Ser Ile Arg Asp Glu Ala Arg His Ala Gly Tyr Ser
                325                 330                 335
cgc gcc ttc gag ttc ccc ggc ttc gtc ccc gcc tac atc cgg ccc ctg      1356
Arg Ala Phe Glu Phe Pro Gly Phe Val Pro Ala Tyr Ile Arg Pro Leu
            340                 345                 350
ttc tgc gag ggt ctc ggc ccc ttc cgc tgg gtg gcc ctt tcc ggc gac      1404
Phe Cys Glu Gly Leu Gly Pro Phe Arg Trp Val Ala Leu Ser Gly Asp
        355                 360                 365
ccg gag gac atc cgc gtc acc gac gag gcc gtc aag gag ctg ttc ccc      1452
Pro Glu Asp Ile Arg Val Thr Asp Glu Ala Val Lys Glu Leu Phe Pro
    370                 375                 380
gac aac gag cac ctc cac cgc tgg atc gac gcg gca ggg gag tac gtc      1500
Asp Asn Glu His Leu His Arg Trp Ile Asp Ala Ala Gly Glu Tyr Val
385                 390                 395                 400
gag ttc gag ggc ctg ccg gcc cgc atc tgc tgg ctc ggc tac ggc gag      1548
Glu Phe Glu Gly Leu Pro Ala Arg Ile Cys Trp Leu Gly Tyr Gly Glu
                405                 410                 415
cgg cac aag gcg gga ctg ctg ttc aac cgt ctc gtc gcc gag ggc aag      1596
Arg His Lys Ala Gly Leu Leu Phe Asn Arg Leu Val Ala Glu Gly Lys
            420                 425                 430
gtg aag gcg ccc atc gtc atc ggc cgt gac cac ctc gac tcc ggt tcc      1644
Val Lys Ala Pro Ile Val Ile Gly Arg Asp His Leu Asp Ser Gly Ser
        435                 440                 445
gtc gcc tcc ccc tac cgg gag acc gag tcc atg ctc gac ggc tcc gac      1692
Val Ala Ser Pro Tyr Arg Glu Thr Glu Ser Met Leu Asp Gly Ser Asp
    450                 455                 460
gcc atc gcc gac tgg ccg ctg ctc aac gcc ctc acc gcc acc tcc tcc      1740
Ala Ile Ala Asp Trp Pro Leu Leu Asn Ala Leu Thr Ala Thr Ser Ser
465                 470                 475                 480
ggc gcg acc tgg gtc tcc ctg cac cac gga ggc ggc gtg ggc atc gga      1788
Gly Ala Thr Trp Val Ser Leu His His Gly Gly Gly Val Gly Ile Gly
                485                 490                 495
cgg tcc atc cac gcg ggc cag gtg tgc gtc gcc gac ggc acg gag ctg      1836
Arg Ser Ile His Ala Gly Gln Val Cys Val Ala Asp Gly Thr Glu Leu
            500                 505                 510
gcc gcc gcg aag ctc acc gcc gtg ctc acc aac gac ccg ggc atg ggc      1884
Ala Ala Ala Lys Leu Thr Ala Val Leu Thr Asn Asp Pro Gly Met Gly
        515                 520                 525
gtc atc cgc cac gtc gac gcc ggc tac gac cgt gcc cac gag gtc gcc      1932
Val Ile Arg His Val Asp Ala Gly Tyr Asp Arg Ala His Glu Val Ala
    530                 535                 540
gtc gag cgc ggg gtc cgt gtc ccc atg ccg ttc gtc agc cgc gag agg      1980
Val Glu Arg Gly Val Arg Val Pro Met Pro Phe Val Ser Arg Glu Arg
545                 550                 555                 560
tag ccatgagcac gctgttccac ggaatctccg agctgaggac cgtctccggg           2033
ctgggcacgc tcagcgacgc cgcgctcatc gtcgaccggg gccgcatcgc ctggatcggc    2093
ccgcgcgccg gggcccccgc cgccgacgcg gcggttgatc tgggcggccg ggccgtgcta    2153
cccggctggg tggactccca cacccacatg atcttcgcgg gggaccgcgc cgccgagttc    2213
gaggcccgca tgaacgggca ggactaccag gcgggcggca tcgcggtgac catgtccgcc    2273
acccgcgagg                                                          2283
<210>  190
<211>  560
<212>  PRT
<213>  Corynebacterium humireducens
<400>  190
Met Thr Glu Ser Pro Arg Thr Ile Arg Ala Pro His Gly Thr Glu Leu
1               5                   10                  15
Ser Ala Lys Ser Trp Gln Thr Glu Ala Pro Leu Arg Met Leu Met Asn
            20                  25                  30
Asn Leu Asp Pro Glu Val Ala Glu Arg Pro Glu Asp Leu Val Val Tyr
        35                  40                  45
Gly Gly Thr Gly Arg Ala Ala Arg Ser Trp Glu Ala Tyr Asp Ala Ile
    50                  55                  60
Ile Glu Thr Leu Arg Asp Leu Glu Glu Asp Glu Thr Leu Leu Val Gln
65                  70                  75                  80
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Ser Gly Lys Pro Val Gly Val Phe Arg Thr Asn Val Trp Ala Pro Arg
                85                  90                  95
Val Leu Ile Ala Asn Ser Asn Leu Val Gly Asp Trp Ala Asn Trp Pro
            100                 105                 110
Glu Phe Arg Arg Leu Glu Ala Glu Gly Leu Met Met Tyr Gly Gln Met
        115                 120                 125
Thr Ala Gly Ser Trp Ile Tyr Ile Ala Thr Gln Gly Ile Leu Gln Gly
    130                 135                 140
Thr Tyr Glu Thr Phe Ala Ala Val Ala Arg Lys Arg Phe Gly Gly Thr
145                 150                 155                 160
Leu Ala Gly Thr Leu Thr Leu Thr Gly Gly Cys Gly Gly Met Gly Gly
                165                 170                 175
Ala Gln Pro Leu Ser Val Thr Leu Asn Gly Gly Val Cys Leu Ile Val
            180                 185                 190
Asp Val Asp Glu Ser Arg Leu Arg Arg Arg Gln Ala Lys Arg Tyr Leu
        195                 200                 205
Asp Glu Val Ala Thr Asp Leu Asp Asp Ala Val Ala Arg Val Ser Ala
    210                 215                 220
Ala Lys Glu Glu Lys Arg Ala Leu Ser Val Gly Leu Val Gly Asn Ala
225                 230                 235                 240
Ala Glu Val Phe Pro Glu Leu Leu Arg Arg His Arg Ala Gly Glu Ile
                245                 250                 255
Thr Val Asp Val Val Thr Asp Gln Thr Ser Ala His Asp Pro Leu Ser
            260                 265                 270
Tyr Leu Pro Thr Glu Ile Thr Val Glu Asp Trp Gln Arg Glu Ala Ala
        275                 280                 285
Glu Asp Pro Ile Thr Phe Thr Lys Lys Ala Arg Glu Ser Met Ala Val
    290                 295                 300
Gln Val Gln Ala Met Val Glu Phe Gln Asp Glu Gly Ala Glu Val Phe
305                 310                 315                 320
Asp Tyr Gly Asn Ser Ile Arg Asp Glu Ala Arg His Ala Gly Tyr Ser
                325                 330                 335
Arg Ala Phe Glu Phe Pro Gly Phe Val Pro Ala Tyr Ile Arg Pro Leu
            340                 345                 350
Phe Cys Glu Gly Leu Gly Pro Phe Arg Trp Val Ala Leu Ser Gly Asp
        355                 360                 365
Pro Glu Asp Ile Arg Val Thr Asp Glu Ala Val Lys Glu Leu Phe Pro
    370                 375                 380
Asp Asn Glu His Leu His Arg Trp Ile Asp Ala Ala Gly Glu Tyr Val
385                 390                 395                 400
Glu Phe Glu Gly Leu Pro Ala Arg Ile Cys Trp Leu Gly Tyr Gly Glu
                405                 410                 415
Arg His Lys Ala Gly Leu Leu Phe Asn Arg Leu Val Ala Glu Gly Lys
            420                 425                 430
Val Lys Ala Pro Ile Val Ile Gly Arg Asp His Leu Asp Ser Gly Ser
        435                 440                 445
Val Ala Ser Pro Tyr Arg Glu Thr Glu Ser Met Leu Asp Gly Ser Asp
    450                 455                 460
Ala Ile Ala Asp Trp Pro Leu Leu Asn Ala Leu Thr Ala Thr Ser Ser
465                 470                 475                 480
Gly Ala Thr Trp Val Ser Leu His His Gly Gly Gly Val Gly Ile Gly
                485                 490                 495
Arg Ser Ile His Ala Gly Gln Val Cys Val Ala Asp Gly Thr Glu Leu
            500                 505                 510
Ala Ala Ala Lys Leu Thr Ala Val Leu Thr Asn Asp Pro Gly Met Gly
        515                 520                 525
Val Ile Arg His Val Asp Ala Gly Tyr Asp Arg Ala His Glu Val Ala
    530                 535                 540
Val Glu Arg Gly Val Arg Val Pro Met Pro Phe Val Ser Arg Glu Arg
545                 550                 555                 560
<210>  191
<211>  1809
<212>  ADN
<213>  Corynebacterium humireducens
<220>
<221>  CDS
<222>  (301)..(1509)
<223>  gen hutI (Imidazolone Propionase)
<400>  191
ctccgacgcc atcgccgact ggccgctgct caacgccctc accgccacct cctccggcgc       60
gacctgggtc tccctgcacc acggaggcgg cgtgggcatc ggacggtcca tccacgcggg      120
ccaggtgtgc gtcgccgacg gcacggagct ggccgccgcg aagctcaccg ccgtgctcac      180
caacgacccg ggcatgggcg tcatccgcca cgtcgacgcc ggctacgacc gtgcccacga      240
ggtcgccgtc gagcgcgggg tccgtgtccc catgccgttc gtcagccgcg agaggtagcc      300
atg agc acg ctg ttc cac gga atc tcc gag ctg agg acc gtc tcc ggg        348
Met Ser Thr Leu Phe His Gly Ile Ser Glu Leu Arg Thr Val Ser Gly
1               5                   10                  15
ctg ggc acg ctc agc gac gcc gcg ctc atc gtc gac cgg ggc cgc atc        396
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```
Leu Gly Thr Leu Ser Asp Ala Ala Leu Ile Val Asp Arg Gly Arg Ile
            20                  25                  30
gcc tgg atc ggc ccg cgc gcc ggg gcc ccc gcc gcc gac gcg gcg gtt        444
Ala Trp Ile Gly Pro Arg Ala Gly Ala Pro Ala Ala Asp Ala Ala Val
        35                  40                  45
gat ctg ggc ggc cgg gcc gtg cta ccc ggc tgg gtg gac tcc cac acc        492
Asp Leu Gly Gly Arg Ala Val Leu Pro Gly Trp Val Asp Ser His Thr
    50                  55                  60
cac atg atc ttc gcg ggg gac cgc gcc gcc gag ttc gag gcc cgc atg        540
His Met Ile Phe Ala Gly Asp Arg Ala Ala Glu Phe Glu Ala Arg Met
65                  70                  75                  80
aac ggg cag gac tac cag gcg ggc ggc atc gcg gtg acc atg tcc gcc        588
Asn Gly Gln Asp Tyr Gln Ala Gly Gly Ile Ala Val Thr Met Ser Ala
                85                  90                  95
acc cgc gag gcc ggc gcc gtc cgc ctc gag cag ctg ctg ctg cgc cgc        636
Thr Arg Glu Ala Gly Ala Val Arg Leu Glu Gln Leu Leu Leu Arg Arg
            100                 105                 110
ctg gcc gat gcg cgc gcc ggg ggc acg acc acg gtg gag acg aag acc        684
Leu Ala Asp Ala Arg Ala Gly Gly Thr Thr Thr Val Glu Thr Lys Thr
        115                 120                 125
ggc tac ggg ctc gac gtg gac tcc gag gcc ctg gcg gcc gac atc gcc        732
Gly Tyr Gly Leu Asp Val Asp Ser Glu Ala Leu Ala Ala Asp Ile Ala
    130                 135                 140
gcc cgg cac gtc gat gac gtc acc ttc ctc ggc gcg cat ctc gtg ccg        780
Ala Arg His Val Asp Asp Val Thr Phe Leu Gly Ala His Leu Val Pro
145                 150                 155                 160
ccg ggg gag gac ccg gac gag tac ctc gct ctc gtg ctc ggc gac atg        828
Pro Gly Glu Asp Pro Asp Glu Tyr Leu Ala Leu Val Leu Gly Asp Met
                165                 170                 175
ctc gac gcc gtc gcg gcc aac gtc agc tgg atc gac gtg ttc tgc gaa        876
Leu Asp Ala Val Ala Ala Asn Val Ser Trp Ile Asp Val Phe Cys Glu
            180                 185                 190
cgc ggg gcc ttc gat gag gcg gcc gcc cgc cgc gtc ctc gag gcc ggg        924
Arg Gly Ala Phe Asp Glu Ala Ala Ala Arg Arg Val Leu Glu Ala Gly
        195                 200                 205
cgg gcg cgg ggt ctg ggg ctg cgc gtg cac ggc aac cag ctc ggg cac        972
Arg Ala Arg Gly Leu Gly Leu Arg Val His Gly Asn Gln Leu Gly His
    210                 215                 220
ggt ccc gga gtg cag ctg gcg gtg gag tac ggc gcc gcc agc gtg gac       1020
Gly Pro Gly Val Gln Leu Ala Val Glu Tyr Gly Ala Ala Ser Val Asp
225                 230                 235                 240
cac gtc aac tac gtg agt gac ggt gac gtg gag gca ctc gcc tcc tcg       1068
His Val Asn Tyr Val Ser Asp Gly Asp Val Glu Ala Leu Ala Ser Ser
                245                 250                 255
gag acg gtg gcc acg gtc ctc ccc gcc tgc gac ctg tcc acg agg cag       1116
Glu Thr Val Ala Thr Val Leu Pro Ala Cys Asp Leu Ser Thr Arg Gln
            260                 265                 270
ccg ctg gcg ccg gcc cgg agg ctt ctc gac gcc ggg gtc cac ctc gcc       1164
Pro Leu Ala Pro Ala Arg Arg Leu Leu Asp Ala Gly Val His Leu Ala
        275                 280                 285
ctc gcc tcc aac ctc aac ccg ggc acg tcg tac acc tcg tcg atg gcc       1212
Leu Ala Ser Asn Leu Asn Pro Gly Thr Ser Tyr Thr Ser Ser Met Ala
    290                 295                 300
ttc tgc gtc acc acc gcg gtg ctg cag cag cac ctc acc ctc gac gag       1260
Phe Cys Val Thr Thr Ala Val Leu Gln Gln His Leu Thr Leu Asp Glu
305                 310                 315                 320
gcc atc cac gcg gcc acc gcc ggt ggg gcg cgg gcg ctg cgg cgt cac       1308
Ala Ile His Ala Ala Thr Ala Gly Gly Ala Arg Ala Leu Arg Arg His
                325                 330                 335

gac atc ggc ggc ggc gtc gac ccc cag ggc cga ccc gcc cgc ggc agc       1356
Asp Ile Gly Gly Gly Val Asp Pro Gln Gly Arg Pro Ala Arg Gly Ser
            340                 345                 350
ctc gtg gtc ggg gcc gcg gca gac ctg cac gtg ctg gac acc ccc cac       1404
Leu Val Val Gly Ala Ala Ala Asp Leu His Val Leu Asp Thr Pro His
        355                 360                 365
gcc atc gat ctg gcc tac cgg ccg ggg atg ccg ctc acg tgg cgg acc       1452
Ala Ile Asp Leu Ala Tyr Arg Pro Gly Met Pro Leu Thr Trp Arg Thr
    370                 375                 380
tac atc cag ggg gtg cag gtc cac ccg gaa ccg cag gat cag tcc gac       1500
Tyr Ile Gln Gly Val Gln Val His Pro Glu Pro Gln Asp Gln Ser Asp
385                 390                 395                 400
ggc cga tga cgcacgatct cctccacgat ccgggccgcg acccgcgcgg                1549
Gly Arg

tccggccgtc gacgtcgaga agcgggttga gttcgacgac atcgaccaga cgcagcttcc      1609
cgctgcgcgc cacggctctg acgagcgtca ggatccgtgc cagatcgacg cccaacgccg      1669
ccggcgcgct cacgccgggg gcgaccgccg cgggcaggac gtcaaggtcg atgctcaggt      1729
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ggacgtccgg ggcgtcctcc aggagctttc cgacgagcgc ctcgcacccg gccgacgtca 1789
tctccgccag ctcgacgtcg 1809
<210> 192
<211> 402
<212> PRT
<213> Corynebacterium humireducens
<400> 192
Met Ser Thr Leu Phe His Gly Ile Ser Glu Leu Arg Thr Val Ser Gly
1 5 10 15
Leu Gly Thr Leu Ser Asp Ala Ala Leu Ile Val Asp Arg Gly Arg Ile
20 25 30
Ala Trp Ile Gly Pro Arg Ala Gly Ala Pro Ala Ala Asp Ala Ala Val
35 40 45
Asp Leu Gly Gly Arg Ala Val Leu Pro Gly Trp Val Asp Ser His Thr
50 55 60
His Met Ile Phe Ala Gly Asp Arg Ala Ala Glu Phe Glu Ala Arg Met
65 70 75 80
Asn Gly Gln Asp Tyr Gln Ala Gly Gly Ile Ala Val Thr Met Ser Ala
85 90 95
Thr Arg Glu Ala Gly Ala Val Arg Leu Glu Gln Leu Leu Leu Arg Arg
100 105 110
Leu Ala Asp Ala Arg Ala Gly Gly Thr Thr Thr Val Glu Thr Lys Thr
115 120 125
Gly Tyr Gly Leu Asp Val Asp Ser Glu Ala Leu Ala Ala Asp Ile Ala
130 135 140
Ala Arg His Val Asp Asp Val Thr Phe Leu Gly Ala His Leu Val Pro
145 150 155 160
Pro Gly Glu Asp Pro Asp Glu Tyr Leu Ala Leu Val Leu Gly Asp Met
165 170 175
Leu Asp Ala Val Ala Ala Asn Val Ser Trp Ile Asp Val Phe Cys Glu
180 185 190
Arg Gly Ala Phe Asp Glu Ala Ala Ala Arg Arg Val Leu Glu Ala Gly
195 200 205
Arg Ala Arg Gly Leu Gly Leu Arg Val His Gly Asn Gln Leu Gly His
210 215 220
Gly Pro Gly Val Gln Leu Ala Val Glu Tyr Gly Ala Ala Ser Val Asp
225 230 235 240
His Val Asn Tyr Val Ser Asp Gly Asp Val Glu Ala Leu Ala Ser Ser
245 250 255
Glu Thr Val Ala Thr Val Leu Pro Ala Cys Asp Leu Ser Thr Arg Gln
260 265 270
Pro Leu Ala Pro Ala Arg Arg Leu Leu Asp Ala Gly Val His Leu Ala
275 280 285
Leu Ala Ser Asn Leu Asn Pro Gly Thr Ser Tyr Thr Ser Ser Met Ala
290 295 300
Phe Cys Val Thr Thr Ala Val Leu Gln Gln His Leu Thr Leu Asp Glu
305 310 315 320
Ala Ile His Ala Ala Thr Ala Gly Gly Ala Arg Ala Leu Arg Arg His
325 330 335
Asp Ile Gly Gly Gly Val Asp Pro Gln Gly Arg Pro Ala Arg Gly Ser
340 345 350
Leu Val Val Gly Ala Ala Ala Asp Leu His Val Leu Asp Thr Pro His
355 360 365
Ala Ile Asp Leu Ala Tyr Arg Pro Gly Met Pro Leu Thr Trp Arg Thr
370 375 380
Tyr Ile Gln Gly Val Gln Val His Pro Glu Pro Gln Asp Gln Ser Asp
385 390 395 400
Gly Arg
<210> 193
<211> 2151
<212> AND
<213> Corynebacterium humireducens
<220>
<221> CDS
<222> (301)..(1851)
<223> gen hutH (Histidin Amoniac lyaza)
<400> 193
ccccggcgtc gtcggtaccg gcccggaatg ccatccgtgc agctcagagc cctgacgggc 60
atctcgtatg cgagatagat tccgcgcaca ccggaaagtc tcgtaagtga gacagccgtg 120
cccttcacgg gctgtcgccg gggcgtgacg gctgacacac tgggaggaac tgcgtccggc 180
tgtcgcgcag gtcgaaccgt ccacgagtca ccgccccgga ggacaggtac cacctgtgcc 240
tgccccgggg ccggtgcccc ggagaaaccg ggacccacca ggaagcaggg gaagccccac 300
atg cag acc atc acc tcc cac atc cgc gtc ggc gtc gga gcg ctc agc 348
Met Gln Thr Ile Thr Ser His Ile Arg Val Gly Val Gly Ala Leu Ser
1 5 10 15
atc gac gag gtc gtg gct gtc gcc cgg cac gac gcc cac gtc gag atc 396
Ile Asp Glu Val Val Ala Val Ala Arg His Asp Ala His Val Glu Ile
20 25 30

```
acc ccg gag gcg ctc gag gcc gtc gcc gcc acc cgt gcc cgc atc gag        444
Thr Pro Glu Ala Leu Glu Ala Val Ala Ala Thr Arg Ala Arg Ile Glu
        35                  40                  45
gaa ctg gcc gac cac ccg acc ccg gtg tac ggc gtg tcc acc ggt ttc        492
Glu Leu Ala Asp His Pro Thr Pro Val Tyr Gly Val Ser Thr Gly Phe
    50                  55                  60
ggc gcc ctg gcc cgc cgc tac atc ccc cag gag atg cgc ctc cag ctg        540
Gly Ala Leu Ala Arg Arg Tyr Ile Pro Gln Glu Met Arg Leu Gln Leu
65                  70                  75                  80
cag cgc agc ctc gtc cgc tcc cat gcc gcc ggc tcc ggc ccc gag gtg        588
Gln Arg Ser Leu Val Arg Ser His Ala Ala Gly Ser Gly Pro Glu Val
                85                  90                  95
gag cgc gag gtc gtc cgg gcg ctc atg ctg ctg cgc ctg tcc aca ctg        636
Glu Arg Glu Val Val Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu
            100                 105                 110
tgc acc ggc cgt acc ggc gtg cgg ccg gtc gtc gcg gag acc tac gcc        684
Cys Thr Gly Arg Thr Gly Val Arg Pro Val Val Ala Glu Thr Tyr Ala
        115                 120                 125
gcg gtg ctc aac gcc ggc atc acc ccc gtc gtc cac gag tac ggc tcg        732
Ala Val Leu Asn Ala Gly Ile Thr Pro Val Val His Glu Tyr Gly Ser
    130                 135                 140
ctc ggc tgc tcc ggc gac ctc tcc ccg ctg gcg cac tgc gcc ctg gcg        780
Leu Gly Cys Ser Gly Asp Leu Ser Pro Leu Ala His Cys Ala Leu Ala
145                 150                 155                 160
ctg ctg ggg gag ggc gag gtc acc acc gct gac ggc cgc cgc ctg ccc        828
Leu Leu Gly Glu Gly Glu Val Thr Thr Ala Asp Gly Arg Arg Leu Pro
                165                 170                 175
gcc gcc gtc gcc ctc gcc gag cac ggc atc gag ccg ctg gtc ctg cgg        876
Ala Ala Val Ala Leu Ala Glu His Gly Ile Glu Pro Leu Val Leu Arg
            180                 185                 190
gag aag gag ggg ctg gca ctc atc aac ggc acc gac ggc atg ctg ggc        924
Glu Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Asp Gly Met Leu Gly
        195                 200                 205
atg ctg tgc ctg gcc atc gct gac ctc gag tgc ctg gcc cgc agc gcc        972
Met Leu Cys Leu Ala Ile Ala Asp Leu Glu Cys Leu Ala Arg Ser Ala
    210                 215                 220
gac atc gcc gcc gcg atg acc gtc gag gcc ctg cgg ggc acc ctc acc       1020
Asp Ile Ala Ala Ala Met Thr Val Glu Ala Leu Arg Gly Thr Leu Thr
225                 230                 235                 240
gtc ttc gcc gcg gac ctg cag gag ctg cgc ccg cac ccg ggt cag gcg       1068
Val Phe Ala Ala Asp Leu Gln Glu Leu Arg Pro His Pro Gly Gln Ala
                245                 250                 255
gcc tcc gcg gcc aac atc cgc gcc gtg gcc gag ggc tcc gcc ata ctg       1116
Ala Ser Ala Ala Asn Ile Arg Ala Val Ala Glu Gly Ser Ala Ile Leu
            260                 265                 270
cag tcc gcc acc gag gaa ttc gcc ctg acc cac gtg cag gac gcc tac       1164
Gln Ser Ala Thr Glu Glu Phe Ala Leu Thr His Val Gln Asp Ala Tyr
        275                 280                 285
tcg gtg cgg tgc gcc ccg cag gtc gcc ggt ggt ttc cgc gac acc ctg       1212
Ser Val Arg Cys Ala Pro Gln Val Ala Gly Gly Phe Arg Asp Thr Leu
    290                 295                 300
gcc cac gcc cgc ctg gtc gcc gac cgg gag ctc gcc tcc gcc gtg gac       1260
Ala His Ala Arg Leu Val Ala Asp Arg Glu Leu Ala Ser Ala Val Asp
305                 310                 315                 320
aac ccc gtg gtg gct ctc gac ggc cgc gtg acc tcc aac ggc aac ttc       1308
Asn Pro Val Val Ala Leu Asp Gly Arg Val Thr Ser Asn Gly Asn Phe
                325                 330                 335
cac ggc gcg ccc gtc ggc tac gcg ctc gac ttc ctc gcc atc gtc acc       1356
His Gly Ala Pro Val Gly Tyr Ala Leu Asp Phe Leu Ala Ile Val Thr
            340                 345                 350
gcc gac ctg gcg agc atc tcc gag cgc cgc acc gac cgg ctt ctc gac       1404
Ala Asp Leu Ala Ser Ile Ser Glu Arg Arg Thr Asp Arg Leu Leu Asp
        355                 360                 365
gtc gcc cgc agc cgc gga ctc aac gcc ttc ctc gcc gac gat ccg ggc       1452
Val Ala Arg Ser Arg Gly Leu Asn Ala Phe Leu Ala Asp Asp Pro Gly
    370                 375                 380
gtg gac tcc ggc cac atg atc gcc cag tac acg cag gcc ggg atc gtc       1500
Val Asp Ser Gly His Met Ile Ala Gln Tyr Thr Gln Ala Gly Ile Val
385                 390                 395                 400
tcc gag ctc aag cgg ctg gcc gcc ccg gcc agc gtg gac tcc atc ccc       1548
Ser Glu Leu Lys Arg Leu Ala Ala Pro Ala Ser Val Asp Ser Ile Pro
                405                 410                 415
tcc tcc gcc atg cag gag gac cac gtg tcc atg ggc tgg tcg gcc ggg       1596
Ser Ser Ala Met Gln Glu Asp His Val Ser Met Gly Trp Ser Ala Gly
            420                 425                 430
cgc aag ctg cgc cgt tcc gtc gac ggg ctg ggg cgg gtg ctc ggc gtc       1644
Arg Lys Leu Arg Arg Ser Val Asp Gly Leu Gly Arg Val Leu Gly Val
        435                 440                 445
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gag gtg ctc acc gca gcc cgg gcc atc gac atg cgc gag cag gag ccc      1692
Glu Val Leu Thr Ala Ala Arg Ala Ile Asp Met Arg Glu Gln Glu Pro
    450                 455                 460
gcg ccg ggg acc cgc gcc gca ctg gac gcc ctg cgc ggc cgt gtg gag      1740
Ala Pro Gly Thr Arg Ala Ala Leu Asp Ala Leu Arg Gly Arg Val Glu
465                 470                 475                 480
ggg ccc ggc ccc gac cgc tac ctg tcc ccg gag atc gag gag tcg gtg      1788
Gly Pro Gly Pro Asp Arg Tyr Leu Ser Pro Glu Ile Glu Glu Ser Val
                485                 490                 495
cag ctg ctc acc tcc ggg gcg ctg ctg gag gcg gtg gag ggg gtc gtc      1836
Gln Leu Leu Thr Ser Gly Ala Leu Leu Glu Ala Val Glu Gly Val Val
            500                 505                 510
gga aag ctg gca tga gcgggcgaat ctcagatatg agactaaagg ggcctccggg      1891
Gly Lys Leu Ala
        515
ccctcgatcc cgactgtgac ctgtcttacc gtcagaagtg tcaccgacac cggccacacc     1951
agcccggtgc tccacacccg acgatgacag ccccgggcca cccggatcgc gggtgccccg     2011
gggccccggc ctgatcggcc cccaccgtag aaggagaccc accccatgac cgagtccccg     2071
cgcaccatcc gtgccccgca cggcaccgag ctcagcgcca agagctggca aaccgaggca     2131
cccctgcgca tgctcatgaa                                                2151
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1               5                   10                  15
Ile Asp Glu Val Val Ala Val Ala Arg His Asp Ala His Val Glu Ile
            20                  25                  30
Thr Pro Glu Ala Leu Glu Ala Val Ala Ala Thr Arg Ala Arg Ile Glu
        35                  40                  45
Glu Leu Ala Asp His Pro Thr Pro Val Tyr Gly Val Ser Thr Gly Phe
    50                  55                  60
Gly Ala Leu Ala Arg Arg Tyr Ile Pro Gln Glu Met Arg Leu Gln Leu
65                  70                  75                  80
Gln Arg Ser Leu Val Arg Ser His Ala Ala Gly Ser Gly Pro Glu Val
                85                  90                  95
Glu Arg Glu Val Val Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu
            100                 105                 110
Cys Thr Gly Arg Thr Gly Val Arg Pro Val Val Ala Glu Thr Tyr Ala
        115                 120                 125
Ala Val Leu Asn Ala Gly Ile Thr Pro Val Val His Glu Tyr Gly Ser
    130                 135                 140
Leu Gly Cys Ser Gly Asp Leu Ser Pro Leu Ala His Cys Ala Leu Ala
145                 150                 155                 160
Leu Leu Gly Glu Gly Glu Val Thr Thr Ala Asp Gly Arg Arg Leu Pro
                165                 170                 175
Ala Ala Val Ala Leu Ala Glu His Gly Ile Glu Pro Leu Val Leu Arg
            180                 185                 190
Glu Lys Glu Gly Leu Ala Leu Ile Asn Gly Thr Asp Gly Met Leu Gly
        195                 200                 205
Met Leu Cys Leu Ala Ile Ala Asp Leu Glu Cys Leu Ala Arg Ser Ala
    210                 215                 220
Asp Ile Ala Ala Ala Met Thr Val Glu Ala Leu Arg Gly Thr Leu Thr
225                 230                 235                 240
Val Phe Ala Ala Asp Leu Gln Glu Leu Arg Pro His Pro Gly Gln Ala
                245                 250                 255
Ala Ser Ala Ala Asn Ile Arg Ala Val Ala Glu Gly Ser Ala Ile Leu
            260                 265                 270
Gln Ser Ala Thr Glu Glu Phe Ala Leu Thr His Val Gln Asp Ala Tyr
        275                 280                 285
Ser Val Arg Cys Ala Pro Gln Val Ala Gly Gly Phe Arg Asp Thr Leu
    290                 295                 300
Ala His Ala Arg Leu Val Ala Asp Arg Glu Leu Ala Ser Ala Val Asp
305                 310                 315                 320
Asn Pro Val Val Ala Leu Asp Gly Arg Val Thr Ser Asn Gly Asn Phe
                325                 330                 335
His Gly Ala Pro Val Gly Tyr Ala Leu Asp Phe Leu Ala Ile Val Thr
            340                 345                 350
Ala Asp Leu Ala Ser Ile Ser Glu Arg Arg Thr Asp Arg Leu Leu Asp
        355                 360                 365
Val Ala Arg Ser Arg Gly Leu Asn Ala Phe Leu Ala Asp Asp Pro Gly
    370                 375                 380
Val Asp Ser Gly His Met Ile Ala Gln Tyr Thr Gln Ala Gly Ile Val
385                 390                 395                 400
Ser Glu Leu Lys Arg Leu Ala Ala Pro Ala Ser Val Asp Ser Ile Pro
                405                 410                 415
Ser Ser Ala Met Gln Glu Asp His Val Ser Met Gly Trp Ser Ala Gly
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            420                 425                 430
Arg Lys Leu Arg Arg Ser Val Asp Gly Leu Gly Arg Val Leu Gly Val
        435                 440                 445
Glu Val Leu Thr Ala Ala Arg Ala Ile Asp Met Arg Glu Gln Glu Pro
    450                 455                 460
Ala Pro Gly Thr Arg Ala Ala Leu Asp Ala Leu Arg Gly Arg Val Glu
465                 470                 475                 480
Gly Pro Gly Pro Asp Arg Tyr Leu Ser Pro Glu Ile Glu Glu Ser Val
                485                 490                 495
Gln Leu Leu Thr Ser Gly Ala Leu Leu Glu Ala Val Glu Gly Val Val
            500                 505                 510
Gly Lys Leu Ala
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agacgggcac gtcgatggat gagagcagcg agaggatgcg caacgtgtgt cgcgcggcgg      180
gcacctgtcc catgtcactc cttacctgtg tgtggtctgt gggtcggcgg tctcgtatgc      240
gggaccacgc tgcgtcgcag ccgggtgtgg cgggaggtcg gtggcgttat cctacggcgc      300
atg acc acc cat gaa tgg aca gga cgc gac gac ggg ccc ggg gcc ggg         348
Met Thr Thr His Glu Trp Thr Gly Arg Asp Asp Gly Pro Gly Ala Gly
1               5                  10                  15
cac gcc cgt tgg cac agc gtc atc acc acc acg acc gac cgg ccg ggg         396
His Ala Arg Trp His Ser Val Ile Thr Thr Thr Thr Asp Arg Pro Gly
            20                  25                  30
gtc gcc ctc gtc ggg ttc gcc tcc gac gag ggg gtc cgc cgc aac ggt         444
Val Ala Leu Val Gly Phe Ala Ser Asp Glu Gly Val Arg Arg Asn Gly
        35                  40                  45
ggc cgc ccc ggc gcc gcc ggc ccc acg gag atc cgc cgt gcc ctg         492
Gly Arg Pro Gly Ala Ala Ala Gly Pro Thr Glu Ile Arg Arg Ala Leu
    50                  55                  60
gcc tcc ctg gcc gtg cac acc gac gtc ccg ctt ctc gac gcc ggc acc         540
Ala Ser Leu Ala Val His Thr Asp Val Pro Leu Leu Asp Ala Gly Thr
65                  70                  75                  80
gtc acc gtc tcc ggt acc gac ctg gag ggc ggg cac gac gca ctg tcc         588
Val Thr Val Ser Gly Thr Asp Leu Glu Gly Gly His Asp Ala Leu Ser
                85                  90                  95
gcg cag gtg gag gag ctg acc cgc gcg ggg cac acc gtc atc gtg ctg         636
Ala Gln Val Glu Glu Leu Thr Arg Ala Gly His Thr Val Ile Val Leu
            100                 105                 110
ggc ggt ggg cat gag acg gcg ttc ggg tcg cac cgc ggg gtg cgc cgg         684
Gly Gly Gly His Glu Thr Ala Phe Gly Ser His Arg Gly Val Arg Arg
        115                 120                 125
gcg ctg ggg cac agt ccg gcg atc atc aac ctc gac gcc cac ttc gac         732
Ala Leu Gly His Ser Pro Ala Ile Ile Asn Leu Asp Ala His Phe Asp
    130                 135                 140
ctg cgg gtc gcg ccg gcc ccg tcc tcg ggt acc ccg ttc cgg cag atc         780
Leu Arg Val Ala Pro Ala Pro Ser Ser Gly Thr Pro Phe Arg Gln Ile
145                 150                 155                 160
gcg gac ctg gcc ggg gag gag ttc cgt tat gcg gtg ctg ggc atc tcg         828
Ala Asp Leu Ala Gly Glu Glu Phe Arg Tyr Ala Val Leu Gly Ile Ser
                165                 170                 175
gtg ccc aac aac acc cgg gcg ctg ttc gac acc gcc cgg gaa ctg ggg         876
Val Pro Asn Asn Thr Arg Ala Leu Phe Asp Thr Ala Arg Glu Leu Gly
            180                 185                 190
gtc cgg gtg acc acc gac gtc gag ctg gcg gag atg acg tcg gcc ggg         924
Val Arg Val Thr Thr Asp Val Glu Leu Ala Glu Met Thr Ser Ala Gly
        195                 200                 205
tgc gag gcg ctc gtc gga aag ctc ctg gag gac gcc ccg gac gtc cac         972
Cys Glu Ala Leu Val Gly Lys Leu Leu Glu Asp Ala Pro Asp Val His
    210                 215                 220
ctg agc atc gac ctt gac gtc ctg ccc gcg gcg gtc gcc ccc ggc gtg        1020
Leu Ser Ile Asp Leu Asp Val Leu Pro Ala Ala Val Ala Pro Gly Val
225                 230                 235                 240
agc gcg ccg gcg gcg ttg ggc gtc gat ctg gca cgg atc ctg acg ctc        1068
Ser Ala Pro Ala Ala Leu Gly Val Asp Leu Ala Arg Ile Leu Thr Leu
                245                 250                 255
gtc aga gcc gtg gcg cgc agc ggg aag ctg cgt ctg gtc gat gtc gtc        1116
Val Arg Ala Val Ala Arg Ser Gly Lys Leu Arg Leu Val Asp Val Val
            260                 265                 270
```

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gaa ctc aac ccg ctt ctc gac gtc gac ggc cgg acc gcg cgg gtc gcg      1164
Glu Leu Asn Pro Leu Leu Asp Val Asp Gly Arg Thr Ala Arg Val Ala
        275                 280                 285
gcc cgg atc gtg gag gag atc gtg cgt cat cgg ccg tcg gac tga          1209
Ala Arg Ile Val Glu Glu Ile Val Arg His Arg Pro Ser Asp
    290                 295                 300
tcctgcggtt ccgggtggac ctgcaccccc tggatgtagg tccgccacgt gagcggcatc    1269
cccggccggt aggccagatc gatggcgtgg ggggtgtcca gcacgtgcag gtctgccgcg    1329
gccccgacca cgaggctgcc gcgggcgggt cggccctggg ggtcgacgcc gccgccgatg    1389
tcgtgacgcc gcagcgcccg cgccccaccg gcggtggccg cgtggatggc ctcgtcgagg    1449
gtgaggtgct gctgcagcac cgcggtggtg acgcagaagg ccatcgacga ggtgtacgac    1509
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1               5                  10                  15
His Ala Arg Trp His Ser Val Ile Thr Thr Thr Thr Asp Arg Pro Gly
            20                  25                  30
Val Ala Leu Val Gly Phe Ala Ser Asp Glu Gly Val Arg Arg Asn Gly
        35                  40                  45
Gly Arg Pro Gly Ala Ala Ala Gly Pro Thr Glu Ile Arg Arg Ala Leu
    50                  55                  60
Ala Ser Leu Ala Val His Thr Asp Val Pro Leu Leu Asp Ala Gly Thr
65                  70                  75                  80
Val Thr Val Ser Gly Thr Asp Leu Glu Gly Gly His Asp Ala Leu Ser
                85                  90                  95
Ala Gln Val Glu Glu Leu Thr Arg Ala Gly His Thr Val Ile Val Leu
            100                 105                 110
Gly Gly Gly His Glu Thr Ala Phe Gly Ser His Arg Gly Val Arg Arg
        115                 120                 125
Ala Leu Gly His Ser Pro Ala Ile Ile Asn Leu Asp Ala His Phe Asp
    130                 135                 140
Leu Arg Val Ala Pro Ala Pro Ser Ser Gly Thr Pro Phe Arg Gln Ile
145                 150                 155                 160
Ala Asp Leu Ala Gly Glu Glu Phe Arg Tyr Ala Val Leu Gly Ile Ser
                165                 170                 175
Val Pro Asn Asn Thr Arg Ala Leu Phe Asp Thr Ala Arg Glu Leu Gly
            180                 185                 190
Val Arg Val Thr Thr Asp Val Glu Leu Ala Glu Met Thr Ser Ala Gly
        195                 200                 205
Cys Glu Ala Leu Val Gly Lys Leu Leu Glu Asp Ala Pro Asp Val His
    210                 215                 220
Leu Ser Ile Asp Leu Asp Val Leu Pro Ala Ala Val Ala Pro Gly Val
225                 230                 235                 240
Ser Ala Pro Ala Ala Leu Gly Val Asp Leu Ala Arg Ile Leu Thr Leu
                245                 250                 255
Val Arg Ala Val Ala Arg Ser Gly Lys Leu Arg Leu Val Asp Val Val
            260                 265                 270
Glu Leu Asn Pro Leu Leu Asp Val Asp Gly Arg Thr Ala Arg Val Ala
        275                 280                 285
Ala Arg Ile Val Glu Glu Ile Val Arg His Arg Pro Ser Asp
    290                 295                 300
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<222>  (301)..(1467)
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gctggccggt ccggacttcc ggtacctcga tcacatcaag ccgatctacg accagcccat      60
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tttcggctac ggccacctga cgtcggaact ctgcagcggt cggctcgggg agctggtgga     180
acgcttcctg gagctgtggg acgcgcccac cacggcgtag cgcctccgtc cggggcgtgt     240
ggccgcaggg tatcgccgat ccggcgtcgt gcgtgcggca acgtctatac actgcagggc     300
atg gac ctc tac gag tac cag gcc ctt gaa ctc ttc gcc gcc cac ggc       348
Met Asp Leu Tyr Glu Tyr Gln Ala Leu Glu Leu Phe Ala Ala His Gly
1               5                  10                  15
gtt ccg gtt ctg tcc gga acg gtg gct gag act ccg gcg gag gca cgc       396
Val Pro Val Leu Ser Gly Thr Val Ala Glu Thr Pro Ala Glu Ala Arg
            20                  25                  30
gcg gcg gcg gag cgg ctg ggc ggg gag tgc gtc gtc aag gcg cag gtg       444
Ala Ala Ala Glu Arg Leu Gly Gly Glu Cys Val Val Lys Ala Gln Val
        35                  40                  45
aag atc ggc ggc cgc ggc aag gcg ggc ggt gtc cgc gtc gcg gcg gcg       492
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Lys Ile Gly Gly Arg Gly Lys Ala Gly Gly Val Arg Val Ala Ala Ala
    50                  55                  60
ccc gag gcg gcc gag cag gcg gcg gag gcg atc ctg ggg atg gac atc      540
Pro Glu Ala Ala Glu Gln Ala Ala Glu Ala Ile Leu Gly Met Asp Ile
65                  70                  75                  80
cgc ggg cac acg gtc gag cgg gtg ctc gtc gtg gag tgc gtg gag atc      588
Arg Gly His Thr Val Glu Arg Val Leu Val Val Glu Cys Val Glu Ile
                85                  90                  95
gag gcg gag tac tac ttc tcg ctg ctc ctc gac cgc gcg cgg cgc tcc      636
Glu Ala Glu Tyr Tyr Phe Ser Leu Leu Leu Asp Arg Ala Arg Arg Ser
            100                 105                 110
tac ctg ggg ttg ttc tcg gtg gag gga ggc gtg gac atc gag aag ctc      684
Tyr Leu Gly Leu Phe Ser Val Glu Gly Gly Val Asp Ile Glu Lys Leu
        115                 120                 125
gcc gcg gag cgg ccg gag gcg ctg gcc cgc gtg gag gtc gac ccc ctc      732
Ala Ala Glu Arg Pro Glu Ala Leu Ala Arg Val Glu Val Asp Pro Leu
    130                 135                 140
gag ggc ttc gac gcc cac gaa ctt gtc gac gcc ctc ccc gcc gac ctc      780
Glu Gly Phe Asp Ala His Glu Leu Val Asp Ala Leu Pro Ala Asp Leu
145                 150                 155                 160
cgc gac aag gtc gtc ccc gtc atc cgg cgg ctc gcc gag gtc ttc cgc      828
Arg Asp Lys Val Val Pro Val Ile Arg Arg Leu Ala Glu Val Phe Arg
                165                 170                 175
gag gag gac gcc acc ctc gtc gag gtg aac ccg ctc gtc ctc acg gtg      876
Glu Glu Asp Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Val
            180                 185                 190
cag ggg gac atc atc gcc ctc gac gcg aag atc acc ctc gac gac aac      924
Gln Gly Asp Ile Ile Ala Leu Asp Ala Lys Ile Thr Leu Asp Asp Asn
        195                 200                 205
gcc gcc ttc cgt cac gac aac cgc gcg gag ctc gcc gag gcc gcc gac      972
Ala Ala Phe Arg His Asp Asn Arg Ala Glu Leu Ala Glu Ala Ala Asp
    210                 215                 220
cac ctc gac ccg atc gag cga cgc gcg agc gag cag ggg ctc aag tac     1020
His Leu Asp Pro Ile Glu Arg Arg Ala Ser Glu Gln Gly Leu Lys Tyr
225                 230                 235                 240
gtc acg ctc gag ggt tcg gtg ggc atc atc ggc aac ggc gcc ggg ctg     1068
Val Thr Leu Glu Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu
                245                 250                 255
gtc atg tcg acc ctc gac gtc gtg tcc ggg gcg ggg gag cgg cac ggc     1116
Val Met Ser Thr Leu Asp Val Val Ser Gly Ala Gly Glu Arg His Gly
            260                 265                 270
ggg cag aag ccg gcg aac ttc ctc gac atc ggc ggt ggc gcc tgc ccg     1164
Gly Gln Lys Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Cys Pro
        275                 280                 285
gag acg atg acc gcg gcc ctg gag atc gtc ctc tcg gac gag cag gtg     1212
Glu Thr Met Thr Ala Ala Leu Glu Ile Val Leu Ser Asp Glu Gln Val
    290                 295                 300
cgc agc gtg ttc gtc aac gtc ttc gga ggc atc acg tcc tgc gac gcg     1260
Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ser Cys Asp Ala
305                 310                 315                 320
gtg gcc acc ggc atc gtg gag gcg ctc act cac ctc ggg gac acg gcc     1308
Val Ala Thr Gly Ile Val Glu Ala Leu Thr His Leu Gly Asp Thr Ala
                325                 330                 335
cgc aag ccg atc gtc gtg cgt ctc gac ggc aac agc gtc gac gag gga     1356
Arg Lys Pro Ile Val Val Arg Leu Asp Gly Asn Ser Val Asp Glu Gly
            340                 345                 350
cgc cgc atc ctc cgc gag tac gat cac ccc ctc gtc acc gtc gtc gac     1404
Arg Arg Ile Leu Arg Glu Tyr Asp His Pro Leu Val Thr Val Val Asp
        355                 360                 365
gac atg gac gag gcc gcg gac cgg gtg gcg gag ctc gcc gcg gtg acc     1452
Asp Met Asp Glu Ala Ala Asp Arg Val Ala Glu Leu Ala Ala Val Thr
    370                 375                 380
ccg agc gtc gtc tag cgaaaggcac cgacatggcg atcttcctca actccgaatc     1507
Pro Ser Val Val
385
ccgcatcatc gtccagggca tcaccgggcg tgaggggcgg gagcacaccg cccggatgct     1567
cgccgccggc gcgaacgtgg tcggcggcac caacccgaag aaggcgggcg agacggtgac     1627
ggtcggcggc cacgagctgc cggtgttcgg caccgtcgcc gacgcacgcg cggccaccga     1687
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catcgacgcc gcgatcccgc                                                 1767
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Met Asp Leu Tyr Glu Tyr Gln Ala Leu Glu Leu Phe Ala Ala His Gly
1               5                   10                  15
Val Pro Val Leu Ser Gly Thr Val Ala Glu Thr Pro Ala Glu Ala Arg
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            20                  25                  30
Ala Ala Ala Glu Arg Leu Gly Gly Glu Cys Val Val Lys Ala Gln Val
        35                  40                  45
Lys Ile Gly Gly Arg Gly Lys Ala Gly Gly Val Arg Val Ala Ala Ala
    50                  55                  60
Pro Glu Ala Ala Glu Gln Ala Ala Glu Ala Ile Leu Gly Met Asp Ile
65                  70                  75                  80
Arg Gly His Thr Val Glu Arg Val Leu Val Val Glu Cys Val Glu Ile
                85                  90                  95
Glu Ala Glu Tyr Tyr Phe Ser Leu Leu Leu Asp Arg Ala Arg Arg Ser
            100                 105                 110
Tyr Leu Gly Leu Phe Ser Val Glu Gly Gly Val Asp Ile Glu Lys Leu
        115                 120                 125
Ala Ala Glu Arg Pro Glu Ala Leu Ala Arg Val Glu Val Asp Pro Leu
    130                 135                 140
Glu Gly Phe Asp Ala His Glu Leu Val Asp Ala Leu Pro Ala Asp Leu
145                 150                 155                 160
Arg Asp Lys Val Val Pro Val Ile Arg Arg Leu Ala Glu Val Phe Arg
                165                 170                 175
Glu Glu Asp Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Val
            180                 185                 190
Gln Gly Asp Ile Ile Ala Leu Asp Ala Lys Ile Thr Leu Asp Asp Asn
        195                 200                 205
Ala Ala Phe Arg His Asp Asn Arg Ala Glu Leu Ala Glu Ala Ala Asp
    210                 215                 220
His Leu Asp Pro Ile Glu Arg Arg Ala Ser Glu Gln Gly Leu Lys Tyr
225                 230                 235                 240
Val Thr Leu Glu Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu
                245                 250                 255
Val Met Ser Thr Leu Asp Val Val Ser Gly Ala Gly Glu Arg His Gly
            260                 265                 270
Gly Gln Lys Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Cys Pro
        275                 280                 285
Glu Thr Met Thr Ala Ala Leu Glu Ile Val Leu Ser Asp Glu Gln Val
    290                 295                 300
Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ser Cys Asp Ala
305                 310                 315                 320
Val Ala Thr Gly Ile Val Glu Ala Leu Thr His Leu Gly Asp Thr Ala
                325                 330                 335
Arg Lys Pro Ile Val Val Arg Leu Asp Gly Asn Ser Val Asp Glu Gly
            340                 345                 350
Arg Arg Ile Leu Arg Glu Tyr Asp His Pro Leu Val Thr Val Val Asp
        355                 360                 365


Asp Met Asp Glu Ala Ala Asp Arg Val Ala Glu Leu Ala Ala Val Thr
    370                 375                 380
Pro Ser Val Val
385
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cacggcccgc aagccgatcg tcgtgcgtct cgacggcaac agcgtcgacg agggacgccg      180
catcctccgc gagtacgatc acccccctcgt caccgtcgtc gacgacatgg acgaggccgc      240
ggaccgggtg gcggagctcg ccgcggtgac cccgagcgtc gtctagcgaa aggcaccgac      300
atg gcg atc ttc ctc aac tcc gaa tcc cgc atc atc gtc cag ggc atc         348
Met Ala Ile Phe Leu Asn Ser Glu Ser Arg Ile Ile Val Gln Gly Ile
1               5                   10                  15
acc ggg cgt gag ggg cgg gag cac acc gcc cgg atg ctc gcc gcc ggc         396
Thr Gly Arg Glu Gly Arg Glu His Thr Ala Arg Met Leu Ala Ala Gly
            20                  25                  30
gcg aac gtg gtc ggc ggc acc aac ccg aag aag gcg ggc gag acg gtg         444
Ala Asn Val Val Gly Gly Thr Asn Pro Lys Lys Ala Gly Glu Thr Val
        35                  40                  45
acg gtc ggc ggc cac gag ctg ccg gtg ttc ggc acc gtc gcc gac gca         492
Thr Val Gly Gly His Glu Leu Pro Val Phe Gly Thr Val Ala Asp Ala
    50                  55                  60
cgc gcg gcc acc gac gcg aac gtg tcc gtg gtg ttc gtg cct gcc ccc         540
Arg Ala Ala Thr Asp Ala Asn Val Ser Val Val Phe Val Pro Ala Pro
65                  70                  75                  80
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ttc gtc cgg gag gcg gtc tgc gag gcc atc gac gcc gcg atc ccg ctc        588
Phe Val Arg Glu Ala Val Cys Glu Ala Ile Asp Ala Ala Ile Pro Leu
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atc gtc gtc atc acc gag ggc gtg ccc gtc cgc gac acc gcc gag atg        636
Ile Val Val Ile Thr Glu Gly Val Pro Val Arg Asp Thr Ala Glu Met
            100                 105                 110
ctg gcg cac gcg cgg acg gag gga ggc acg cgg atc atc ggc ccg aac        684
Leu Ala His Ala Arg Thr Glu Gly Gly Thr Arg Ile Ile Gly Pro Asn
        115                 120                 125
tgc ccc ggc atc atc ccc gcg gat atc agc ggc ccc ggc ccc gtg gga        732
Cys Pro Gly Ile Ile Pro Ala Asp Ile Ser Gly Pro Gly Pro Val Gly
    130                 135                 140
ctg atc tcg aag tcg ggc acg ctg acg tac cag atg atg cac gcg ctt        780
Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln Met Met His Ala Leu
145                 150                 155                 160
tcc gac gtc ggc atc tcc acc gcc ctc ggc atc ggc ggc gac ccc ctc        828
Ser Asp Val Gly Ile Ser Thr Ala Leu Gly Ile Gly Gly Asp Pro Leu
                165                 170                 175
atc ggc acc gcc tac atc gac gcg ctc agc gcc ttc gag gag gac ccc        876
Ile Gly Thr Ala Tyr Ile Asp Ala Leu Ser Ala Phe Glu Glu Asp Pro
            180                 185                 190
gac acc cgg gcc atc gtc atg atc ggc gag atc ggc ggc gac gcc gag        924
Asp Thr Arg Ala Ile Val Met Ile Gly Glu Ile Gly Gly Asp Ala Glu
        195                 200                 205
gaa cgc gcc gcc gac tac atc cgg gag cac gtg acc aaa ccc gtc gtc        972
Glu Arg Ala Ala Asp Tyr Ile Arg Glu His Val Thr Lys Pro Val Val
    210                 215                 220
ggc tac gtc gcc ggg ttc acc gcc ccg gag ggc aag acc atg ggg cac       1020
Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly Lys Thr Met Gly His
225                 230                 235                 240
gca ggt gcc atc gtc acc ggt tcc gtc ggc acg gcg cag gcc aag aag       1068
Ala Gly Ala Ile Val Thr Gly Ser Val Gly Thr Ala Gln Ala Lys Lys
                245                 250                 255
gag gcg ctc gag gcg gcc ggt gtc cgg gtg ggc acc acg ccg acg gag       1116
Glu Ala Leu Glu Ala Ala Gly Val Arg Val Gly Thr Thr Pro Thr Glu
            260                 265                 270
acc gcg gag atc atg cgg ggg att gtc gag ggg atg tag gctgcccggg       1165
Thr Ala Glu Ile Met Arg Gly Ile Val Glu Gly Met
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tcgcgtcggc ggcctatcat cggagcatgc tggagaccgg acgcacccac cccctggcag     1225
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Ala Asn Val Val Gly Gly Thr Asn Pro Lys Lys Ala Gly Glu Thr Val
        35                  40                  45
Thr Val Gly Gly His Glu Leu Pro Val Phe Gly Thr Val Ala Asp Ala
    50                  55                  60
Arg Ala Ala Thr Asp Ala Asn Val Ser Val Val Phe Val Pro Ala Pro
65                  70                  75                  80
Phe Val Arg Glu Ala Val Cys Glu Ala Ile Asp Ala Ala Ile Pro Leu
                85                  90                  95
Ile Val Val Ile Thr Glu Gly Val Pro Val Arg Asp Thr Ala Glu Met
            100                 105                 110
Leu Ala His Ala Arg Thr Glu Gly Gly Thr Arg Ile Ile Gly Pro Asn
        115                 120                 125
Cys Pro Gly Ile Ile Pro Ala Asp Ile Ser Gly Pro Gly Pro Val Gly
    130                 135                 140
Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln Met Met His Ala Leu
145                 150                 155                 160
Ser Asp Val Gly Ile Ser Thr Ala Leu Gly Ile Gly Gly Asp Pro Leu
                165                 170                 175
Ile Gly Thr Ala Tyr Ile Asp Ala Leu Ser Ala Phe Glu Glu Asp Pro
            180                 185                 190
Asp Thr Arg Ala Ile Val Met Ile Gly Glu Ile Gly Gly Asp Ala Glu
        195                 200                 205
Glu Arg Ala Ala Asp Tyr Ile Arg Glu His Val Thr Lys Pro Val Val
    210                 215                 220
Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly Lys Thr Met Gly His
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225                 230                 235                 240
Ala Gly Ala Ile Val Thr Gly Ser Val Gly Thr Ala Gln Ala Lys Lys
                245                 250                 255
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            260                 265                 270
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ttgtaaaccg taggttgcga gttcaagtct cgtctccagc tctgctctcc acgaggtggg      180
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ggtgatgggc cgtagaatgg gcggcagcaa gcaccgtccc ccacctcaag gagtcagcac      300
atg gcc aac atc agg gtc gcg atc gtc ggt tac ggc aac ctc ggc aag        348
Met Ala Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Lys
1               5                   10                  15
tcc gtc gag aag ctc atc ggc cag cag ccg gac atg gag ctc gcg ggc        396
Ser Val Glu Lys Leu Ile Gly Gln Gln Pro Asp Met Glu Leu Ala Gly
            20                  25                  30
gtg ttc tcg cgt cgc gac gca ctg gac acc ctc gac ccg gcc acc ccg        444
Val Phe Ser Arg Arg Asp Ala Leu Asp Thr Leu Asp Pro Ala Thr Pro
        35                  40                  45
gtc ctg ccc gtc gcg gag ttc ggt gag cac acc gac aag ttc gac gtc        492
Val Leu Pro Val Ala Glu Phe Gly Glu His Thr Asp Lys Phe Asp Val
    50                  55                  60
gcc gtc ctc tgc ctc ggc tcc gcc acc gac atc ccg gag cag gcc ccc        540
Ala Val Leu Cys Leu Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro
65                  70                  75                  80
gag ttc atc cgc cac gcc aac acg gtc gac acc tac gac aac cac cgc        588
Glu Phe Ile Arg His Ala Asn Thr Val Asp Thr Tyr Asp Asn His Arg
                85                  90                  95
gac atc ccg cgc cac cgc gcc gag atg gac agg gtg gcc agg gag aac        636
Asp Ile Pro Arg His Arg Ala Glu Met Asp Arg Val Ala Arg Glu Asn
            100                 105                 110
ggc acc gtc gcc atc gtc tcc acc ggc tgg gac ccg ggc atg ttc tcc        684
Gly Thr Val Ala Ile Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser
        115                 120                 125
ctc aac cgc acc atc ggc cag gcg ctc ctg ccg ggc ggc cag cag cag        732
Leu Asn Arg Thr Ile Gly Gln Ala Leu Leu Pro Gly Gly Gln Gln Gln
    130                 135                 140
acc ttc tgg ggt ccg ggc ctc tcg cag ggc cac tct gac gcg gtg cgc        780
Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Val Arg
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cgc gtc gcg ggc gtg aag aag ggc gtg cag tac acc atc ccc tcc ccg        828
Arg Val Ala Gly Val Lys Lys Gly Val Gln Tyr Thr Ile Pro Ser Pro
                165                 170                 175
gag gcc ctc gag gcg gcc cgc aag ggt gag tcg ggt ctc agc ggc aag        876
Glu Ala Leu Glu Ala Ala Arg Lys Gly Glu Ser Gly Leu Ser Gly Lys
            180                 185                 190
cag gcc cac ctg cgc cgc tgc ttc atc gtg gcg gac gag gcc gac cac        924
Gln Ala His Leu Arg Arg Cys Phe Ile Val Ala Asp Glu Ala Asp His
        195                 200                 205
gag cgc atc gag aac gag atc cgc acc atg ccc gac tac ttc gtc ggc        972
Glu Arg Ile Glu Asn Glu Ile Arg Thr Met Pro Asp Tyr Phe Val Gly
    210                 215                 220
tac gag gtg gag gtc aac ttc atc gac gag gcc acc ttc gac gcc gag       1020
Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ala Glu
225                 230                 235                 240
cac acc ggc atg ccg cac ggc ggg cac gtc atc acg gcg ggt gac acc       1068
His Thr Gly Met Pro His Gly Gly His Val Ile Thr Ala Gly Asp Thr
                245                 250                 255
ggc ggc tac gtc cag tcc atc gag tac aac ctc gac ctg gac cgg aac       1116
Gly Gly Tyr Val Gln Ser Ile Glu Tyr Asn Leu Asp Leu Asp Arg Asn
            260                 265                 270
ccg gac ttc acc ggt gcc gtc gcc ctg gca tac gcc cgt gcg gcc cac       1164
Pro Asp Phe Thr Gly Ala Val Ala Leu Ala Tyr Ala Arg Ala Ala His
        275                 280                 285
cgt ctg cgt gag gcg ggc cag gcc ggc gcc tac acc gtc ctc gag gtc       1212
Arg Leu Arg Glu Ala Gly Gln Ala Gly Ala Tyr Thr Val Leu Glu Val
    290                 295                 300
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gcc ccg tac ctg atc tcc ccg acg ccg ctc gag gag ctc atc gcc cgc       1260
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305                 310                 315                 320
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Asp Val

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Val Phe Ser Arg Arg Asp Ala Leu Asp Thr Leu Asp Pro Ala Thr Pro
        35                  40                  45
Val Leu Pro Val Ala Glu Phe Gly Glu His Thr Asp Lys Phe Asp Val
    50                  55                  60
Ala Val Leu Cys Leu Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro
65                  70                  75                  80
Glu Phe Ile Arg His Ala Asn Thr Val Asp Thr Tyr Asp Asn His Arg
                85                  90                  95
Asp Ile Pro Arg His Arg Ala Glu Met Asp Arg Val Ala Arg Glu Asn
            100                 105                 110
Gly Thr Val Ala Ile Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser
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Leu Asn Arg Thr Ile Gly Gln Ala Leu Leu Pro Gly Gly Gln Gln Gln
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Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Val Arg
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Arg Val Ala Gly Val Lys Lys Gly Val Gln Tyr Thr Ile Pro Ser Pro
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Glu Ala Leu Glu Ala Ala Arg Lys Gly Glu Ser Gly Leu Ser Gly Lys
            180                 185                 190
Gln Ala His Leu Arg Arg Cys Phe Ile Val Ala Asp Glu Ala Asp His
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Glu Arg Ile Glu Asn Glu Ile Arg Thr Met Pro Asp Tyr Phe Val Gly
    210                 215                 220
Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ala Glu
225                 230                 235                 240
His Thr Gly Met Pro His Gly Gly His Val Ile Thr Ala Gly Asp Thr
                245                 250                 255
Gly Gly Tyr Val Gln Ser Ile Glu Tyr Asn Leu Asp Leu Asp Arg Asn
            260                 265                 270
Pro Asp Phe Thr Gly Ala Val Ala Leu Ala Tyr Ala Arg Ala Ala His
        275                 280                 285
Arg Leu Arg Glu Ala Gly Gln Ala Gly Ala Tyr Thr Val Leu Glu Val
    290                 295                 300
Ala Pro Tyr Leu Ile Ser Pro Thr Pro Leu Glu Glu Leu Ile Ala Arg
305                 310                 315                 320
Asp Val
```

YÊU CẦU BẢO HỘ

1. Hệ phân cắt glyxin chứa các enzym GcvP, GcvT và GcvH, khác biệt ở chỗ, hệ này chứa ít nhất một polypeptit trong số các polypeptit sau:

a) enzym GcvP có độ tương đồng trình tự ít nhất bằng 80% so với trình tự nêu trong SEQ ID NO.40,

b) enzym GcvT có độ tương đồng trình tự ít nhất bằng 80% so với trình tự nêu trong SEQ ID NO.42,

c) enzym GcvH có độ tương đồng trình tự ít nhất bằng 80% so với trình tự nêu trong SEQ ID NO.38.

2. Hệ phân cắt glyxin theo điểm 1, khác biệt ở chỗ, hệ này chứa hai, tốt hơn nếu tất cả ba polypeptit nêu trên.

3. Hệ phân cắt glyxin theo điểm 2, khác biệt ở chỗ, hệ này chứa các polypeptit sau:

a) enzym GcvP có độ tương đồng trình tự ít nhất bằng 95% hoặc 98% so với trình tự nêu trong SEQ ID NO.40,

b) enzym GcvT có độ tương đồng trình tự ít nhất bằng 95% hoặc 98% so với trình tự nêu trong SEQ ID NO.42,

c) enzym GcvH có độ tương đồng trình tự ít nhất bằng 95% hoặc 98% so với trình tự nêu trong SEQ ID NO.38.

4. Hệ phân cắt glyxin theo điểm bất kỳ trong số các điểm nêu trên, khác biệt ở chỗ, hệ này chứa ít nhất một polypeptit bổ sung được chọn từ nhóm bao gồm:

a) enzym LipA có độ tương đồng trình tự ít nhất bằng 80% so với trình tự nêu trong SEQ ID NO.48,

b) enzym LipB có độ tương đồng trình tự ít nhất bằng 80% so với trình tự nêu trong SEQ ID NO.50,

c) enzym Lpd có độ tương đồng trình tự ít nhất bằng 80% so với trình tự nêu trong SEQ ID NO.52,

d) enzym LplA có độ tương đồng trình tự ít nhất bằng 80% so với trình tự nêu trong SEQ ID NO.94,

e) enzym GcvL có độ tương đồng trình tự ít nhất bằng 80% so với trình tự nêu trong SEQ ID NO.96.

5. Polypeptit cấu thành các enzym của hệ phân cắt glyxin, được chọn từ nhóm bao gồm:

a) enzym GcvP có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.40,

b) enzym GcvT có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.42,

c) enzym GcvH có độ tương đồng trình tự ít nhất bằng 80%, tốt hơn nếu ít nhất bằng 85% hoặc 90%, tốt hơn nữa nếu ít nhất bằng 92%, 94%, 96% hoặc 98%, tốt nhất nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.38.

6. Polynucleotit, mã hoá các enzym của hệ phân cắt glyxin, được chọn từ nhóm bao gồm:

a) polynucleotit (gcvP), mã hoá enzym GcvP và có độ tương đồng trình tự ít nhất bằng 70% hoặc 75%, tốt hơn nếu ít nhất bằng 80% hoặc 85%, tốt hơn nữa nếu ít nhất bằng 90% hoặc 95%, tốt nhất nếu ít nhất bằng 98% hoặc 100%, so với trình tự có vị trí từ 301 đến 3162 như nêu trong SEQ ID NO.39 và/hoặc lai hóa trong các điều kiện nghiêm ngặt với polynucleotit có trình tự bổ sung với trình tự có vị trí từ 301 đến 3162 như nêu trong SEQ ID NO.39;

b) polynucleotit (gcvT), mã hoá enzym GcvT và có độ tương đồng trình tự ít nhất bằng 70% hoặc 75%, tốt hơn nếu ít nhất bằng 80% hoặc 85%, tốt hơn nữa nếu ít nhất bằng 90% hoặc 95%, tốt nhất nếu ít nhất bằng 98% hoặc 100%, so với trình tự có vị trí từ 301 đến 1404 như nêu trong SEQ ID NO.41 và/hoặc lai hóa trong các điều kiện nghiêm ngặt với polynucleotit có trình tự bổ sung với trình tự có vị trí từ 301 đến 1404 như nêu trong SEQ ID NO.41;

c) polynucleotit (gcvH), mã hoá enzym GcvH và có độ tương đồng trình tự ít nhất bằng 70% hoặc 75%, tốt hơn nếu ít nhất bằng 80% hoặc 85%, tốt hơn nữa nếu ít

nhất bằng 90% hoặc 95%, tốt nhất nếu ít nhất bằng 98% hoặc 100%, so với trình tự có vị trí từ 301 đến 699 như nêu trong SEQ ID NO.37 và/hoặc lai hóa trong các điều kiện nghiêm ngặt với polynucleotit có trình tự bổ sung với trình tự có vị trí từ 301 đến 699 như nêu trong SEQ ID NO.37.

7. Vectơ, khác biệt ở chỗ, vectơ này chứa ít nhất một polynucleotit, tốt hơn nếu ít nhất hai hoặc ba polynucleotit theo điểm 6.

8. Vi sinh vật tái tổ hợp, khác biệt ở chỗ, vi sinh vật này chứa ít nhất một hệ phân cắt glyxin theo điểm bất kỳ trong số các điểm từ 1 đến 4 và/hoặc polynucleotit mã hoá hệ phân cắt glyxin này và/hoặc ít nhất một polypeptit theo điểm 5 và/hoặc polynucleotit mã hoá polypeptit này hoặc các polynucleotit mã hoá các polypeptit này và/hoặc ít nhất một polynucleotit theo điểm 6 và/hoặc vectơ theo điểm 7.

9. Vi sinh vật tái tổ hợp theo điểm 8, khác biệt ở chỗ, hệ phân cắt glyxin và/hoặc polynucleotit mã hoá hệ này có mặt dưới dạng được biểu hiện quá mức.

10. Vi sinh vật tái tổ hợp theo điểm 8 hoặc 9, khác biệt ở chỗ, vi sinh vật này là chủng sản sinh lượng lớn L-methionin có ít nhất một, tốt hơn nếu ít nhất hai hoặc ba, tốt hơn nữa nếu ít nhất bốn hoặc năm polynucleotit trong số các polynucleotit sau:

a) polynucleotit giảm hoạt lực (mcbR), mã hoá miền gắn kết ADN thuộc loại HTH tetR (McbR), tốt hơn nếu miền gắn kết ADN có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.2,

b) polynucleotit giảm hoạt lực (gen thrB), mã hoá homoserin kinaza (ThrB, EC 2.7.1.39), tốt hơn nếu homoserin kinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.4,

c) polynucleotit giảm hoạt lực (pgi), mã hoá glucoza-6-phosphat isomeraza (Pgi, EC 5.3.1.9), tốt hơn nếu glucoza-6-phosphat isomeraza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.6,

d) polynucleotit giảm hoạt lực (pck), mã hoá phosphoenolpyruvat carboxykinaza (Pck, EC 4.1.1.32), tốt hơn nếu phosphoenolpyruvat carboxykinaza có

độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.8,

e) polynucleotit giảm hoạt lực (metQ), mã hoá lipoprotein gắn kết D-methionin (MetQ), tốt hơn nếu lipoprotein gắn kết D-methionin có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.10,

f) polynucleotit giảm hoạt lực (metP), mã hoá protein vận chuyển methionin (MetP), tốt hơn nếu protein vận chuyển methionin có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.12,

g) polynucleotit giảm hoạt lực (metN), mã hoá protein vận chuyển methionin phụ thuộc ATP (MetN), tốt hơn nếu protein vận chuyển methionin phụ thuộc vào ATP có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.14,

h) polynucleotit giảm hoạt lực (metK), mã hoá S-adenosylmethionin synthaza (MetK), tốt hơn nếu S-adenosylmethionin synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.16,

i) polynucleotit giảm hoạt lực (metI), mã hoá permeaza hệ nhập methionin (MetI), tốt hơn nếu permeaza hệ nhập methionin có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.18,

j) polynucleotit giảm hoạt lực (dapA), mã hoá 4-hydroxy-tetrahydrodipicolinat synthaza (DapA), tốt hơn nếu 4-hydroxy-tetrahydrodipicolinat synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.20,

k) polynucleotit được biểu hiện quá mức (CBS), mã hoá xystein synthaza (CBS), tốt hơn nếu xystein synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.22,

l) polynucleotit giảm hoạt lực, mã hoá đoạn tương đồng cg3031, tốt hơn nếu đoạn tương đồng cg3031 có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.24,

m) polynucleotit được biểu hiện quá mức (aecD), mã hoá xystathionin beta-lyaza (AecD), tốt hơn nếu xystathionin beta-lyaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.26,

n) polynucleotit được biểu hiện quá mức (asd), mã hoá aspartat semialdehyt dehydrogenaza (Asd), tốt hơn nếu aspartat semialdehyt dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.28,

o) polynucleotit được biểu hiện quá mức (metH), mã hoá 5-metyltetrahydrofolat homoxystein metyltransferaza (MetH, EC 2.1.1.13),

p) polynucleotit được biểu hiện quá mức (brnE), mã hoá tiểu đơn vị nhỏ hơn của protein vận chuyển đối với các axit amin mạch nhánh (BrnE), tốt hơn nếu tiểu đơn vị có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.30,

q) polynucleotit được biểu hiện quá mức (brnF), mã hoá tiểu đơn vị lớn hơn của protein vận chuyển đối với các axit amin mạch nhánh (BrnF), tốt hơn nếu tiểu đơn vị có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.32,

r) polynucleotit được biểu hiện quá mức (cysE), mã hoá serin axetyltransferaza (CysE), tốt hơn nếu serin axetyltransferaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.34,

s) polynucleotit được biểu hiện quá mức (cysK), mã hoá xystein synthaza (CysK), tốt hơn nếu xystein synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.36,

t) polynucleotit được biểu hiện quá mức (glyA), mã hoá serin hydroxymetyltransferaza (GlyA), tốt hơn nếu serin hydroxymetyltransferaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.44,

u) polynucleotit được biểu hiện quá mức (hom), mã hoá homoserin dehydrogenaza chịu tác động ngược tuỳ ý (Hom), tốt hơn nếu homoserin dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.46,

v) polynucleotit được biểu hiện quá mức (lysC), mã hoá aspartat kinaza chịu tác động ngược tuỳ ý (LysC), tốt hơn nếu aspartat kinaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.54,

w) polynucleotit được biểu hiện quá mức (metB), mã hoá xystathionin gama-synthaza (MetB), tốt hơn nếu xystathionin gama-synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.56,

x) polynucleotit được biểu hiện quá mức (metF), mã hoá 5,10-metylentetrahydrofolat reductaza (MetF), tốt hơn nếu 5,10-metylentetrahydrofolat reductaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.58,

y) polynucleotit được biểu hiện quá mức (metX), mã hoá homoserin O-axetyltransferaza (MetX), tốt hơn nếu homoserin O-axetyltransferaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.60,

z) polynucleotit được biểu hiện quá mức (metY), mã hoá O-axetylhomoserin lyaza (MetY), tốt hơn nếu O-axetylhomoserin lyaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.62,

aa) polynucleotit được biểu hiện quá mức (pyc), mã hoá pyruvat carboxylaza (Pyc), tốt hơn nếu pyruvat carboxylaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.64,

bb) polynucleotit được biểu hiện quá mức (serA), mã hoá D-3-phosphoglyxerat dehydrogenaza chịu tác động ngược tuỳ ý (SerA), tốt hơn nếu D-3-phosphoglyxerat dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.66,

cc) polynucleotit được biểu hiện quá mức (serB), mã hoá phosphoserin phosphataza (SerB), tốt hơn nếu phosphoserin phosphataza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.68,

dd) polynucleotit được biểu hiện quá mức (serC), mã hoá phosphoserin aminotransferaza (SerC), tốt hơn nếu phosphoserin aminotransferaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.70,

ee) polynucleotit được biểu hiện quá mức (ald), mã hoá alanin dehydrogenaza (Ald), tốt hơn nếu alanin dehydrogenaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.72,

ff) polynucleotit được biểu hiện quá mức (cysD), mã hoá tiểu đơn vị của sulphat adenylyltransferaza (CysD), tốt hơn nếu tiểu đơn vị có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.74,

gg) polynucleotit được biểu hiện quá mức (cysH), mã hoá adenosin phosphosulphat reductaza (CysH), tốt hơn nếu adenosin phosphosulphat reductaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.76,

hh) polynucleotit được biểu hiện quá mức (cysI), mã hoá sulphit reductaza (CysI), tốt hơn nếu sulphit reductaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.78,

ii) polynucleotit được biểu hiện quá mức (cysJ), mã hoá (CysJ), tốt hơn nếu (CysJ) có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.80,

jj) polynucleotit được biểu hiện quá mức (cysN), mã hoá tiểu đơn vị của sulphat adenylyltransferaza (CysN), tốt hơn nếu tiểu đơn vị có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.82,

kk) polynucleotit được biểu hiện quá mức (cysY), mã hoá xystathionin beta-synthaza (CysY), tốt hơn nếu xystathionin beta-synthaza có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.84,

ll) polynucleotit được biểu hiện quá mức (cysZ), mã hoá protein vận chuyển sulphat giả định (CysZ), tốt hơn nếu protein vận chuyển sulphat có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.86,

mm) polynucleotit được biểu hiện quá mức (metE), mã hoá 5-metyltetrahydropteroyltriglutamat-homoxystein metyltransferaza (MetE), tốt hơn nếu protein có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.88,

nn) polynucleotit được biểu hiện quá mức (ptH1), mã hoá peptidyl-ARN vận chuyển hydrolaza 1 (PtH1), tốt hơn nếu peptidyl-ARN vận chuyển hydrolaza 1 có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.90,

oo) polynucleotit được biểu hiện quá mức (ptH2), mã hoá peptidyl-ARN vận chuyển hydrolaza 2 (PtH2), tốt hơn nếu peptidyl-ARN vận chuyển hydrolaza 2 có độ tương đồng trình tự ít nhất bằng 90%, 95% hoặc 98%, tốt hơn nếu bằng 100%, so với trình tự nêu trong SEQ ID NO.92.

11. Vi sinh vật tái tổ hợp theo điểm bất kỳ trong số các điểm từ 8 đến 10, khác biệt ở chỗ, vi sinh vật này là vi khuẩn *Coryneform*, cụ thể là *Corynebacterium*, tốt hơn là *C. glutamicum* hoặc *C. humireducens*.

12. Phương pháp sản xuất lượng lớn axit L-amin, khác biệt ở chỗ, hệ phân cắt glyxin theo điểm bất kỳ trong số các điểm từ 1 đến 4 và/hoặc ít nhất một polypeptit theo điểm 5 và/hoặc ít nhất một polynucleotit theo điểm 6 và/hoặc vectơ theo điểm 7 và/hoặc vi sinh vật tái tổ hợp theo điểm bất kỳ trong số các điểm từ 8 đến 11 được sử dụng trong phương pháp này.

13. Phương pháp theo điểm 12, khác biệt ở chỗ, axit L-amin được sản xuất lượng lớn được chọn từ L-alanin, L-valin, axit L-amin thuộc họ glutamat, cụ thể là L-glutamat, L-glutamin, L-prolin và L-arginin, và axit L-amin thuộc họ aspartat, cụ thể là L-aspartat, L-asparagin, L-methionin, L-lysin, L-isoleuxin và L-threonin.

14. Phương pháp theo điểm 13, khác biệt ở chỗ, axit L-amin được sản xuất lượng lớn là L-methionin.

15. Phương pháp theo điểm bất kỳ trong số các điểm nêu trên, khác biệt ở chỗ, chỉ lượng nhỏ glyxin có mặt dưới dạng sản phẩm phụ.