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(54) Title: ENZYMATIC PROCESSES FOR THE PRODUCTION OF 4-SUBSTITUTED 3-HYDROXYBUTYRIC ACID DERIVATIVES AND VICINAL CYANO, HYDROXY SUBSTITUTED CARBOXYLIC ACID ESTERS

(57) Abstract: The present invention provides methods and composition for preparing 4-substituted 3-hydroxybutyric acid derivatives by halohydrin dehalogenase-catalyzed conversion of 4-halo-3-hydroxybutyric acid derivatives. The present invention further provides methods and compositions for preparing 4-halo-3-hydroxybutyric acid derivatives by ketoreductase-catalyzed conversion of 4-halo-3-ketobutyric acid derivatives. The present invention also provides methods and compositions for preparing vicinal cyano, hydroxyl substituted carboxylic acid esters.

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ENZYMATIC PROCESSES FOR THE PRODUCTION OF
4-SUBSTITUTED 3-HYDROXYBUTYRIC ACID DERIVATIVES
AND VICINAL CYANO, HYDROXY SUBSTITUTED CARBOXYLIC ACID ESTERS

CROSS-REFERENCE TO RELATED APPLICATION

This application is a continuation in part of U.S.S.N. 10/639,159, filed August 11, 2003, which claims the benefit under 35 U.S.C. § 119(e) of U.S.S.N. 60/402,436, filed August 9, 2002, both of which are incorporated herein by reference in their entireties.

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FIELD OF THE INVENTION

The present invention relates to novel enzymatic methods and compositions for preparing 4-substituted 3-hydroxybutyric acid derivatives and vicinal cyano, hydroxy substituted carboxylic acid esters.

BACKGROUND

4-substituted 3-hydroxybutyric acid derivatives and vicinal cyano, hydroxy substituted carboxylic acid esters are commercially important intermediates in the synthesis of pharmaceuticals. Nonracemic chiral 4-substituted 3-hydroxybutyric acid esters may be utilized in the synthesis of HMG-CoA reductase inhibitors, such as atorvastatin, fluvastatin, rosuvastatin, and itavastatin. For example, an ester of (R)-4-cyano-3-hydroxybutyric acid and an ester of (3R,5R)-6-cyano-3,5-dihydroxyhexanoic acid are key intermediates for the production of the cholesterol lowering agent atorvastatin. Methods have been described for producing certain 4-substituted 3-hydroxybutyric acid esters. Isbell, et al., Carbohydrate Res., 72:301 (1979), report a method for synthesizing an (R)-4-cyano-3-hydroxybutyric acid

ester by reacting the monohydrate calcium salt of threonine with hydrogen bromide to produce a dibromo derivative of threonine, which is then converted to a vicinal bromohydrin. The hydroxyl group of the bromohydrin is protected prior to reaction with sodium cyanide. Id.

5 Acta Chem. Scand., B37, 341 (1983) reports a method for producing a 4-cyano-3-hydroxybutyrate from a 4-bromo-3-hydroxybutyrate that requires protecting the hydroxy group with a protecting group prior to reaction with sodium cyanide. Recent routes to synthesize 4-cyano-3-hydroxybutyrate esters involve the uncatalyzed chemical reaction of a 4-bromo- or 4-chloro- 3-hydroxybutyrate ester, without protection of the hydroxyl group, 10 with a cyanide salt. By-products, however, are formed under the basic conditions created by the basic cyanide anion, which are particularly problematic to remove from the product. 4-Cyano-3-hydroxybutyrate esters are high boiling liquids and vacuum fractional distillation is required to separate the 4-cyano-3-hydroxybutyrate ester from these by-products. The distillation conditions are prone to generate additional by-products and the distillation is 15 troublesome to operate successfully.

The use of a 4-chloro-3-hydroxybutyric acid ester as a starting material in the synthesis of a 4-cyano-3-hydroxybutyric acid ester is more economically attractive than the use of a 4-bromo-3-hydroxybutyric acid ester, but requires more forcing conditions in its reaction with cyanide salts due to the lower reactivity of the chloro substituent compared to 20 the bromo substituent. While the cyanation of 4-chloro-3-hydroxybutyrate esters proceeds with alkali cyanide and high temperature, these forcing conditions lead to substantial by-product formation, requiring extensive isolation and purification procedures that result in additional yield loss. U.S. Pat. No. 5,908,953 discloses that, besides unreacted starting material, crude lower alkyl esters of (R)-4-cyano-3-hydroxybutyric acid may contain 25 hydroxyacrylate, cyanoacrylate, 3-cyanobutyrolactone, 3-hydroxybutyrolactone, γ -crotonolactone, 3-cyano-4-hydroxybutyrate lower alkyl ester, 3,4-dicyanobutyrate lower alkyl ester and high-boiling uncharacterized compounds. U.S. Pat. No. 5,908,953 further describes a purification method for lower alkyl esters of (R)-4-cyano-3-hydroxybutyric acid that involves distillation of a crude mixture in the presence of a solvent that has a boiling 30 point of 50°C to 160°C at 10 Torr. Using such distillation methods, the decomposition of unreacted starting material is said to be minimized, which otherwise can result in a dramatic overall loss in (R)-4-cyano-3-hydroxybutyric acid lower alkyl ester production. U.S. Pat. No.

6,140,527 describes an alternative approach for treating crude lower alkyl esters of (R)-4-cyano-3-hydroxybutyric acid that involves removal of the dehydrated by-products, such as 4-hydroxycrotonic acid esters, by chemical reaction, which renders these components water soluble and extractable. Thus, although these methods utilize a readily available starting material, significant yield loss and product purification requirements make them commercially undesirable. Accordingly, more efficient methods for producing nonracemic chiral 4-substituted 3-hydroxybutyric acid esters under milder conditions would be highly desirable.

Halohydrin dehalogenases, also referred to as haloalcohol dehalogenases or halohydrin hydrogen-halide lyases, catalyze the elimination of hydrogen halide, as proton and halide ion, from vicinal halohydrins to produce the corresponding epoxide. These enzymes also catalyze the reverse reaction. Nagasawa et al., Appl. Microbiol. Biotechnol. vol. 36 (1992) pp. 478-482, disclose activity of a certain halohydrin hydrogen-halide lyase on 4-chloro-3-hydroxybutyronitrile among other vicinal halohydrins. Nakamura et al., Biochem. Biophys. Research Comm. vol. 180 (1991) pp. 124-130 and Tetrahedron vol. 50 (1994) pp 11821-11826, disclose activity of a halohydrin hydrogen-halide lyase to catalyze the reaction of certain epoxides with cyanide to form the corresponding beta-hydroxynitriles. In these references and U.S. Patent 5,210,031, Nakamura et al. disclose a reaction of epihalohydrin with alkali cyanide in the presence of a certain halohydrin hydrogen-halide lyase to produce the corresponding 4-halo-3-hydroxy-butyronitrile. In U.S. Patent No. 5,166,061, Nakamura et al. disclose a reaction of a 1,3-dihalo-2-propanol with alkali cyanide in the presence of certain dehalogenating enzymes to produce the corresponding 4-halo-3-hydroxybutyronitrile. In Tetrahedron vol. 50 (1994) pp 11821-11826, Nakamura et al. disclose the reaction of 1,3-dichloro-2-propanol with cyanide using a purified halohydrin hydrogen-halide lyase to produce 4-chloro-3-hydroxybutyronitrile.

Lutje-Spelberg et al., Org. Lett., vol. 2 (2001) pp 41-43, discloses activity of a halohydrin dehalogenase to catalyze the reaction of certain styrene oxides with azide to form the corresponding 1-phenyl-2-azido-ethanol.

SUMMARY OF THE INVENTION

In one aspect, the present invention is directed to a method for producing a 4-cyano-3-hydroxybutyric acid ester or amide from a 4-halo-3-hydroxybutyric acid ester or amide, the method comprising:

- 5 (a) providing a 4-halo-3-hydroxybutyric acid ester or amide,
wherein the halo substituent is selected from the group consisting of chlorine, bromine, and iodine; and
(b) contacting the 4-halo-3-hydroxybutyric acid ester or amide with a halohydrin dehalogenase and cyanide under conditions sufficient to form a reaction mixture for
10 converting the 4-halo-3-hydroxybutyric acid ester or amide to a 4-cyano-3-hydroxybutyric acid ester or amide.

In a further aspect of the present invention, the 4-halo-3-hydroxybutyric acid ester or amide in step (a) is provided by a method comprising:

- providing a 4-halo-3-ketobutyric acid ester or amide,
15 wherein the halo substituent is selected from the group consisting of chlorine, bromine, and iodine; and
contacting the 4-halo-3-ketobutyric acid ester or amide with a ketoreductase, a cofactor, and a cofactor regeneration system under conditions sufficient to form a reaction mixture for converting the 4-halo-3-ketobutyric acid ester or amide to the 4-halo-3-
20 hydroxybutyric acid ester or amide.

In another aspect, the present invention is directed to a method for producing a 4-cyano-3-hydroxybutyric acid ester from a 4-halo-3-ketobutyric acid ester, the method comprising:

- (a) providing a 4-halo-3-ketobutyric acid ester,
25 wherein the halo substituent is selected from the group consisting of chlorine, bromine, and iodine; and
(b) contacting the 4-halo-3-ketobutyric acid ester with a ketoreductase, a cofactor, a cofactor regeneration system, cyanide, and a halohydrin dehalogenase to form a reaction mixture for converting the 4-halo-3-ketobutyric acid ester to a 4-cyano-3-hydroxybutyric acid
30 ester.

In another embodiment, the present invention is directed to a method for producing a 4-nucleophile substituted-3-hydroxybutyric acid ester or amide from a 4-halo-3-hydroxybutyric acid ester or amide, the method comprising:

- (a) providing a 4-halo-3-hydroxybutyric acid ester or amide,
5 wherein the halo substituent is selected from the group consisting of chlorine, bromine, and iodine; and
- (b) contacting the 4-halo-3-hydroxybutyric acid ester or amide with a halohydrin dehalogenase and a nucleophile under conditions suitable to form a reaction mixture for converting the 4-halo-3-hydroxybutyric acid ester or amide to a 4-nucleophile substituted-3-hydroxybutyric acid or amide.
10

In a further embodiment, the present invention is directed to a method for producing a 4-nucleophile substituted-3-hydroxybutyric acid esters or amide, the method comprising:

- (a) providing a 4-halo-3-ketobutyric acid ester or amide
 wherein the halo substituent is selected from the group consisting of chlorine,
15 bromine, and iodine; and
- (b) contacting the 4-halo-3-ketobutyric acid ester or amide with a ketoreductase, a cofactor, a cofactor regeneration system, a nucleophile, and a halohydrin dehalogenase to form a reaction mixture for converting the 4-halo-3-ketobutyric acid ester or amide to a 4-nucleophile substituted-3-hydroxybutyric acid ester or amide.

20 In another aspect, the present invention is directed to a composition comprising:

- (a) a halohydrin dehalogenase;
(b) a nucleophile; and
(c) a 4-halo-3-hydroxybutyric acid ester or amide.

25 The present invention further provides compositions that are useful in the production of vicinal cyano, hydroxy substituted carboxylic acid esters, as well as additional related methods for converting vicinal halo, hydroxy substituted carboxylic acid esters to vicinal cyano, hydroxy substituted carboxylic acid esters.

BRIEF DESCRIPTION OF THE DRAWINGS

30 Figure 1 depicts the amounts of ethyl 4-chloro-3-hydroxybutyrate (chlorohydrin) and ethyl 4-cyano-3-hydroxybutyrate (cyanohydrin) analyzed in test reactions of ethyl 4-chloro-

3-hydroxybutyrate with cyanide in aqueous solutions at various pHs in the presence or absence of a halohydrin dehalogenase (HHDH), as described in Example 21.

Figure 2 depicts a 3944 bp expression vector (pCK110700) of the present invention comprising a p15A origin of replication (p15 ori), a lacI repressor, a T5 promoter, a T7
5 ribosomal binding site (T7g10), and a chloramphenicol resistance gene (camR).

Figure 3 depicts a 4036 bp expression vector (pCK110900) of the present invention comprising a p15A origin of replication (p15 ori), a lacI repressor, a CAP binding site, a lac promoter (lac), a T7 ribosomal binding site (T7g10 RBS), and a chloramphenicol resistance gene (camR).

10 Figure 4 depicts the percent conversion vs. time for the reactions of ethyl (S)-4-chloro-3-hydroxybutyrate with aqueous hydrocyanic acid in the presence of various halohydrin dehalogenase enzymes that are described in Examples 25 through 29.

DETAILED DESCRIPTION OF THE INVENTION

15 The present invention provides enzymatic methods and compositions for producing various 4-substituted 3-hydroxybutyric acid esters and amides from corresponding 4-halo-3-hydroxybutyric acid ester and amide substrates. The present invention also provides methods and compositions for producing vicinal cyano, hydroxy substituted carboxylic acid esters from vicinal halo, hydroxy substituted carboxylic acids.

I. HALOHYDRIN DEHALOGENASE-CATALYZED CONVERSION OF 4-HALO-3-HYDROXYBUTYRIC ACID DERIVATIVES

20 The present invention provides a method for producing a 4-nucleophile substituted-3-hydroxybutyric acid ester or amide from a 4-halo-3-hydroxybutyric acid ester or amide, the
25 method comprising:

- (a) providing a 4-halo-3-hydroxybutyric acid ester or amide,
wherein the halo substituent is selected from the group consisting of
chlorine, bromine, and iodine; and
- (b) contacting the 4-halo-3-hydroxybutyric acid ester or amide with a halohydrin

30 dehalogenase and a nucleophile under conditions suitable to form a reaction mixture for converting the 4-halo-3-hydroxybutyric acid ester or amide to a 4-nucleophile substituted-3-hydroxybutyric acid ester or amide. Significantly, the invention method provides a process

for the manufacture of 4-substituted 3-hydroxybutyric acid esters and amides in which by-product formation is minimized.

Nucleophiles suitable for use in the practice of the present invention are those that are capable of displacing the halo substituent of the 4-halo-3-hydroxybutyric acid ester or amide substrate. Typical nucleophiles utilized in the present invention are anionic nucleophiles. Exemplary nucleophiles include cyanide (CN^-), azide (N_3^-), and nitrite (ONO^-).

In a specific embodiment, the present invention provides a method for producing 4-cyano-3-hydroxybutyric acid esters or amides from 4-halo-3-hydroxybutyric acid esters or amides via a halohydrin dehalogenase-catalyzed reaction, the method comprising:

(a) providing a 4-halo-3-hydroxybutyric acid ester or amide;

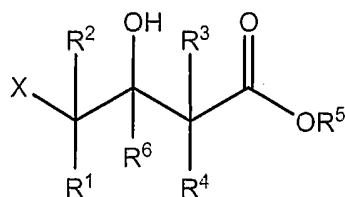
wherein the halo substituent is selected from the group consisting of chlorine, bromine, and iodine; and

(b) contacting the 4-halo-3-hydroxybutyric acid ester or amide with a halohydrin dehalogenase and cyanide under conditions suitable to form a reaction mixture for converting the 4-halo-3-hydroxybutyric acid ester or amide to a 4-cyano-3-hydroxybutyric acid ester or amide.

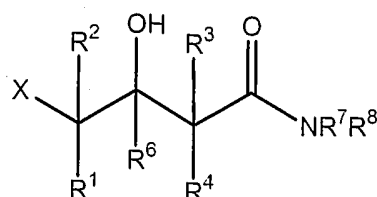
As used herein, the term "cyanide" refers to cyanide anion (CN^-), hydrocyanic acid (HCN), and mixtures thereof. Cyanide may be provided in the form of a cyanide salt, typically an alkali salt (for example, NaCN , KCN , and the like), in the form of hydrocyanic acid (gaseous or in solution), or mixtures thereof.

4-halo-3-hydroxybutyric acid esters and amides employed in the practice of the present invention may be prepared according to the methods described herein, or alternatively, using methods that are well known to those having ordinary skill in the art. Such methods are described, for example, in U.S. Patent No. 5,891,685; Hallinan, et al., Biocatalysis and Biotransformation, 12:179-191 (1995); Russ. Chem. Rev., 41:740 (1972); Kataoka, et al., Appl. Microbiol. Biotechnol., 48:699-703 (1997); and U.S. Patent No. 5,430,171.

Suitable 4-halo-3-hydroxybutyric acid ester and amide substrates employed in the practice of the present invention include those having the structure IA and 1B, respectively:



IA



IB

wherein:

X is a halogen selected from the group consisting of chlorine, bromine, and iodine;

5 R^1 , R^2 , R^3 , R^4 , and R^6 are each independently selected from the group consisting of hydrogen, fluorine, an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted lower alkenyl, an optionally substituted aryl, an optionally substituted arylalkyl, amino, an optionally substituted lower alkylamino, an optionally substituted cycloalkylamino, an optionally substituted lower alkoxy, an optionally substituted cycloalkoxy, an optionally substituted aryloxy, and an optionally substituted arylalkoxy; and

R^5 is selected from the group consisting of an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted aryl, and an optionally substituted arylalkyl; and

15 R^7 and R^8 are each independently selected from the group consisting of hydrogen, an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted aryl, and an optionally substituted arylalkyl.

"Optionally substituted" refers herein to the replacement of hydrogen with a monovalent radical. Suitable substitution groups include, for example, hydroxyl, alkyl, a lower alkyl, an alkoxy, a lower alkoxy, an alkenyl, a lower alkenyl, nitro, amino, cyano, 20 halogen (i.e., halo), thio, and the like. Other suitable substitution groups include carboxy (i.e. a carboxylate or carboxylic acid group), carboalkoxy (i.e. an ester group), carbamide (i.e. an amide group), and acyl (i.e. forming a ketone),

The term "lower alkyl" is used herein to refer to branched or straight chain alkyl groups having from one to about six carbon atoms that are unsubstituted or substituted, e.g., 25 with one or more halo, hydroxyl or other groups, including, e.g., methyl, ethyl, propyl, isopropyl, *n*-butyl, *i*-butyl, *t*-butyl, trifluoromethyl, and the like. The term "cycloalkyl" refers to carbocyclic alkyl moieties having from 3 to about 6 carbon atoms, as well as heterocyclic alkyl moieties having from 3 to about 6 atoms, where at least one ring atom is a heteroatom,

and the other atoms are carbon atoms. "Heteroatom" refers herein to oxygen, nitrogen, or sulfur.

The term "lower alkenyl" is used herein to refer to a branched or straight chain group having one or more double bonds and from 2 to about 6 carbon atoms. Lower alkenyl groups employed in the practice of the present invention may be optionally substituted with the groups described herein, including, for example, halo, hydroxyl, lower alkyl, and the like.

As used herein, the term "lower alkoxy" refers to $-OR$ where R is a lower alkyl or a lower alkenyl. Suitable lower alkoxy groups employed in the practice of the present invention include methoxy, ethoxy, *t*-butoxy, trifluoromethoxy, and the like. The term "aryloxy" refers herein to $RO-$, where R is an aryl. As used herein, the term "aryl" refers to monocyclic and polycyclic aromatic groups having from 3 to about 14 backbone carbon or heteroatoms, and includes both carbocyclic aryl groups and heterocyclic aryl groups. Carbocyclic aryl groups are aryl groups in which all ring atoms in the aromatic ring are carbon. Heterocyclic aryl groups are aryl groups that have from 1 to about 4 heteroatoms as ring atoms in an aromatic ring with the remainder of the ring atoms being carbon atoms. Exemplary aryl groups employed as substituents in the present invention include, for example, phenyl, pyridyl, pyrimidinyl, naphthyl, and the like.

The term "arylalkyl" refers herein to an alkyl group substituted with an aryl group. Exemplary arylalkyl groups include benzyl, picolyl, and the like. Substituted arylalkyl groups may be substituted in either or both aryl and alkyl portions of the arylalkyl group. As used herein, the term "arylalkoxy" refers to $RO-$ where R is an arylalkyl.

The term "cycloalkoxy" refers herein to $RO-$, where R is an optionally substituted C_3 - C_8 cycloalkyl. The term "amino" is used herein to refer to the group $-NH_2$. The term "lower alkylamino" refers herein to the group $-NRR'$ where R is hydrogen or a lower alkyl, and R' is a lower alkyl. The term "cycloalkylamino" refers herein to the group $-NR$ where R is an optionally substituted divalent aliphatic radical having from 3 to about 8 carbon atoms, so that N and R form a cyclic structure, for example, pyrrolidino, piperidino, and the like.

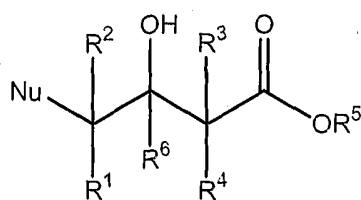
Specific 4-halo-3-hydroxybutyric acid esters of compound IA that may be employed in the practice of the present invention include ethyl 4-chloro-3-hydroxybutyric acid ester (i.e., where X is chlorine, R^1 , R^2 , R^3 , R^4 , and R^6 are hydrogen, and R^5 is ethyl), methyl 4-chloro-3-hydroxybutyric acid ester (i.e., where X is chlorine, R^1 , R^2 , R^3 , R^4 and R^6 are hydrogen and R^5 is methyl), ethyl 4-bromo-3-hydroxybutyric acid ester (i.e., where X is

bromine, R^1 , R^2 , R^3 , R^4 , and R^6 are hydrogen, and R^5 is ethyl), methyl 4-bromo-3-hydroxybutyric acid ester (i.e., where X is bromine, R^1 , R^2 , R^3 , R^4 , and R^6 are hydrogen, and R^5 is methyl), t-butyl-4-chloro-3-hydroxybutyric acid ester (i.e., where X is chlorine, R^1 , R^2 , R^3 , R^4 , and R^6 are hydrogen, and R^5 is t-butyl), t-butyl-4-bromo-3-hydroxybutyric acid ester (i.e., where X is bromine, R^1 , R^2 , R^3 , R^4 , and R^6 are hydrogen, and R^5 is t-butyl), and t-butyl-4-iodo-3-hydroxybutyric acid ester (i.e., where X is iodine, R^1 , R^2 , R^3 , R^4 , and R^6 are hydrogen, and R^5 is t-butyl). In certain embodiments, at least one of R^1 , R^2 , R^3 , R^4 , and R^6 is a lower alkyl, such as, for example, methyl, ethyl, or propyl.

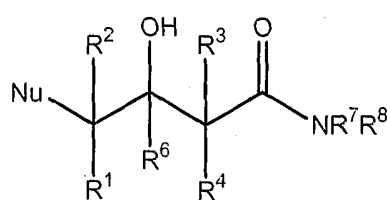
Suitable 4-halo-3-hydroxybutyric acid amides of compound IB that may be employed in the practice of the present invention include 4-chloro-3-hydroxybutyric amide (i.e., where X is chlorine, R^1 , R^2 , R^3 , R^4 , R^6 , R^7 , and R^8 are hydrogen), 4-bromo-3-hydroxybutyric amide (i.e., where X is bromine, and R^1 , R^2 , R^3 , R^4 , R^6 , R^7 , and R^8 are hydrogen), and 4-iodo-3-hydroxybutyric amide (i.e., where X is iodine, R^1 , R^2 , R^3 , R^4 , R^6 , R^7 , and R^8 are hydrogen). In certain embodiments, at least one of R^1 , R^2 , R^3 , R^4 , and R^6 is a lower alkyl, such as, for example, methyl, ethyl, or propyl.

The 4-halo substituent of the 4-halo-3-hydroxybutyric acid ester and amide substrates is preferably selected from chlorine and bromine. Particularly preferred are 4-chloro-3-hydroxybutyric acid ester and amide substrates.

4-substituted-3-hydroxybutyric acid esters and amides produced by the methods of the present invention include those having the structure IIA and IIB, respectively:



IIA

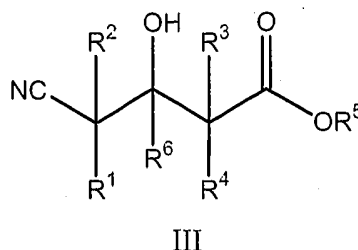


IIB

where:

R^1 , R^2 , R^3 , R^4 , R^5 , R^6 , R^7 , and R^8 are as defined for structures IA and IB; and Nu is selected from the group consisting of $-CN$, $-N_3$, and $-ONO$.

When 4-halo-3-hydroxybutyric acid ester substrates having the structure of compound IA are reacted with cyanide and halohydrin dehalogenase, 4-cyano-3-hydroxybutyric acid ester products are generated that have the structure of compound III:



5 where R^1 , R^2 , R^3 , R^4 , R^5 , and R^6 are as defined for structure IA .

Halohydrin dehalogenases are employed in the practice of the present invention to catalyze the conversion of a 4-halo-3-hydroxybutyric acid ester or amide to the corresponding 4-nucleophile substituted-3-hydroxybutyric acid ester or amide in the presence of a nucleophile. The terms "halohydrin dehalogenase" and "HHDH" are used

10 interchangeably herein to refer to an enzyme that, in the process of the present invention, catalyzes the conversion of a vicinal halo, hydroxy substituted carboxylic ester or amide to a vicinal cyano, hydroxyl substituted carboxylic ester or amide, such as, for example, 4-halo-3-hydroxybutyric acid ester and/or amide to a 4-nucleophile substituted-3-hydroxybutyric acid ester and/or amide, respectively, in the presence of a nucleophile such as cyanide.

15 Suitable halohydrin dehalogenases include naturally occurring (wild type) halohydrin dehalogenases, as well as non-naturally occurring halohydrin dehalogenases generated by human manipulation. Exemplary naturally occurring and non-naturally occurring halohydrin dehalogenases and halohydrin dehalogenase-encoding polynucleotides include those described herein.

20 Naturally occurring halohydrin dehalogenase encoding genes have been identified in *Agrobacterium radiobacter* AD1 (*hheC*), *Agrobacterium tumefaciens* (*halB*), *Corynebacterium* sp. (*hheA* encoding Ia and *hhB* encoding Ib), *Arthrobacter* sp. (*hheA*_{AD2}), and *Mycobacterium* sp. GP1 (*hheB*_{GP1}). See van Hylckama Vlieg, J.E.T., L. Tang, J.H. Lutje Spelberg, T. Smilda, G.J. Poelarends, T. Bosma, A.E.J. van Merode, M.W. Fraaije & Dick B.

25 Janssen, "Halohydrin Dehalogenases are structurally and mechanistically related to short-chain dehydrogenases/reductases (2001) *Journal of Bacteriology*, 183:5058-5066 (provides the amino acid sequences for these halohydrin dehalogenases in an alignment).

These naturally occurring halohydrin dehalogenases have been characterized to some extent. HHDH from *Agrobacterium radiobacter* AD1 is a homotetramer of 28 kD subunits.

Corynebacterium sp. N-1074 produces two HHDH enzymes, one of which is composed of 28 kD subunits (Ia), while the other is composed of related subunits of 35 and/or 32 kD (Kb).

HHDH from some sources is easily inactivated under oxidizing conditions in a process that leads to dissociation of the subunits, has a broad pH optimum from pH 8 to 9 and an optimal

5 temperature of 50°C (Tang, Enz. Microbiol. Technol. (2002) 30:251-258; Swanson, Curr. Opinion Biotechnol. (1999) 10:365-369). The optimal pH for HHDH catalyzed epoxide formation is 8.0 to 9.0 and the optimal temperature ranges from 45 to 55°C (Van Hylekama Vlieg, et al., J. Bacteriol. (2001) 183:5058-5066; Nakamura, et al., Appl. Environ. Microbiol. (1994) 60:1297-1301; Nagasawa, et al., Appl. Microbiol. Biotechnol. (1992) 36:478-482).

10 The optimal pH for the reverse reaction, ring opening by chloride has been reported for the two *Cornebacterium* sp. N-1074 enzymes and is 7.4 (Ia) or 5 (Ib). Polynucleotides encoding the halohydrin dehalogenase from *Agrobacterium radiobacter* AD1 are provided herein as SEQ ID NOS: 13, 15, and 17. The polynucleotides corresponding to SEQ ID NOS: 13, 15, and 17 are variants that encode the same amino acid sequence (the translated sequences are

15 provided as SEQ ID NOS: 14, 16, and 18).

Non-naturally occurring halohydrin dehalogenases can be generated using known methods, including, for example, mutagenesis, directed evolution, and the like. Several illustrative methods are described hereinbelow. The enzymes can be readily screened for activity using the method described in Example 4. Such screening methods may also be

20 readily applied to identifying other naturally occurring halohydrin dehalogenases. Suitable non-naturally occurring halohydrin dehalogenases include those corresponding to SEQ ID NOS: 24 (HHDH B-03), 26 (HHDH C-04), 28 (HHDH E-01), 30 (S01056858), 32 (HHDH 2G5), 34 (HHDH Mz1.1A5), 36 (HHDH cys1.10), 38 (HHDH cys2.12), 74 (HHDH B-12), 76 (HHDH Mz1/4H6), 78 (HHDH F-04), 80 (HHDH A-08), 82 (HHDH G9), 84 (HHDH F9),

25 86 (HHDH H10), 88 (HHDH A1), 90 (HHDH A-03), 92 (HHDH E-03), 94 (HHDH S00827801), 96 (HHDH S00890554), 98 (HHDH S00994580), 100 (HHDH S01018044), 102 (HHDH S01035939), 104 (HHDH S01009684), 106 (HHDH S00817219), 108 (HHDH S00708827), 110 (HHDH S00772501), 112 (HHDH S01035968), and 114 (HHDH S01040430). Exemplary polynucleotide sequences that encode these halohydrin

30 dehalogenases include those corresponding to SEQ ID NOS: 23, 25, 27, 29, 31, 33, 35, 37, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, and 113, respectively. Additional non-naturally occurring halohydrin dehalogenases that are suitable

for use in the practice of the present invention are provided in the patent application entitled, "Improved Halohydrin Dehalogenases and Related Polynucleotides," corresponding to Attorney Docket No. 0353.110US, filed on August 11, 2003, and assigned U.S. application serial number 60/494,382, and in the patent application entitled, "Improved Halohydrin Dehalogenases and Related Polynucleotides," corresponding to Attorney Docket No. 0353.210US, filed on February 18, 2004, and assigned U.S. application serial number _____, both of which are incorporated herein by reference in their entireties.

Halohydrin dehalogenases that are suitable for use in the practice of the present invention, whether naturally occurring or non-naturally occurring, can be readily identified by those having ordinary skill in the art using the method described in Example 4 and the vicinal halo, hydroxyl substituted substrate and nucleophile of interest.. Halohydrin dehalogenases employed in the practice of the present invention typically exhibit an activity of at least about 1 $\mu\text{mol}/\text{min}/\text{mg}$ in the assay described in Example 4. Halohydrin dehalogenases employed in the practice of the present invention may exhibit an activity of at least about 10 $\mu\text{mol}/\text{min}/\text{mg}$, and sometimes at least about 10^2 $\mu\text{mol}/\text{min}/\text{mg}$, and up to about 10^3 $\mu\text{mol}/\text{min}/\text{mg}$ or higher, in the assay described in Example 4.

Halohydrin dehalogenase may be provided to the reaction mixture in the form of purified enzyme, cell extract, cell lysate, or whole cells transformed with gene(s) encoding halohydrin dehalogenase(s). Whole cells transformed with halohydrin dehalogenase encoding genes and/or cell extracts and/or cell lysates thereof may be employed in a variety of different forms, including solid (e.g., lyophilized, spray dried, and the like) or semi-solid (e.g., a crude paste). The cell extracts or cell lysates may be partially purified by precipitation (ammonium sulfate, polyethyleneimine, heat treatment or the like), followed by a desalting procedure prior to lyophilization (e.g., ultrafiltration, dialysis, and the like). Any of the cell preparations may be stabilized by crosslinking using known crosslinking agents, such as, for example, glutaraldehyde or immobilization to a solid phase (e.g., Eupergit C, and the like).

The solid reactants (e.g., enzyme, salts, etc.) may be provided in a variety of different forms, including powder (e.g., lyophilized, spray dried, and the like), solution, emulsion, suspension, and the like. The reactants can be readily lyophilized or spray dried using methods and equipment that are known to those having ordinary skill in the art. For example,

the protein solution can be frozen at -80°C in small aliquots, then added to a prechilled lyophilization chamber, followed by the application of a vacuum. After the removal of water from the samples, the temperature is typically raised to 4°C for two hours before release of the vacuum and retrieval of the lyophilized samples.

5 In carrying out the conversion of 4-halo-3-hydroxybutyric acid ester or amide substrate to the corresponding 4-nucleophile substituted-3-hydroxybutyric ester or amide product, the substrate is typically contacted with the halohydrin dehalogenase and nucleophile in a solvent. Suitable solvents for carrying out the conversion of 4-halo-3-hydroxybutyric acid ester or amide to 4-nucleophile substituted-3-hydroxybutyric acid ester
10 or amide include water, organic solvents (e.g. ethyl acetate, butyl acetate, 1-octanol, heptane, octane, methyl t-butyl ether (MTBE), toluene, and the like), ionic liquids (e.g., 1-ethyl 4-methylimidazolium tetrafluoroborate, 1-butyl-3-methylimidazolium tetrafluoroborate, 1-butyl-3-methylimidazolium hexafluorophosphate, and the like), and co-solvent systems, including aqueous co-solvent systems, and the like. Preferred solvents are aqueous solvents,
15 including water and aqueous co-solvent systems.

Exemplary aqueous co-solvent systems have water and one or more organic solvent. In general, an organic solvent component of an aqueous co-solvent system is selected such that it does not completely inactivate the enzyme catalysts employed in the invention method. Appropriate co-solvent systems can be readily identified by measuring enzyme activity with
20 the substrate of interest in the candidate solvent system, utilizing the enzyme assay described in Example 4.

The organic solvent component of an aqueous co-solvent system may be miscible with the aqueous component, providing a single liquid phase, or may be partly miscible or immiscible with the aqueous component, providing two liquid phases. Typically, when an
25 aqueous co-solvent system is employed, it is selected to be biphasic, with water dispersed in an organic solvent, or vice-versa. Generally, when an aqueous co-solvent system is utilized, it is desirable to select an organic solvent that can be readily separated from the aqueous phase. In general, the ratio of water to organic solvent in the co-solvent system is typically in the range of from about 90:10 to about 10:90 (v/v) organic solvent to water, and between
30 80:20 and 20:80 (v/v) organic solvent to water. The co-solvent system may be pre-formed prior to addition to the reaction mixture, or it may be formed *in situ* in the reaction vessel.

The aqueous solvent (water or aqueous co-solvent system) may be pH-buffered or unbuffered. The conversion of the 4-halo-3-hydroxybutyric acid ester or amide to the 4-nucleophile substituted-3-hydroxybutyric acid ester or amide may be carried out at a pH of about 5 or above. Generally, the conversion is carried out at a pH of about 10 or below, usually in the range of from about 5 to about 10.. Typically, the conversion is carried out at a pH of about 9 or below, usually in the range of from about 5 to about 9. Preferably, the conversion is carried out at a pH of about 8 or below, usually in the range of from about 5 to about 8, and more preferably in the range of from about 6 to about 8. This conversion may also be carried out at a pH of about 7.8 or below, or 7.5 or below. Alternatively, the conversion may be carried out a neutral pH, i.e., about 7.

During the course of conversion, the pH of the reaction mixture may change. The pH of the reaction mixture may be maintained at a desired pH or within a desired pH range by the addition of an acid or a base during the course of conversion. Alternatively, the pH change may be controlled by using an aqueous solvent that comprises a buffer. Suitable buffers to maintain desired pH ranges are known in the art and include, for example, phosphate buffer, triethanolamine buffer, and the like. Combinations of buffering and acid or base addition may also be used.

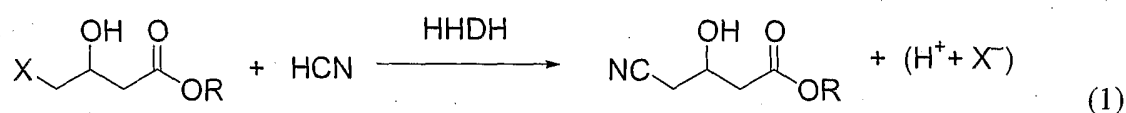
As described above, when conversion to 4-cyano-3-hydroxybutyric acid derivative is desired, the cyanide may be provided in the form of a cyanide salt, typically an alkali salt (for example, NaCN, KCN, and the like), in the form of hydrocyanic acid (gaseous or in solution), or mixtures thereof. Hydrocyanic acid is a weak acid. In aqueous solutions within several pH units of its pKa (pKa = 9.1 in water) cyanide is present as both CN^- and HCN in equilibrium concentrations. At pH values below about 9, cyanide is predominantly present as HCN.

When the cyanide is provided by a cyanide salt, the reaction mixture is typically buffered or acidified or both to provide the desired pH. Suitable acids for acidification of basic cyanide salts solutions include organic acids, for example carboxylic acids, sulfonic acids, phosphonic acids, and the like, mineral acids, for example hydrohalic acids (such as hydrochloric acid), sulfuric acid, phosphoric acid, and the like, acidic salts, for example dihydrogenphosphate salts (e.g. KH_2PO_4), bisulfate salts (e.g. NaHSO_4) and the like, as well as hydrocyanic acid. The acids or acid salts used to acidify the cyanide salt may be selected to also provide a buffer in the resulting solution. For example, acidification with phosphoric

acid or a dihydrogenphosphate salt may be used to provide a phosphate buffered solution of HCN in the phosphate buffer range (about pH 6-8).

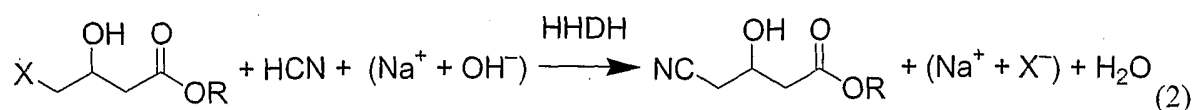
When the cyanide is provided by hydrocyanic acid and a higher pH than that so created is desired, the reaction mixture is typically buffered or made less acidic by adding a base to provide the desired pH. Suitable bases for neutralization of hydrocyanic acid are organic bases, for example amines, alkoxides and the like, and inorganic bases, for example, hydroxide salts (e.g. NaOH), carbonate salts (e.g. NaHCO₃), bicarbonate salts (e.g. K₂CO₃), basic phosphate salts (e.g. K₂HPO₄, Na₃PO₄), and the like, as well as cyanide salts.

For pH values below about 9, at which cyanide is predominantly present as HCN, equation (1) describes the halohydrin dehalogenase catalyzed reaction of a 4-halo-3-hydroxybutyric acid ester with the HCN in unbuffered aqueous reaction mixtures.

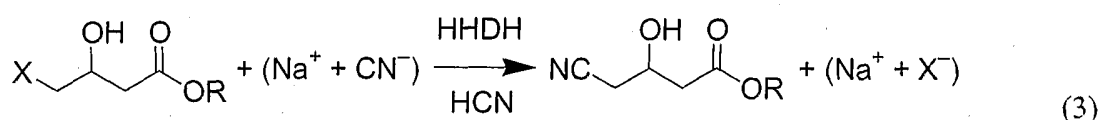


The consumption of the hydrocyanic acid, a weak acid (pK_a ~9) and release of the hydrohalic acid, a strong acid (pK_a <0), causes the pH of the reaction mixture to drop if the aqueous hydrohalic acid (H⁺ + X⁻) is not otherwise neutralized. The pH of the reaction mixture may be maintained at the desired level by standard buffering techniques, wherein the buffer neutralizes the hydrohalic acid up to the buffering capacity provided, or by the addition of a base concurrent with the course of the conversion. Such addition may be done manually while monitoring the reaction mixture pH or, more conveniently, by using an automatic titrator as a pH stat. A combination of partial buffering capacity and base addition can also be used for process control.

When the pH is maintained by buffering or by addition of a base over the course of the conversion, an aqueous halide salt rather than aqueous hydrohalic acid is the product of the overall process. For example, equation (2) represents the overall process when aqueous sodium hydroxide (Na⁺ + OH⁻) is added over the course of the reaction to maintain an initial pH below about 9.



In the embodiment wherein a cyanide salt is added as the base to neutralize the hydrohalic acid as it is produced, the neutralization regenerates HCN and maintains the total cyanide concentration (HCN + CN⁻) as well as the pH in the reaction mixture. This can be advantageous if the rate of conversion otherwise decreases as cyanide concentration decreases. For example, equation (3) represents the overall process when aqueous sodium cyanide (Na⁺ + CN⁻) is added over the course of the reaction to maintain an initial pH. While the cyanide is present predominantly as HCN in the reaction mixture, the HCN concentration is maintained while the conversion in net consumes the added basic cyanide salt.



When base addition is employed to neutralize the hydrohalic acid released during the halohydrin dehalogenase-catalyzed reaction of a 4-halo-3-hydroxybutyrate ester or amide to a 4-cyano-3-hydroxybutyric acid ester or amide, the progress of the conversion may be monitored by the amount of base added to maintain the pH. Typically bases added to unbuffered or partially buffered reaction mixtures over the course of conversion are added in aqueous solutions.

When the nucleophile is the conjugate anion of a stronger acid, having a pK_a significantly below the initial pH of the reaction solution, the nucleophile is present predominantly in its anionic form so that, unlike with HCN, a proton is not released on its reaction. Accordingly, the reaction mixture pH in reactions of such nucleophiles may be maintained without stoichiometric buffering or base addition. For example, the conjugate acid of azide, hydrazoic acid has a pK_a of 4.7 and the conjugate acid of nitrite, nitrous acid, has a pK_a of 3.3. Accordingly, at neutral pH, these nucleophiles are present predominantly in their anionic form, N₃⁻ and ONO⁻, respectively. That is, the neutral reaction mixture comprises aqueous azide and nitrite salt, respectively. Their reaction in such mixtures releases halide anion to form aqueous halide salt, not aqueous hydrohalic acid.

Those having ordinary skill in the art can readily determine the quantities of HHDH, 4-halo-3-hydroxybutyric acid ester or amide substrate and nucleophile to use based on, for example, the activity of HHDH as determined by the method in Example 4, the quantity of product desired, and the like. To illustrate, the amount of 4-halo-3-hydroxybutyric acid ester or amide can be in the range of from about 10 to about 500 g/L using about 10 mg to about 30 g of halohydrin dehalogenase. The stoichiometric amount of nucleophile can be readily determined. Further illustrative examples are provided herein.

Suitable conditions for carrying out the HHDH-catalyzed conversion of the present invention include a wide variety of conditions which can be readily optimized by routine experimentation that includes contacting the HHDH, 4-halo-3-hydroxybutyric acid ester or amide substrate, and nucleophile at an experimental pH and temperature and detecting product, for example, using the methods described in the Examples provided herein. The HHDH-catalyzed conversion of 4-halo-3-hydroxybutyric acid ester or amide to 4-nucleophile substituted-3-hydroxybutyric acid ester or amide is typically carried out at a temperature in the range of from about 15°C to about 75°C. More typically, the reaction is carried out at a temperature in the range of from about 20°C to about 55°C, and typically from about 20°C to about 45°C. The reaction may also be carried out under ambient conditions.

The HHDH-catalyzed conversion of 4-halo-3-hydroxybutyric acid ester or amide to 4-nucleophile substituted-3-hydroxybutyric acid ester or amide is generally allowed to proceed until essentially complete or near complete conversion of substrate. Conversion of substrate to product can be monitored using known methods by detecting substrate and/or product. Suitable methods include gas chromatography, HPLC, and the like. Yields of the 4-nucleophile substituted-3-hydroxybutyric acid ester or amide generated in the reaction mixture are generally greater than about 50%, may also be greater than about 60%, may also be greater than about 70%, may be also be greater than about 80%, and are often greater than about 90%.

The 4-nucleophile substituted-3-hydroxybutyric acid ester or amide may be collected from the reaction mixture and optionally purified using methods that are known to those having ordinary skill in the art, as well as those described in the Examples.

Preferred 4-halo-3-hydroxybutyric acid ester or amide substrates of the present invention are chiral, being stereogenic at the 3-position, and may be racemic or non-racemic. Certain halohydrin dehalogenase enzymes used in the process of the present invention

convert the chiral substrate to the 4-cyano-3-hydroxybutyric acid ester or amide with retention of the absolute stereochemistry at the stereogenic 3-position. Non-racemic chiral 4-halo-3-hydroxybutyric acid ester or amide substrates may be converted to substantially equally non-racemic 4-cyano-3-hydroxybutyric acid ester or amide products with little or no loss in stereopurity. The Examples show embodiments of the invention providing high retention of enantiopurity. (Due to conventions for designating stereochemistry, the enantiomer of ethyl 4-chloro-3-hydroxybutyrate designated as (S) and the enantiomer ethyl 4-cyano-3-hydroxybutyrate designated as (R) have the identical stereoconfiguration at the 3-position.)

In other embodiments of the present invention, certain halohydrin dehalogenase enzymes may be stereospecific for one stereoisomer of the chiral 4-halo-3-hydroxybutyric acid ester or amide substrate. The process of the present invention using such stereospecific enzymes may be used to react one stereoisomer of a stereoisomeric mixture of a 4-halo-3-hydroxybutyric acid ester or amide, for example a racemic mixture, while leaving the other stereoisomer substantially unreacted, thereby providing a kinetic resolution of the mixture.

A further significant characteristic of the present invention is that the purity of the 4-nucleophile substituted-3-hydroxybutyric acid ester or amide products generated is very high without the need for extensive purification procedures such as vacuum distillation. Typically, the purity of 4-nucleophile substituted-3-hydroxybutyric acid ester or amide products generated in accordance with the methods of the present invention are at least about 80%, usually at least about 90%, and typically at least about 95%. Product purity may be determined by conventional methods such as HPLC or gas chromatography.

II. KETOREDUCTASE-CATALYZED PRODUCTION OF HALOHYDRINS

The present invention further provides an enzymatic method for generating a 4-halo-3-hydroxybutyric acid ester or amide by:

- (a) providing a 4-halo-3-ketobutyric acid ester or amide,
wherein the halo substituent is selected from the group consisting of chlorine, bromine, and iodine; and
- (b) contacting the 4-halo-3-ketobutyric acid ester or amide with a ketoreductase, a cofactor, and a cofactor regeneration system under conditions suitable to form a reaction

mixture for converting the 4-halo-3-ketobutyric acid ester or amide to the 4-halo-3-hydroxybutyric acid ester or amide.

The terms "ketoreductase" and "KRED" are used interchangeably herein to refer to an enzyme that, in the process of the present invention, catalyzes the reduction of a 4-halo-3-ketobutyric acid ester or amide to the corresponding 4-halo-3-hydroxybutyric acid ester or amide. Such catalytic activity may be detected in an assay such as that described in Example 4, hereinbelow.

As used herein, the term "cofactor" refers to a non-protein compound that operates in combination with an enzyme which catalyzes the reaction of interest. Suitable cofactors employed in the practice of the present invention include NADP^+ (nicotinamide-adenine dinucleotide phosphate), NADPH (i.e., the reduced form of nicotinamide adenine dinucleotide phosphate), NAD^+ (i.e., nicotinamide adenine dinucleotide), and NADH (i.e., the reduced form of NAD^+), and the like. The reduced form of the cofactor is regenerated by reducing the oxidized cofactor with a cofactor regeneration system.

In the present process, the ketoreductase catalyzes the reduction of the 4-halo-3-ketobutyric acid ester or amide by the reduced form of the cofactor. Equation (4) describes the ketoreductase-catalyzed reduction of a 4-halo-3-ketobutyric acid ester by NADH or NADPH , which are represented as alternatives by the designation NAD(P)H .



Ketoreductases that are suitable for carrying out the reduction of 4-halo-3-ketobutyric acid ester or amide to 4-halo-3-hydroxybutyric acid ester or amide include both naturally occurring ketoreductases, as well as non-naturally occurring ketoreductases generated by human manipulation. Exemplary naturally occurring and non-naturally occurring ketoreductases and ketoreductase-encoding polynucleotides include those described herein.

Naturally occurring KRED enzymes can be found in a wide range of bacteria and yeasts. Several naturally occurring KRED gene and enzyme sequences have been reported in the literature, such as, *Candida magnoliae* (Genbank Acc. No. JC7338; GI:11360538), *Candida parapsilosis* (Genbank Ac. No. BAA24528.1; GI:2815409), *Sporobolomyces*

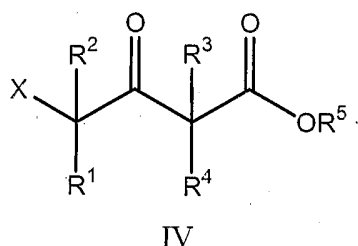
salmicolor (Genbank Acc. No. AF160799; GI 6539734). Polynucleotide sequences encoding the ketoreductase from *Candida magnoliae* are provided as SEQ ID NOS: 1 (CR2-5), 3 (CR1-2), 5 (CR1-3), and 7 (CR2-4). SEQ ID NOS: 1 (CR2-5), 5 (CR1-3), and 7 (CR2-4) are variants that encode the *C. magnoliae* protein (SEQ ID NOS: 2, 6, and 8). SEQ ID NO: 3 (CR1-2) encodes a variant that differs from the *C. magnoliae* protein by one amino acid change (SEQ ID NO: 4). Enzymatic reduction of β -keto esters has been reported for a carbonyl reductase from *Rhodococcus erythropolis* (Peters, Appl. Microbiol. Biotechnol. (1992) 38:334-340; Zelinski, J. Biotechnol. (1994) 33:283-292), an aldehyde reductase from *Sporobolomyces salmonicolor* AKU 4429 (Shimizu, Biotechnol. Lett. (1990) 12:593-596; Appl. Environ. Microbiol. (1990) 56:2374-2377). Enzymes such as those derived from *S. cerevisiae* (J. Org. Chem. (1991) 56:4778; Biosci. Biotech. Biochem. (1994) 58:2236), *Sporobolomyces salmonicolor* (Biochim. Biophys. Acta (1992) 1122:57), *Sporobolomyces* sp. (Biosci. Biotech. Biochem. (1993) 57:303; Japanese patent publication JP2566960), *Candida albicans* (Biosci. Biotech. Biochem. (1993) 57:303), *Candida macedoniensis* (Arch. Biochem. Biophys. (1992) 294-469), *Geotrichium candidum* (Enzyme Microbiol. Technol. (1992) 14:731) have been used for the reduction of ethyl 4-chloro-3-acetoacetate (ECAA). U.S. Pat. No. 6,168,935 describes the use of glycerol dehydrogenase (Tetrahedron Lett. (1988) 29:2453), alcohol dehydrogenase (ADH) from *Thermoanaerobium brockii* (JACS (1985) 107:4028), or *Sulfolobus solfataricus* (Biotechnol. Lett. (1991) 13:31) or *Pseudomonas* sp. (U.S. Pat. No. 5,385,833; J. Org. Chem. (1992) 57:1526).

Suitable non-naturally occurring ketoreductases can be readily identified by applying known methods, including mutagenesis, directed evolution, and the like, followed by screening for activity using the method described in Example 4. For example, these methods can be readily applied to naturally occurring ketoreductases, including the ones described herein. Exemplary non-naturally occurring ketoreductases are provided herein as SEQ ID NOS: 40 (KRED krh133c), 42 (KRED krh215), 44 (KRED krh267), 46 (KRED krh287), 48 (KRED krh320), 50 (KRED krh326), 52 (KRED krh408), 54 (KRED krh417), 56 (KRED krh483), 58 (KRED krh476), 60 (KRED krh495), 114 (KRED S01040430), 116 (KRED S01091361), 118 (KRED S01091625), and 120 (KRED S01094648). The polynucleotide sequences that encode them are provided herein as SEQ ID NOS: 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 113, 115, 117, and 119, respectively. Additional non-naturally occurring ketoreductases that are suitable for use in the practice of the present invention are provided in

the patent application entitled, "Improved Ketoreductase Polypeptides and Related Polynucleotides," corresponding to Attorney Docket No. 0190.110US/15077US01, filed on August 11, 2003, and assigned U.S. application serial number 60/494,195, and in the patent application entitled, "Improved Ketoreductase Polypeptides and Related Polynucleotides,"
 5 corresponding to Attorney Docket No. 0190.210US/15077US02, both of which are incorporated herein by reference in their entireties.

Ketoreductases employed in the practice of the present invention typically exhibit an activity of at least about 1 $\mu\text{mol}/\text{min}/\text{mg}$ in the assay described in Example 4, using the 4-halo-3-ketobutyric acid ester or amide substrate of interest. Ketoreductases employed in
 10 the practice of the present invention may exhibit an activity of at least 1 $\mu\text{mol}/\text{min}/\text{mg}$ to about 10 $\mu\text{mol}/\text{min}/\text{mg}$ and sometimes at least about 10^2 $\mu\text{mol}/\text{min}/\text{mg}$, up to about 10^3 $\mu\text{mol}/\text{min}/\text{mg}$ or higher.

4-halo-3-ketobutyric acid esters and amides employed in the practice of the present invention can be readily purchased or synthesized using known methods. Exemplary 4-halo-
 15 3-ketobutyric acid ester substrates include those having the structure IV:



where:

X is a halogen selected from the group consisting of chlorine, bromine, and iodine;

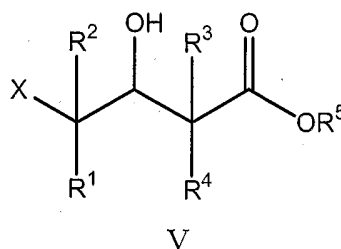
20 and

R^1 , R^2 , R^3 , R^4 , and R^5 are selected as described for structure 1A.

Specific 4-halo-3-ketobutyric acid esters that may be employed in the practice of the present invention include ethyl 4-chloro-3-ketobutyric acid ester (i.e., where X is chlorine, R^1 , R^2 , R^3 , and R^4 are each hydrogen, and R^5 is ethyl), methyl 4-chloro-3-ketobutyric acid
 25 ester (i.e., where X is chlorine, R^1 , R^2 , R^3 , and R^4 are each hydrogen, and R^5 is methyl), ethyl 4-bromo-3-ketobutyric acid ester (i.e., where X is bromine, R^1 , R^2 , R^3 , and R^4 are each hydrogen, and R^5 is ethyl), ethyl 4-iodo-3-ketobutyric acid ester (i.e., where X is iodine, R^1 , R^2 , R^3 , and R^4 are each hydrogen, and R^5 is ethyl), methyl 4-bromo-3-ketobutyric acid ester (i.e., where X is bromine, R^1 , R^2 , R^3 , and R^4 are each hydrogen, and R^5 is methyl), methyl

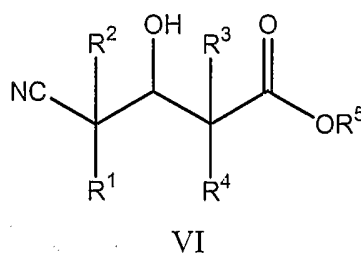
4-iodo-3-ketobutyric acid ester (i.e., where X is iodine, R^1 , R^2 , R^3 , and R^4 are each hydrogen, and R^5 is methyl), t-butyl-4-chloro-3-ketobutyric acid ester (i.e., where X is chlorine, R^1 , R^2 , R^3 , and R^4 are each hydrogen, and R^5 is t-butyl), t-butyl-4-bromo-3-ketobutyric acid ester (i.e., where X is bromine, R^1 , R^2 , R^3 , and R^4 are each hydrogen, and R^5 is t-butyl), and t-butyl-4-iodo-3-ketobutyric acid ester (i.e., where X is iodine, R^1 , R^2 , R^3 , and R^4 are each hydrogen, and R^5 is t-butyl). In certain embodiments, at least one of R^1 , R^2 , R^3 , and R^4 is a lower alkyl, such as, for example, methyl, ethyl, or propyl.

When 4-halo-3-ketobutyric acid ester substrates having the structure of compound IV are reduced during the KRED-catalyzed conversion of the present invention, 4-halo-3-hydroxybutyric acid esters are generated having the structure V:



where X, R^1 , R^2 , R^3 , R^4 and R^5 are as described for structure IV.

4-halo-3-hydroxybutyric acid esters or amides produced by the ketoreductase-catalyzed reduction method of the present invention can then be readily used in the halohydrin dehalogenase-catalyzed conversions of the present invention. For example, 4-halo-3-hydroxybutyric acid esters corresponding to structure V can be used as substrate for conversion by HHDH in the presence of cyanide to generate 4-cyano-3-hydroxybutyric acid esters having the structure VI:



where R^1 , R^2 , R^3 , R^4 , and R^5 are as described as for compound V.

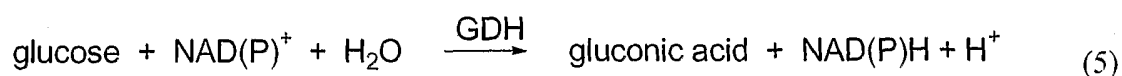
The term "cofactor regeneration system" refers herein to a set of reactants that participate in a reaction that reduces the oxidized form of the cofactor (e.g., NADP to NADPH). Cofactors oxidized by the ketoreductase-catalyzed reduction of the 4-halo-3-ketobutyric acid ester or amide are regenerated in reduced form by the cofactor regeneration

system. Cofactor regeneration systems comprise a stoichiometric reductant that is a source of reducing hydrogen equivalents and is capable of reducing the oxidized form of the cofactor. The cofactor regeneration system may further comprise a catalyst, for example an enzyme catalyst, that catalyzes the reduction of the oxidized form of the cofactor by the reductant.

5 Cofactor regeneration systems to regenerate NADH or NADPH from NAD or NADP, respectively, are known in the art and may be used in the present invention.

Suitable cofactor regeneration systems employed in the practice of the present invention include glucose and glucose dehydrogenase, formate and formate dehydrogenase, glucose-6-phosphate and glucose-6-phosphate dehydrogenase, isopropyl alcohol and
10 secondary alcohol dehydrogenase, phosphite and phosphite dehydrogenase, molecular hydrogen and hydrogenase, and the like, and may be used in combination with either NADP/NADPH or NAD/NADH as the cofactor. Electrochemical regeneration using hydrogenase may also be used as a cofactor regeneration system. See, e.g., U.S. Patent Nos. 5,538,867 and 6,495,023, both of which are incorporated herein by reference. Chemical
15 cofactor regeneration systems comprising a metal catalyst and a reducing agent (for example, molecular hydrogen or formate) are also suitable. See, e.g., PCT publication WO 2000053731, which is incorporated herein by reference.

The terms "glucose dehydrogenase" and "GDH" are used interchangeably herein to refer to an NAD or NADP-dependent enzyme that catalyzes the conversion of D-glucose and
20 NAD or NADP to gluconic acid and NADH or NADPH, respectively. Equation (5) describes the glucose dehydrogenase-catalyzed reduction of NAD or NADP by glucose.



25 Glucose dehydrogenases that are suitable for use in the practice of the present invention include both naturally occurring glucose dehydrogenases, as well as non-naturally occurring glucose dehydrogenases. Naturally occurring glucose dehydrogenase encoding genes have been reported in the literature. For example, the *Bacillus subtilis* 61297 GDH gene was expressed in *E. coli* and was reported to exhibit the same physicochemical
30 properties as the enzyme produced in its native host (Vasantha, et al., Proc. Natl. Acad. Sci. USA (1983) 80:785). The gene sequence of the *B. subtilis* GDH gene, which corresponds to

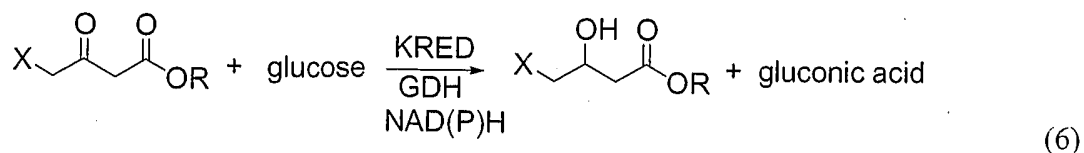
Genbank Acc. No. M12276, was reported by Lampel, et al. (J. Bacteriol. (1986) 166:238-243) and in corrected form by Yamane, et al. (Microbiology (1996) 142:3047-3056) as Genbank Acc. No. D50453. Naturally occurring GDH genes also include those that encode the GDH from *B. cereus* ATCC 14579 (Nature (2003) 423:87-91; Genbank Acc. No. AE017013) and *B. megaterium* (Eur. J. Biochem. (1988) 174:485-490, Genbank Acc. No. X12370; J. Ferment. Bioeng. (1990) 70:363-369, Genbank Acc. No. GI216270). Glucose dehydrogenases from *Bacillus* sp. are provided herein as SEQ ID NOS: 10 and 12 (encoded by polynucleotide sequences corresponding to SEQ ID NOS: 9 and 11, respectively).

Non-naturally occurring glucose dehydrogenases may be generated using known methods, such as, for example, mutagenesis, directed evolution, and the like. GDH enzymes having suitable activity, whether naturally occurring or non-naturally occurring, may be readily identified using the assay described in Example 4. Exemplary non-naturally occurring halohydrin dehalogenases are provided herein as SEQ ID NOS: 62 (GDH 2313), 64 (GDH 2331), 66 (GDH 2279), 68 (GDH 2379), 122 (GDH S01024744), 124 (GDH S01052992), and 126 (GDH S01063714). The polynucleotide sequences that encode them are provided herein as SEQ ID NOS: 61, 63, 65, 67, 121, 123, and 125, respectively. Additional non-naturally occurring glucose dehydrogenases that are suitable for use in the practice of the present invention are provided in the patent application entitled, "Improved Glucose Dehydrogenase Polypeptides and Related Polynucleotides," corresponding to Attorney Docket No. 0352.110US/15076US01, filed on August 11, 2003, and assigned U.S. application serial number 60/494,300, and in the patent application entitled, "Improved Glucose Dehydrogenase Polypeptides and Related Polynucleotides," corresponding to Attorney Docket No. 0352.210US/15076US02, filed on February 18, 2004, and assigned U.S. application serial number _____, both of which are incorporated herein by reference in their entireties.

Glucose dehydrogenases employed in the practice of the present invention may exhibit an activity of at least about 10 $\mu\text{mol}/\text{min}/\text{mg}$ and sometimes at least about 10² $\mu\text{mol}/\text{min}/\text{mg}$ or about 10³ $\mu\text{mol}/\text{min}/\text{mg}$, up to about 10⁴ $\mu\text{mol}/\text{min}/\text{mg}$ or higher in the assay described in Example 4.

When glucose and glucose dehydrogenase are employed as the cofactor regeneration system, as the 4-halo-3-ketobutyric acid ester or amide is reduced by the ketoreductase and NADH or NADPH, the resulting NAD or NADP is reduced by the coupled oxidation of

glucose to gluconic acid by the glucose dehydrogenase. The net reaction is described by equation (6), which is the summation of equations (4) and (5):



The ketoreductase-catalyzed reduction of 4-halo-3-ketobutyric acid ester or amide is generally carried out in a solvent. The solvent may be a co-solvent system, such as, for example, an aqueous co-solvent system. Suitable solvents (including co-solvent systems) for carrying out this conversion are the same as those described above for the HHDH-catalyzed conversion of 4-halo-3-hydroxybutyric acid esters and amides to 4-cyano-3-hydroxybutyric acid esters and amides.

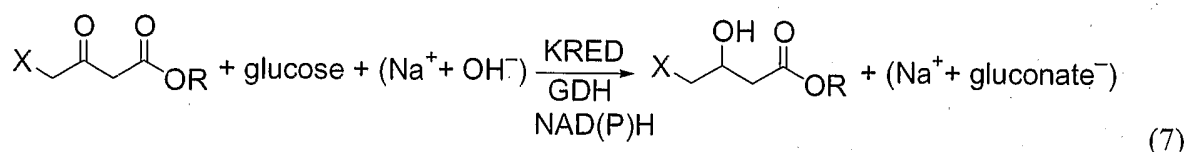
The aqueous solvent (water or aqueous co-solvent system) may be pH-buffered or unbuffered. The conversion of the 4-halo-3-ketobutyric acid ester or amide to the 4-halo-3-hydroxybutyric acid ester or amide may be carried out at a pH of about 5 or above.

Generally, the conversion is carried out at a pH of about 10 or below, usually in the range of from about 5 to about 10. Typically, the conversion is carried out at a pH of about 9 or below, usually in the range of from about 5 to about 9. Preferably, the conversion is carried out at a pH of about 8 or below, usually in the range of from about 5 to about 8, and more preferably in the range of from about 6 to about 8. Alternatively, the conversion may be carried out at neutral pH, i.e., about 7.

When the glucose/glucose dehydrogenase cofactor regeneration system is employed, the co-production of gluconic acid ($\text{pK}_a = 3.6$), as represented in equation (6) causes the pH of the reaction mixture to drop if the resulting aqueous gluconic acid is not otherwise neutralized. The pH of the reaction mixture may be maintained at the desired level by standard buffering techniques, wherein the buffer neutralizes the gluconic acid up to the buffering capacity provided, or by the addition of a base concurrent with the course of the conversion. Suitable buffers and procedures for buffering and suitable bases and procedures for the addition of base during the course of the conversion are the same as those described above for the HHDH-catalyzed conversion of 4-halo-3-hydroxybutyrate esters and amides to 4-cyano-3-hydroxybutyrate esters and amides.

In the ketoreductase-catalyzed reduction of the 4-halo-3-ketobutyric acid ester or amide using glucose/glucose dehydrogenase for cofactor regeneration, when the pH is maintained by buffering or by addition of a base over the course of the conversion, an aqueous gluconate salt rather than aqueous gluconic acid is the product of the overall process.

- 5 For example, equation (7) represents the overall process when aqueous sodium hydroxide ($\text{Na}^+ + \text{OH}^-$) is added over the course of the reaction to maintain the pH:



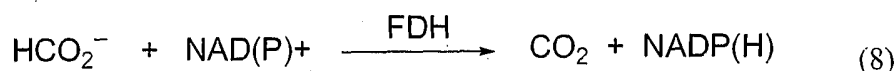
- 10 When base addition is employed to neutralize the gluconic acid released during the ketoreductase-catalyzed reduction of a 4-halo-3-ketobutyric acid ester or amide using the glucose/glucose dehydrogenase cofactor regeneration system, the progress of the conversion may be monitored by the amount of base added to maintain the pH. Typically bases added to unbuffered or partially buffered reaction mixtures over the course of conversion are added in aqueous solutions.

- The terms "formate dehydrogenase" and "FDH" are used interchangeably herein to refer to an NAD or NADP-dependent enzyme that catalyzes the conversion of formate and NAD or NADP to carbon dioxide and NADH or NADPH, respectively. Formate dehydrogenases that are suitable for use in the practice of the present invention include both naturally occurring formate dehydrogenases, as well as non-naturally occurring formate dehydrogenases. Formate dehydrogenases include those corresponding to SEQ ID NOS: 70 (*Pseudomonas sp.*) and 72 (*Candida boidinii*), which are encoded by polynucleotide sequences corresponding to SEQ ID NOS: 69 and 71, respectively. Formate dehydrogenases employed in the practice of the present invention, whether naturally occurring or non-naturally occurring, may exhibit an activity of at least about 1 $\mu\text{mol}/\text{min}/\text{mg}$, sometimes at least about 10 $\mu\text{mol}/\text{min}/\text{mg}$, or at least about 10^2 $\mu\text{mol}/\text{min}/\text{mg}$, up to about 10^3 $\mu\text{mol}/\text{min}/\text{mg}$ or higher, and can be readily screened for activity in the assay described in Example 4.

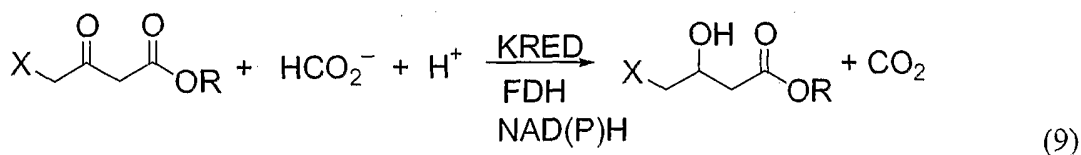
- As used herein, the term "formate" refers to formate anion (HCO_2^-), formic acid (HCO_2H), and mixtures thereof. Formate may be provided in the form of a salt, typically an

alkali or ammonium salt (for example, HCO_2Na , KHCO_2NH_4 , and the like), in the form of formic acid, typically aqueous formic acid, or mixtures thereof. Formic acid is a moderate acid. In aqueous solutions within several pH units of its pK_a ($\text{pK}_a = 3.7$ in water) formate is present as both HCO_2^- and HCO_2H in equilibrium concentrations. At pH values above about 4, formate is predominantly present as HCO_2^- . When formate is provided as formic acid, the reaction mixture is typically buffered or made less acidic by adding a base to provide the desired pH, typically of about 5 or above. Suitable bases for neutralization of formic acid are as described for neutralization of hydrocyanic acid, above.

For pH values above about 5, at which formate is predominantly present as HCO_2^- , equation (8) describes the formate dehydrogenase-catalyzed reduction of NAD or NADP by formate.

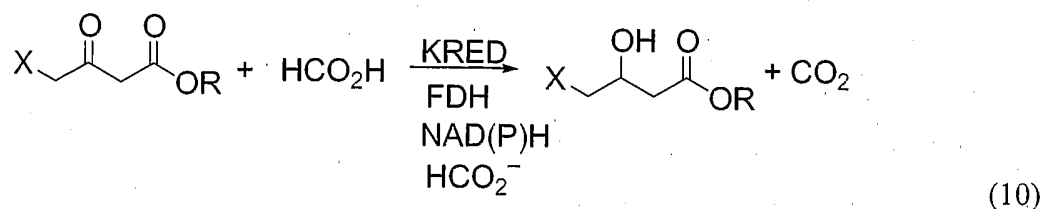


When formate and formate dehydrogenase are employed as the cofactor regeneration system, as the 4-halo-3-ketobutyric acid ester or amide is reduced by the ketoreductase and NADH or NADPH, the resulting NAD or NADP is reduced by the coupled oxidation of formate to carbon dioxide by the formate dehydrogenase. The net reaction is described by equation (9), which is the summation of equations (4) and (8):



Equation (9) shows that when the formate/formate dehydrogenase cofactor regeneration system is employed for the reduction of the 4-halo-3-ketobutyric acid ester or amide in aqueous solution with pH above about 5, protons in solution are consumed and the reaction causes the pH of the reaction mixture to rise if it is not otherwise buffered or re-acidified. The pH of the reaction mixture may be maintained at the desired level by standard buffering techniques, wherein the buffer releases protons up to the buffering capacity provided, or by the addition of an acid concurrent with the course of the conversion. Suitable acids to add during the course of the reaction to maintain the pH include organic acids, for example carboxylic acids, sulfonic acids, phosphonic acids, and the like, mineral acids, for

example hydrohalic acids (such as hydrochloric acid), sulfuric acid, phosphoric acid, and the like, acidic salts, for example dihydrogenphosphate salts (e.g. KH_2PO_4), bisulfate salts (e.g. NaHSO_4) and the like. Particularly preferred is formic acid, whereby both the formate concentration and the pH of the solution are maintained. For example, equation (10) represents the overall process when formic acid (HCO_2H) is added over the course of the reaction to maintain an initial pH above about 5. While the formate is present predominantly as HCO_2^- in the reaction mixture, the HCO_2^- concentration is maintained while the conversion in net consumes the added formic acid.



When acid addition is employed to maintain the pH during the ketoreductase-catalyzed reduction of a 4-halo-3-ketobutyric acid ester or amide using the formate/formate dehydrogenase cofactor regeneration system, the progress of the conversion may be monitored by the amount of acid added to maintain the pH. Typically, acids added to unbuffered or partially buffered reaction mixtures over the course of conversion are added in aqueous solutions.

In carrying out the methods of the present invention, either the oxidized or reduced form of the cofactor may be provided initially. As described above, the cofactor regeneration system converts oxidized cofactor to its reduced form, which is then utilized in the reduction of the ketoreductase substrate (i.e., 4-halo-3-ketobutyric acid ester or amide) to the corresponding halohydrin.

As with the halohydrin dehalogenases, the ketoreductase and enzymes of the cofactor regeneration system may be provided to the reaction mixture for converting 4-halo-3-ketobutyric acid ester or amide in the form of purified enzyme, cell extract, cell lysate, or whole cells transformed with gene(s) encoding the ketoreductase and enzymes of the cofactor regeneration system. The genes encoding the enzymes can be transformed into host cells either separately, or together into the same host cell. For example, in one embodiment one set of host cells can be transformed with ketoreductase encoding gene(s) and another set can

be transformed with cofactor regeneration system enzyme (e.g., GDH, FDH, and the like) encoding gene(s). Both sets of transformed cells can be utilized together in the reaction mixture in the form of whole cells or cell lysates or cell extract derived therefrom.

Alternatively, a host cell can be transformed with genes encoding both ketoreductase and a cofactor regeneration system enzyme, such that each cell expresses both ketoreductase and the cofactor regeneration system enzyme. In a further embodiment, the host cell can be transformed with genes encoding ketoreductase, a cofactor regeneration system enzyme, and a halohydrin dehalogenase. These cells can be utilized in the methods of the present invention to provide the enzymes in the form of whole cells, cell lysate, or cell extract. As described for the reaction mixture of the HHDH-catalyzed method, the solid reactants (i.e., enzymes, salts, cofactor regeneration system, cofactor, and the like) may be provided in a variety of different forms, including powder (e.g., lyophilized, spray dried, and the like), solution, emulsion, suspension, and the like.

The quantities of reactants used in the reduction step will generally vary depending on the quantities of 4-halo-3-hydroxybutyric acid ester or amide desired, and concomitantly the amount of ketoreductase substrate employed. The following guidelines can be used to determine the amounts of ketoreductase, cofactor, and cofactor regeneration system to use. Generally, 4-halo-3-ketobutyric acid esters and amides are employed at a concentration of about 10 to 500 grams/liter using from about 10 mg to about 5 g of ketoreductase and about 25 mg to about 5 g of cofactor. Those having ordinary skill in the art will readily understand how to vary these quantities to tailor them to the desired level of productivity and scale of production. Appropriate quantities of cofactor regeneration system may be readily determined by routine experimentation based on the amount of cofactor and/or ketoreductase utilized. In general, the reductant (e.g. glucose, formate) is utilized at levels above the equimolar level of ketoreductase substrate to achieve essentially complete or near complete conversion of the ketoreductase substrate.

The order of addition of reactants is not critical. The reactants may be added together at the same time to a solvent (e.g., monophasic solvent, biphasic aqueous co-solvent system, and the like), or alternatively, some of the reactants may be added separately, and some together at different time points. For example, the cofactor regeneration system, cofactor, ketoreductase, and ketoreductase substrate may be added first to the solvent

For improved mixing efficiency when an aqueous co-solvent system is used, the cofactor regeneration system, ketoreductase, and cofactor are usually added and mixed into the aqueous phase first. The organic phase may then be added and mixed in, followed by addition of the ketoreductase substrate. Alternatively, the ketoreductase substrate may be premixed in the organic phase, prior to addition to the aqueous phase.

As for the halohydrin dehalogenase-catalyzed conversion of 4-halo-3-hydroxybutyric acid esters and amides, suitable conditions for carrying out the ketoreductase-catalyzed reduction of 4-halo-3-ketobutyric acids esters and amides of the present invention include a wide variety of conditions that can be readily determined by those having ordinary skill in the art. Suitable temperatures for carrying out the ketoreductase-catalyzed reduction step are typically in the range of from about 15°C to about 75°C. Usually, the reactions are carried out at a temperature in the range of from about 20°C to about 55°C, and preferably from about 20°C to about 45°C. The reaction may also be carried out under ambient conditions,

As in the halohydrin dehalogenase-catalyzed reaction, the ketoreductase-catalyzed reaction is allowed to proceed until essentially complete or near complete conversion of substrate is observed using methods that are known in the art. As in the halohydrin dehalogenase-catalyzed reaction, the progression of the ketoreductase-catalyzed reaction may be monitored by monitoring the amount of base or acid added to counter the pH change that may otherwise occur with the particular cofactor regeneration system that is used, as described above.

The ketoreductase-catalyzed reduction of the 4-halo-3-ketobutyric acid ester or amide substrate generates a new stereogenic carbon at the 3-position of the 4-halo-3-hydroxybutyric acid ester or amide product. Typically, the 4-halo-3-hydroxybutyric acid ester or amide is generated with a relatively high stereoselectivity at the 3-position. Thus, the 4-halo-3-hydroxybutyric acid esters and amides generated by the ketoreductase-catalyzed reduction of 4-halo-3-ketobutyric acid esters and amides are typically chiral and non-racemic. The ketoreductase reactions used in the present invention typically generate preferred nonracemic, chiral 4-halo-3-hydroxybutyric acid esters having an e.e. of at least about 90% e.e., usually at least about 95% e.e., and typically at least about 99% e.e. The Examples illustrate embodiments providing ethyl (S)-4-chloro-3-hydroxybutyrate with greater than 99% e.e.

As used herein, the term "enantiomeric excess" or "e.e." refers to the absolute difference between the mole or weight fractions of major ($F_{(+)}$) and minor ($F_{(-)}$) enantiomers

(i.e., $|F_{(+)} - F_{(-)}|$), where $F_{(+)} + F_{(-)} = 1$. Percent e.e. is $100 \times |F_{(+)} - F_{(-)}|$. Enantiomeric composition can be readily characterized by using the gas chromatography method described in Example 6, hereinbelow, and using methods that are known in the art.

As described above, when these nonracemic chiral 4-halo-3-hydroxybutyric acid esters or amides are used as substrates in the halohydrin dehalogenase-catalyzed reactions of the present invention, the resulting 4-substituted-4-hydroxybutyric acid esters or amides are substantially equally nonracemic, with little or no loss in stereopurity. The combination of the high stereoselectivity of the ketoreductase-catalyzed production of the nonracemic 4-halo-3-hydroxybutyric acid esters or amides and the high stereofidelity of the halohydrin dehalogenase-catalyzed conversion of them to the corresponding nonracemic 4-cyano-3-hydroxybutyric acid esters or amides provides a particularly attractive inventive process for the overall production of nonracemic 4-cyano-3-hydroxybutyric acid esters or amides of high e.e. from 4-halo-3-ketobutyric acid esters or amides.

A further significant characteristic of the present invention is that the yield of chiral products generated is very high. Typically, the yields of 4-halo-3-hydroxybutyric acid ester or amide and 4-nucleophile substituted-3-hydroxybutyric acid ester or amide products generated in accordance with the methods of the present invention are at least about 70%, usually at least about 80%, typically at least about 90%, and may be at least about 95%. The computation of product yield is based on initial substrate quantity provided and the amount of product formed in the reaction mixture. Product 4-halo-3-hydroxybutyric acid ester or amide may be optionally purified prior to contacting with the halohydrin dehalogenase. As used herein, the term "purified" refers to a process in which a separation process is applied to a mixture, resulting in an increase in concentration of one component relative to other components in the mixture. Suitable purification processes employed in the practice of the present invention include, for example, filtration, solid or liquid phase extraction, distillation, and the like.

If the 4-halo-3-hydroxybutyric acid ester or amide is purified from the ketoreductase reaction mixture, it is subsequently added to a solvent (e.g., a monophasic solvent, a biphasic aqueous co-solvent system) with the halohydrin dehalogenase and nucleophile.

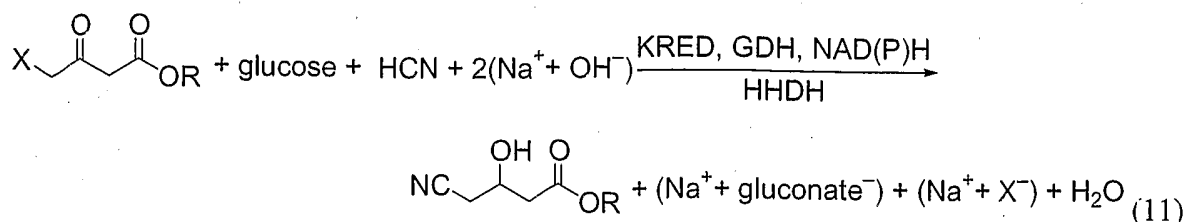
III. ENZYMATIC CONVERSION OF 4-HALO-3-KETOBUTYRIC ACID
ESTER/AMIDE TO 4-NUCLEOPHILE SUBSTITUTED-3-HYDROXYBUTYRIC
ACID ESTER/AMIDE IN A SINGLE REACTION VESSEL

The present invention provides a method for carrying out the conversion of 4-halo-3-ketobutyric acid esters and amides to the corresponding 4-nucleophile substituted-3-hydroxybutyric acid esters and amides in a single reaction vessel, the method comprising contacting the 4-halo-3-ketobutyric acid ester or amide with a ketoreductase, a cofactor, a cofactor regeneration system, a nucleophile, and a halohydrin dehalogenase to form a reaction mixture for converting the 4-halo-3-ketobutyric acid ester or amide to a 4-nucleophile substituted-3-hydroxybutyric acid ester or amide

Mechanistically, this single-vessel method proceeds via ketoreductase-catalyzed conversion of the 4-halo-3-ketobutyric acid ester or amide to provide the 4-halo-3-hydroxybutyric acid ester or amide *in situ*, and consequent halohydrin dehalogenase-catalyzed conversion of the 4-halo-3-hydroxybutyric acid ester or amide to the corresponding 4-nucleophile substituted-3-hydroxybutyric acid ester or amide. Significantly, the 4-halo-3-hydroxybutyric acid ester or amide produced by the ketoreductase-catalyzed reaction is not separated or recovered prior to its contact with halohydrin dehalogenase and nucleophile (e.g., cyanide and the like) for its conversion to 4-nucleophile substituted-3-hydroxybutyric acid ester or amide.

Suitable reactants (substrates, enzymes, cofactors), solvents, pH, temperature, and other reaction conditions and procedures for the single-vessel conversion of 4-halo-3-ketobutyric acid ester or amide to 4-nucleophile substituted-3-hydroxybutyric acid ester or amide are the same as those described above for the carrying out the halohydrin dehalogenase-catalyzed conversion of 4-halo-3-hydroxybutyric acid esters and amides to the corresponding 4-nucleophile substituted-3-hydroxybutyric acid esters and amides.

When glucose and glucose dehydrogenase are used as the cofactor regeneration system and two equivalents of base are added during the course of the reaction to neutralize both the gluconic acid and hydrohalic acid produced and maintain the initial pH of the reaction mixture (for initial pHs in the range of about 5 to about 9), the overall process in a single-vessel reaction is described by equation (11), which is the summation of equations (2) and (7), wherein aqueous sodium hydroxide is illustrated as the base.



Other single-vessel overall process equations can result from summing equations describing other options for conducting the halohydrin dehalogenase-catalyzed reaction (e.g., using a cyanide salt as the base) and/or the ketoreductase reaction (e.g. using formate and formate dehydrogenase as the cofactor regeneration system), as described above for the separately conducted reactions.

It will also be understood that the same single-vessel result may be obtained by first conducting the ketoreductase reaction separately as described above, then subsequently adding halohydrin dehalogenase and cyanide into the ketoreductase reaction mixture and conducting the halohydrin dehalogenase reaction in the presence of the ketoreductase reaction components.

An embodiment of a single-vessel process for converting a 4-halo-3-ketobutyric acid ester to a 4-cyano-3-hydroxybutyric acid ester is illustrated in Example 24.

IV. HALOHYDRIN DEHALOGENASE-CATALYZED CONVERSION OF VICINAL HALO, HYDROXY SUBSTITUTED CARBOXYLIC ACID ESTERS TO VICINAL CYANO, HYDROXY SUBSTITUTED CARBOXYLIC ACID ESTERS

In addition to 4-halo-3-hydroxybutyric acid ester substrates, it has been discovered that halohydrin dehalogenases can be used to catalyze the conversion of other vicinal halo, hydroxy substituted carboxylic acid ester substrates to their corresponding vicinal cyano, hydroxy substituted carboxylic acid esters, using the same conditions as described in part I. Thus, the present invention also provides a method for producing a vicinal cyano, hydroxy substituted carboxylic acid ester from a vicinal halo, hydroxy substituted carboxylic acid ester, the method comprising:

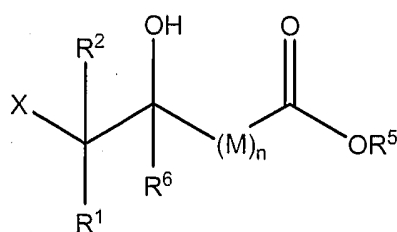
- (a) providing a vicinal halo, hydroxy substituted carboxylic acid ester, wherein the halo substituent is selected from the group consisting of chlorine, bromine, and iodine; and

(b) contacting the vicinal halo, hydroxy substituted carboxylic acid ester with a halohydrin dehalogenase and cyanide under conditions suitable to form a reaction mixture for converting the vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted carboxylic acid ester.

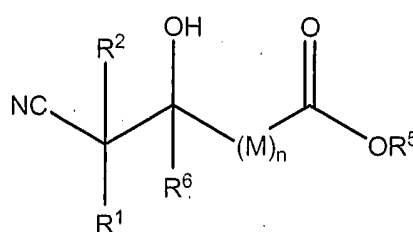
As used herein, the term "vicinal halo, hydroxy substituted" refers to halogen and hydroxyl group substitutions on adjacent carbons. The term "vicinal cyano, hydroxy substituted" is used herein to refer to cyano ($C\equiv N$) and hydroxyl groups substitutions on adjacent carbons. Vicinal halo, hydroxyl substituted carboxylic acid esters that are suitable for use in the practice of the present invention include those that are not 4-halo-3-hydroxybutyric acid ester. Concomitantly, vicinal cyano, hydroxy substituted carboxylic acid ester product generated by these methods include those that are not 4-cyano-3-hydroxybutyric acid ester.

Preferred vicinal halo, hydroxy substituted carboxylic acid ester substrates of the present invention are chiral, being stereogenic at the hydroxy-substituted carbon, and may be racemic or non-racemic. In these embodiments, certain halohydrin dehalogenase enzymes used in the process of the present invention convert the chiral vicinal halo, hydroxyl substituted carboxylic acid ester substrate to the corresponding vicinal cyano, hydroxy substituted carboxylic acid ester with retention of the absolute stereochemistry at the stereogenic hydroxy-substituted carbon. Non-racemic chiral vicinal halo, hydroxy substituted carboxylic acid ester substrates may be converted to substantially equally non-racemic vicinal cyano, hydroxy substituted carboxylic acid ester products with little or no loss in stereopurity.

Suitable vicinal halo, hydroxy substituted carboxylic acid esters employed in the practice of the present invention include those having the structure VII, which provide vicinal cyano, hydroxy substituted carboxylic acid ester having the corresponding structure VIII.



VII



VIII

where:

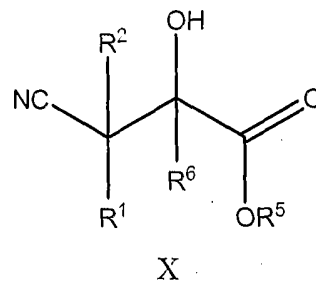
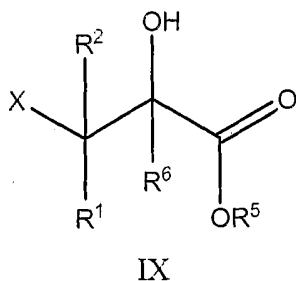
X, R¹, R², R⁵, and R⁶ are as defined for structure IA, and

n is zero or from 1 to 9, inclusive, and

each M_n is independently selected from -C(=O)- (i.e., carbonyl) or -CRⁿR^{n'}-, wherein Rⁿ and R^{n'} are each independently selected from the group consisting of hydrogen, fluorine, an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted lower alkenyl, an optionally substituted aryl, an optionally substituted arylalkyl, amino, an optionally substituted lower alkylamino, an optionally substituted cycloalkylamino, an optionally substituted lower alkoxy, an optionally substituted cycloalkoxy, an optionally substituted aryloxy, an optionally substituted aryl, hydroxyl, nitro, amino, cyano, carboxy (i.e. a carboxylate or carboxylic acid group), carboalkoxy (i.e. an ester group), carbamide (i.e. an amide group), and acyl (i.e. forming a ketone).

Suitable vicinal halo, hydroxy substituted carboxylic acid esters have the structure VII with n=1, and include the 4-halo-3-hydroxybutyric acid esters previously described.

Other suitable vicinal halo, hydroxy substituted carboxylic acid esters have the structure VII with n=0, thereby having structure IX, which provide vicinal cyano, hydroxy substituted carboxylic acid ester having the corresponding structure X.



where:

X, R¹, R², R⁵, and R⁶ are as defined for structure VII.

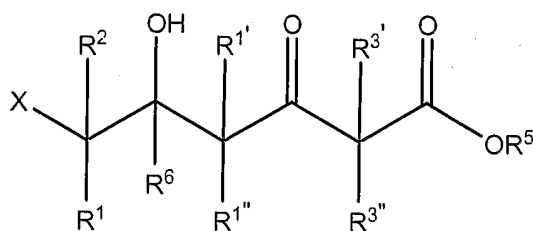
Suitable vicinal halo, hydroxy substituted carboxylic acid esters having the structure IX include 4-halo-2-hydroxypropionic acid esters. With respect to structures VII and IX, X is typically chlorine or bromine, and preferably chlorine. With respect to structures VII through X, R¹, R², R⁵, and R⁶ are preferably each independently either hydrogen or a lower alkyl.

Other suitable vicinal halo, hydroxy substituted carboxylic acid esters have the structure VII with n from 2 to 9, inclusive. Typically, n is from 2 to 8, inclusive, and more typically, from 2 to 7, inclusive, and usually, from 2 to 6, inclusive. Suitable vicinal halo, hydroxy substituted carboxylic acid esters having n=2 include 5-halo-4-hydroxypentanoic

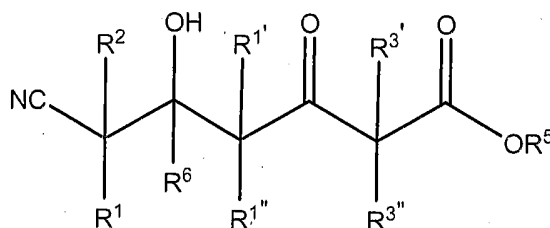
acid esters. Suitable vicinal halo, hydroxy substituted carboxylic acid esters having $n=3$ include 6-halo-5-hydroxyhexanoic acid esters. Suitable vicinal halo, hydroxy substituted carboxylic acid esters having $n=4$ include 7-halo-6-hydroxyheptanoic acid esters. Suitable vicinal halo, hydroxy substituted carboxylic acid esters having $n=5$ include 8-halo-7-

5 hydroxyoctanoic acid esters. Suitable vicinal halo, hydroxy substituted carboxylic acid esters having $n=6$ include 9-halo-8-hydroxynonanoic acid esters. Suitable vicinal halo, hydroxy substituted carboxylic acid esters having $n=7$ include 10-halo-9-hydroxydecanoic acid esters. Suitable vicinal halo, hydroxy substituted carboxylic acid esters having $n=8$ include 11-halo-10-hydroxyundecanoic acid esters. Suitable vicinal halo, hydroxy substituted carboxylic acid
 10 esters having $n=9$ include 12-halo-11-hydroxydodecanoic acid esters.

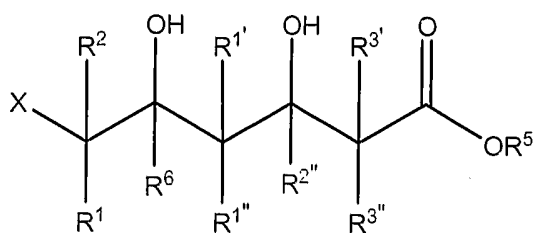
Preferred vicinal halo, hydroxy substituted carboxylic acid esters are 6-halo-5-hydroxy-3-oxohexanoic acid esters having the structure XI and 6-halo-3,5-dihydroxyhexanoic acid esters having the structure XIII, which provide vicinal cyano, hydroxy substituted carboxylic acid ester having the structures XII and XIV, respectively.



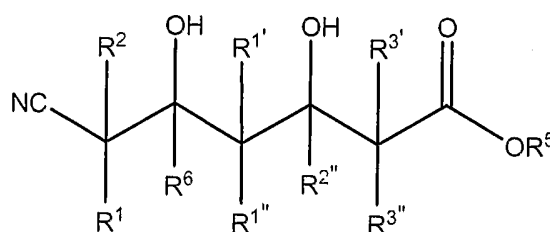
XI



XII



XIII



XIV

20 where for XI, XII, XIII, and XIV:

X, R^1 , R^2 , R^5 , and R^6 are as defined for structure VII. $R^{1'}$, $R^{1''}$, $R^{2'}$, $R^{2''}$, $R^{3'}$, and $R^{3''}$ are as defined for R^n and $R^{n''}$ in structure VII. Preferably, R^1 , R^2 , R^6 , $R^{1'}$, $R^{1''}$, $R^{2'}$, $R^{3'}$, and $R^{3''}$ are each independently either hydrogen or a lower alkyl. X is typically chlorine or bromine.

25 Preferred 6-halo-5-hydroxy-hexanoic acid esters of structure XI or XIII have $X=Cl$.

Specific 6-halo-5-hydroxy-3-oxohexanoic acid esters of structure XI that may be employed in the practice of the present invention include t-butyl 6-chloro-5-hydroxy-3-oxohexanoic acid ester (i.e., where X is chlorine, R^1 , R^2 , R^6 , $R^{1'}$, $R^{1''}$, $R^{2''}$, $R^{3'}$, and $R^{3''}$ are hydrogen and R^5 is t-butyl) and t-butyl 6-bromo-5-hydroxy-3-oxohexanoic acid ester (i.e., where X is bromine, R^1 , R^2 , R^6 , $R^{1'}$, $R^{1''}$, $R^{2''}$, $R^{3'}$, and $R^{3''}$ are hydrogen, and R^5 is t-butyl). When employed in the method of the present invention, these substrates yield the corresponding vicinal cyano, hydroxyl substituted product having structure XII, where R^1 , R^2 , R^6 , $R^{1'}$, $R^{1''}$, $R^{2''}$, $R^{3'}$, and $R^{3''}$ are hydrogen and R^5 is t-butyl.

Specific 6-halo-3,5-dihydroxyhexanoic acid esters having the structure XIII that may be employed in the practice of the present invention include t-butyl 6-chloro-3,5-dihydroxyhexanoic acid ester (i.e., where X is chlorine, R^1 , R^2 , R^6 , $R^{1'}$, $R^{1''}$, $R^{2''}$, $R^{3'}$, and $R^{3''}$ are hydrogen, and R^5 is t-butyl) and t-butyl 6-bromo-3,5-dihydroxyhexanoic acid ester (i.e., where X is bromine, R^1 , R^2 , R^6 , $R^{1'}$, $R^{1''}$, $R^{2''}$, $R^{3'}$, and $R^{3''}$ are hydrogen, and R^5 is t-butyl). When employed in the method of the present invention, these 6-halo-3,5-dihydroxyhexanoic acid ester substrates yield vicinal cyano, hydroxyl substituted product having structure XIV, where R^1 , R^2 , R^6 , $R^{1'}$, $R^{1''}$, $R^{2''}$, $R^{3'}$, and $R^{3''}$ are hydrogen, and R^5 is t-butyl.

Suitable halohydrin dehalogenases for catalyzing the conversion of vicinal halo, hydroxy substituted carboxylic acid ester substrate to vicinal cyano hydroxyl substituted carboxylic acid product include both naturally occurring and non-naturally occurring halohydrin dehalogenases, as previously described in part I *supra*. Halohydrin dehalogenases may be readily identified using the assay described in Example 4 (part (3)) and substituting for ethyl (S)-4-chloro-3-hydroxybutyrate the vicinal halo, hydroxyl substituted carboxylic acid substrate of interest. Conditions that are suitable to form a reaction mixture for converting the vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted carboxylic acid ester are the same as described for converting 4-halo-3-hydroxybutyric acid esters to their corresponding 4-cyano-3-hydroxybutyric acid esters (see part I *supra*), e.g., cyanide sources, methods for controlling pH, temperatures, solvents and co-solvent systems, and the like. Exemplary methods for converting 6-halo-5-hydroxy-3-oxohexanoic acid esters (structure XI) and 6-halo-3,5-dihydroxyhexanoic acid esters (structure XIII) to their corresponding vicinal cyano, hydroxy substituted carboxylic acid esters (i.e., structures XII and XIV, respectively) are provided in Examples 32-41 hereinbelow.

V. COMPOSITIONS

The present invention further provides compositions that are useful for the enzymatic conversion of 4-halo-3-hydroxybutyric acid ester or amide to 4-nucleophile substituted-3-hydroxybutyric acid ester or amide. These compositions comprise a halohydrin dehalogenase, a 4-halo-3-hydroxybutyric acid ester or amide, and a nucleophile. In a preferred composition, the nucleophile is cyanide.

In a further embodiment, the present invention provides compositions useful for preparing 4-nucleophile substituted-3-hydroxybutyric acid esters and amides that have a ketoreductase, a cofactor regeneration system, a cofactor, and a halohydrin dehalogenase. These compositions may further include a 4-halo-3-ketobutyric acid ester or amide.

Any of the previously described ketoreductases, components of a cofactor regeneration system, cofactors, halohydrin dehalogenases, 4-halo-3-ketobutyric acid esters or amides, 4-halo-3-hydroxybutyric acid esters or amides, and nucleophiles may be employed in these compositions.

The present invention also provides compositions that are useful for carrying out the conversion of a vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted carboxylic acid ester or amide. These compositions comprise a halohydrin dehalogenase, a cyanide, and a vicinal halo, hydroxyl substituted carboxylic acid ester.

Compositions of the present invention may be in solid (e.g., a powder) or liquid (e.g., solution, emulsion, suspension, and the like) form. For example, the composition may be in the form of a lyophilized or spray dried powder. Alternatively, the composition may further comprise a solvent.

The compositions may further include components for pH control or processability, including, for example, a salt, an acid, a base, a buffer, a solubilizing agent, etc.

VI. HALOHYDRIN DEHALOGENASES, KETOREDUCTASES, AND COFACTOR REGENERATION SYSTEM ENZYMES AND CORRESPONDING POLYNUCLEOTIDES

In addition to the specific enzymes and polynucleotides described herein, those having ordinary skill in the art will recognize that known techniques can be readily applied in

the discovery of both naturally occurring and non-naturally occurring polynucleotides encoding enzymes suitable for use in the practice of the present invention. See, e.g., Ling, et al., "Approaches to DNA mutagenesis: an overview," Anal. Biochem., 254(2):157-78 (1997); Dale, et al., "Oligonucleotide-directed random mutagenesis using the phosphorothioate method," Methods Mol. Biol., 57:369-74 (1996); Smith, "In vitro mutagenesis," Ann. Rev. Genet., 19:423-462 (1985); Botstein, et al., "Strategies and applications of in vitro mutagenesis," Science, 229:1193-1201 (1985); Carter, "Site-directed mutagenesis," Biochem. J., 237:1-7 (1986); Kramer, et al., "Point Mismatch Repair," Cell, 38:879-887 (1984); Wells, et al., "Cassette mutagenesis: an efficient method for generation of multiple mutations at defined sites," Gene, 34:315-323 (1985); Minshull, et al., "Protein evolution by molecular breeding," Current Opinion in Chemical Biology, 3:284-290 (1999); Christians, et al., "Directed evolution of thymidine kinase for AZT phosphorylation using DNA family shuffling," Nature Biotechnology, 17:259-264 (1999); Cramer, et al., "DNA shuffling of a family of genes from diverse species accelerates directed evolution," Nature, 391:288-291; Cramer, et al., "Molecular evolution of an arsenate detoxification pathway by DNA shuffling," Nature Biotechnology, 15:436-438 (1997); Zhang, et al., "Directed evolution of an effective fucosidase from a galactosidase by DNA shuffling and screening," Proceedings of the National Academy of Sciences, U.S.A., 94:454-4509; Cramer, et al., "Improved green fluorescent protein by molecular evolution using DNA shuffling," Nature Biotechnology, 14:315-319 (1996); Stemmer, "Rapid evolution of a protein in vitro by DNA shuffling," Nature, 370:389-391 (1994); Stemmer, "DNA shuffling by random fragmentation and reassembly: In vitro recombination for molecular evolution," Proceedings of the National Academy of Sciences, U.S.A., 91:10747-10751 (1994); WO 95/22625; WO 97/0078; WO 97/35966; WO 98/27230; WO 00/42651; and WO 01/75767. These and other known methods can be readily applied, for example, together with the assays described herein, to identify other ketoreductases, halohydrin dehalogenases, and cofactor regeneration system enzymes having the activities described herein, as well as other desirable properties, e.g., altered temperature and/or pH optimums, solvent resistance, and the like. For example, a ketoreductase may be mutated or evolved to generate libraries that can be screened to identify a ketoreductase having a preference for one cofactor type over another, for example, NAD versus NADP, or vice-versa.

Polynucleic acid sequences encoding the enzymes employed in the present invention may be codon optimized for optimal production from the host organism selected for expression. Those having ordinary skill in the art will recognize that tables and other references providing codon preference information for a wide range of organisms are readily available. See e.g., Henaut and Danchin, "*Escherichia coli* and *Salmonella*," Neidhardt, et al. eds., ASM Press, Washington, D.C. (1996) pp. 2047-2066.

Enzymes employed in the practice of the present invention may be produced by transforming a vector containing a polynucleotide encoding halohydrin dehalogenase, ketoreductase, or a cofactor regeneration system enzyme into a host cell using well known molecular biology techniques. See, e.g., Berger and Kimmel, "Guide to Molecular Cloning Techniques", Methods in Enzymology, Volume 152, Academic Press, Inc., San Diego, CA; Sambrook, et al., "Molecular Cloning—A Laboratory Manual," 2nd Ed., Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989; and "Current Protocols in Molecular Biology," F.M. Ausubel, et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc. (supplemented through 1999). Methods for making the enzymes are illustrated in Examples 1 and 2.

The foregoing and other aspects of the invention may be better understood in connection with the following non-limiting examples.

EXAMPLES

Example 1: Construction of Expression Constructs for Expression of Halohydrin Dehalogenase, Ketoreductase, and Glucose Dehydrogenase.

(1) Halohydrin Dehalogenase (HHDH)

The gene for the halohydrin dehalogenase was codon optimized for expression in *E. coli* based on the amino acid sequence of the halohydrin dehalogenase from *Agrobacterium* sp. The gene was synthesized using 60-mer oligomers, and cloned into expression vector pCK110700 (depicted in Figure 2) under the control of a T5 promoter. The vectors were transformed into *E. coli* TOP10 (Invitrogen, Carlsbad, CA) from which plasmid DNA was prepared using standard methods. The plasmid DNA was then transformed into *E. coli* BL21 (Stratagene, La Jolla, CA), the expression host, using standard methods. Several clones were

found in the expression library that expressed active HHDH. The genes from these clones were sequenced (see SEQ ID Nos: 13 (HHDH.1), 15 (HHDH.2), and 17 (HHDH.16) which encode polypeptide sequences SEQ ID Nos. 14, 16, and 18, respectively).

(2) Ketoreductase (KRED)

The gene for the ketoreductase was codon optimized for expression in *E. coli* based on the amino acid sequence of the ketoreductase from *Candida magnoliae*. The gene was synthesized using 60-mer oligomers, and cloned into the *Sfi*I cloning sites of expression vector, pCK110900 (depicted in Figure 3), under the control of a lac promoter and lacI repressor gene. The expression vector contains the p15A origin of replication and the chloroamphenicol resistance gene. The plasmids were transformed into an *E. coli* expression host using standard methods. Several clones were found that expressed active ketoreductase and their genes were sequenced to confirm the DNA sequences (see SEQ ID Nos: 1 (Ketoreductase 1), 3 (Ketoreductase 2), 5 (Ketoreductase 3), and 7 (Ketoreductase 4), which encode for polypeptide sequences SEQ ID Nos. 2, 4, 6, and 8, respectively).

(3) Glucose Dehydrogenase (GDH)

The genes for the glucose dehydrogenase were amplified using the polymerase chain reaction (PCR) from genomic DNA preparations of *Bacillus subtilis* and *Bacillus megaterium*. The primers for the amplification reactions were designed using the published *B. subtilis* and *B. megaterium* glucose dehydrogenase gene sequences, and were as follows:

B. subtilis forward primer (SEQ ID NO: 19) :

5'-GAATTCGCCCATATGTATCCGGATTAAAAGG-3'

B. subtilis reverse primer (SEQ ID NO: 20):

5'-TGGCCGGATCCTCATTAACCGCGGCCTGCCTGGA-3'

B. megaterium forward primer (SEQ ID NO: 21):

5'-GAATTCGCCCATATGTATAAAGATTAGAAAGG-3'

B. megaterium reverse primer (SEQ ID NO 22):

5'-GGCCGGATCCTCATTATCCGCGTCCTGCTTGGA-3'

The PCR products were cloned into the *Sfi*I cloning sites of expression vector, pCK110900 (depicted in Figure 3), under the control of a lac promoter and lacI repressor gene. The expression vector contains the p15A origin of replication and the chloroamphenicol resistance gene. The plasmids were transformed into an *E. coli* expression

host using standard methods. Several clones were found to express active GDH and the genes were sequenced to confirm the sequences (see SEQ ID Nos: 9 (Glucose dehydrogenase S06-3) and 11 (Glucose dehydrogenase M02-6), which encode for polypeptide sequences SEQ ID Nos. 10 and 12, respectively).

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(4) Formate Dehydrogenase (FDH)

The genes for the formate dehydrogenase were codon optimized for expression in *E. coli* based on the amino acid sequences of the formate dehydrogenase from *Pseudomonas* species strain 101 (Protein Database Accession ID 2NAD_A) and *Candida boidinii* (Genbank
10 Accession No. CAA09466). The genes were synthesized using 60-mer oligomers, and cloned into the *Sfi*I cloning sites of expression vector, pCK110900 (depicted in Figure 3), under the control of a lac promoter and lacI repressor gene. The expression vector contains the p15A origin of replication and the chloroamphenicol resistance gene. The plasmids were transformed into an *E. coli* expression host using standard methods. Clones were found that
15 expressed active formate dehydrogenase and the genes were sequenced to confirm the DNA sequences (see SEQ ID NOS: 69 and 71, which encode for polypeptide sequences SEQ ID Nos. 70 and 72, respectively.)

Example 2: Production of Enzyme

20 (1) HHDH enzyme:

In an aerated agitated fermentor, 10.0L of growth medium containing 0.528g/L ammonium sulphate; 7.5g/L of di-potassium hydrogen phosphate trihydrate; 3.7g/L of potassium dihydrogen phosphate; 2g/L of Tastone-154 yeast extract; 0.05g/L ferrous sulphate; and 3ml/L of a trace element solution containing 2g/L of calcium chloride
25 dihydrate, 2.2g/L of zinc sulfate septahydrate, 0.5g/L manganese sulfate monohydrate, 1g/L cuprous sulfate heptahydrate: 0.1g/l sodium borate decahydrate and 0.5g/L EDTA, was brought to a temperature of 30 °C. The fermentor was inoculated with a late exponential culture of *Escherichia coli* BL21 (Stratagene, La Jolla, CA) equipped with plasmid containing HHDH polynucleotides as described in Example 1, then grown in a shake flask containing
30 LB, 1% glucose (Sigma Chemical Co., St. Louis, MO), and 30µg/ml chloroamphenicol (Sigma Chemical Co., St. Louis, MO) to a starting optical density at 600 nm (OD₆₀₀) of 0.5 to 2.0. The fermenter was agitated at 500-1500 rpm and air was supplied to the fermentation

vessel at 1.0-15.0 L/min to maintain a dissolved oxygen level of 30% saturation or greater. The pH of the culture was controlled at 7.0 by addition of 20% v/v ammonium hydroxide. After the culture reached an OD₆₀₀ of 40, the temperature was reduced to 25°C and the expression of halohydrin dehalogenase was induced by the addition of isopropyl-β-D-thiogalactoside (IPTG) (Sigma Chemical Corp., St. Louis, MO) to a final concentration of 1mM. The culture was grown for another 15 hours. After the induction, the cells were harvested by centrifugation and washed with 10 mM potassium phosphate buffer, pH 7.0. The cell paste was used directly in the downstream recovery process or was stored at -80°C until use.

(2) Ketoreductase enzyme:

In an aerated agitated fermentor, 10.0L of growth medium containing 0.528g/L ammonium sulphate, 7.5g/L of di-potassium hydrogen phosphate trihydrate, 3.7g/L of potassium dihydrogen phosphate, 2g/L of Tastone-154 yeast extract, 0.05g/L ferrous sulphate, and 3ml/L of a trace element solution containing 2g/L of calcium chloride dihydrate, 2.2g/L of zinc sulfate septahydrate, 0.5g/L manganese sulfate monohydrate, 1g/L cuprous sulfate heptahydrate, 0.1g/L sodium borate decahydrate and 0.5g/L EDTA, was brought to a temperature of 30 °C.

The fermentor was inoculated with a late exponential culture of *Escherichia coli* W3110 (pCR2-5) grown in a shake flask containing LB, 1% glucose (Sigma Chemical Co., St. Louis, MO), and 30 µg/ml chloroamphenicol (Sigma Chemical Co., St. Louis, MO) to a starting optical density at 600 nm (OD₆₀₀) of 0.5 to 2.0. The fermentor was agitated at 500-1500rpm and air was supplied to the fermentation vessel at 1.0-15.0 L/min, and the pH of the culture was controlled at 7.0 by addition of 20% v/v ammonium hydroxide. After the culture reached an OD₆₀₀ of 40, the temperature was reduced to 25 °C and the expression of glucose dehydrogenase was induced by the addition of isopropyl-β-D-thiogalactoside (IPTG) (Sigma Chemical Corp., St. Louis, MO) to a final concentration of 1 mM. The culture was grown for another 15 hours. After the induction, the cells were harvested by centrifugation and washed with 10 mM potassium phosphate buffer, pH 7.0. The cell paste was used directly in the downstream recovery process or was stored at -80 °C until use.

(3) Glucose dehydrogenase enzyme:

In an aerated agitated fermentor, 10.0L of growth medium containing 0.528g/L ammonium sulphate; 7.5g/L of di-potassium hydrogen phosphate trihydrate; 3.7g/L of potassium dihydrogen phosphate; 2g/L of Tastone-154 yeast extract; 0.05g/L ferrous sulphate; and 3ml/L of a trace element solution containing 2g/L of calcium chloride dihydrate, 2.2g/L of zinc sulfate septahydrate, 0.5g/L manganese sulfate monohydrate, 1g/L cuprous sulfate heptahydrate; 0.1g/l sodium borate decahydrate and 0.5g/L EDTA, was brought to a temperature of 30 °C.

The fermentor was inoculated with a late exponential culture of (pGDHS06 or pGDHM02) grown in a shake flask containing LB, 1% glucose (Sigma Chemical Co., St. Louis, MO), and 30 µg/ml chloroamphenicol (Sigma Chemical Co., St. Louis, MO) to a starting optical density at 600 nm (OD_{600}) of 0.5 to 2.0. The fermenter was agitated at 500-1500rpm and air was supplied to the fermentation vessel at 1.0-15.0L/min, and the pH of the culture was controlled at 7.0 by addition of 20% v/v ammonium hydroxide. After the culture reached an OD_{600} of 40, the temperature was reduced to 25 °C and the expression of glucose dehydrogenase was induced by the addition of isopropyl-β-D-thiogalactoside (IPTG) (Sigma Chemical Corp., St. Louis, MO) to a final concentration of 1mM. The culture was grown for another 15 hours. After the induction, the cells were harvested by centrifugation and washed with 10 mM potassium phosphate buffer, pH 7.0. The cell paste was used directly in the downstream recovery process or was stored at -80 °C until use.

(4) Formate Dehydrogenase

In an aerated agitated fermenter, 10.0L of autoclaved minimal medium containing 3.5g/L of $NaNH_4HPO_4 \cdot 4H_2O$, 7.5g/L of $K_2HPO_4 \cdot 3 H_2O$, and 3.7g/L of KH_2PO_4 (see Lageveen, et al., 1988, Appl. Environ. Microbiol. 54:2924. (1988)), 2g/L NH_4Cl , 0.528g/L $(NH_4)_2SO_4$, pH 7.0, 5 ml/L of R2 trace elements (see Reisenberg, et al. Appl. Microbiol. Biotechnol 1990 34:77), 20ml/L of 10% yeast extract solution in water, 5 ml/L 1 M $MgSO_4$, 40 ml/L of 50% glucose solution in water were added. The temperature of the medium was brought to 30 °C.

Chloroamphenicol was added from a concentrated stock solution, to a final concentration of 30 µg/ml. The fermenter was inoculated with an overnight culture of

Escherichia coli W3110 (pFDHPS3 or PFDHCB13) grown in a shake flask containing the above minimal medium with R2 trace element solution, pH 7.0, 0.2% yeast extract, 1% glucose, and 30 µg/ml chloroamphenicol to a starting optical density at 600 nm (OD₆₀₀) of 0.04 – 0.1. The air was supplied to the fermentation vessel at 5.0 L/min. the pH of the culture was maintained at 7.0 using a concentrated solution of potassium hydroxide in water. The culture was grown to an OD₆₀₀ of 12-15, at which time a feed solution of 50% glucose, 6% ammonium chloride and 0.5% magnesium sulfate was initiated at a rate that resulted in a final dissolved oxygen concentration of 30-40% of air saturation. The feed pump rate was controlled such that the dissolved oxygen in the fermenter was maintained around 30% at airflow rate of 10 L/min and agitation rate of 600 rpm. After the culture reached an OD₆₀₀ of 15 and had been exposed to the feeding regimen for a few hours, the expression of the formate dehydrogenase was induced by the addition of 1mM of IPTG. The culture was grown for another 8-18 hours before it was harvested by centrifugation.

Example 3: Enzyme Preparation

(1) Ketoreductase

The cell paste was washed by suspending 1 volume wet weight of cell paste in 3 volumes of 100mM Tris/sulfate (pH 7.2) followed by centrifugation at 5000g for 40 minutes in a Sorval 12BP. The washed cell paste was suspended in 2 volumes of 100mM Tris/sulfate (pH 7.2). The intracellular KRED was released from the cells by passing the suspension through a homogenizer in two passes using a pressure of 14,000 psig for the first pass and 8,000 psig for the second pass. The lysate was warmed to room temperature, then a 10% w/v solution of polyethyleneimine (PEI), pH 7.2, was added to the lysate to a final PEI concentration of 0.75% w/v and stirred for 30 minutes. The treated homogenate was centrifuged at 10,000 rpm in a Beckman lab centrifuge for 60 minutes. The supernatant was decanted and dispensed in shallow containers, frozen at –20 °C and lyophilized.

(2) Glucose Dehydrogenase

The cell paste was washed by suspending 1 volume wet weight of cell paste in 3 volumes of 100mM Tris/sulfate (pH 7.2) followed by centrifugation at 5000g for 40 minutes in a Sorval 12BP. The washed cell paste was suspended in 2 volumes of 100mM Tris/sulfate (pH 7.2). The intracellular HHDH was released from the cells by passing the suspension

through a homogenizer in two passes using a pressure of 14,000 psig for the first pass and 8,000 psig for the second pass. The homogenate was centrifuged at 10,000 rpm in a Beckman lab centrifuge for 60 minutes. The supernatant was decanted and dispensed in shallow containers, frozen at -20°C and lyophilized.

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(3) Halohydrin Dehalogenase

The cell paste was washed by suspending 1 volume wet weight of cell paste in 3 volumes of 100mM Tris/sulfate (pH 7.2) followed by centrifugation at 5000g for 40 minutes in a Sorval 12BP. The washed cell paste was suspended in 2 volumes of 100mM Tris/sulfate (pH 7.2). The intracellular HHDH was released from the cells by passing the suspension through a homogenizer in two passes using a pressure of 14,000 psig for the first pass and 8,000 psig for the second pass. The cell lysate was allowed to cool to 4°C between passes through the homogenizer. The homogenate was centrifuged at 10,000 rpm in a Beckman lab centrifuge for 60 minutes. The supernatant was decanted and dispensed in shallow containers, frozen at -20°C and lyophilized to a powder that was stored at -80°C .

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To assess the quality of the preparation after fermentation, cell lysate containing the expressed halohydrin dehalogenase enzyme was assayed according to the following protocol. Approximately 50 μl of clarified cell lysate in 100mM Tris- SO_4 , 100mM NaCN, pH 8.0 was mixed with 10mM ethyl-(S)-4-chloro-3-hydroxybutyrate (Sigma Aldrich, St. Louis, MO or prepared in accordance with the ketoreductase-catalyzed methods described herein). The total reaction volume was 0.2 ml. The reaction was incubated at room temperature for 30 min to 1 hour. The reaction was extracted with 7 volumes of ethyl acetate and the organic layer removed to a 1.8 ml GC vial. The organic layer was analyzed by GC for presence of the ethyl-(R)-4-cyano-3-hydroxybutyrate product. The amount of product produced was determined by comparison to a standard curve prepared and analyzed under the same conditions.

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(4) Formate Dehydrogenase

Cell lysate containing expressed formate dehydrogenase was prepared by homogenization of cell paste in 1 volume 100 mM triethanolamine (pH 7.0) at 4°C . The cell lysate was allowed to cool to 4°C between passes through the homogenizer. Cell lysate was

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clarified by centrifugation at 4°C. The clarified lysate was assayed as described in Example 4.

Example 4: Characterization of Enzyme Activity

(1) Ketoreductase (KRED)

To a solution of ethyl 4-chloro-3-ketobutyric acid ester (10 mM) in 100 mM potassium phosphate buffer (pH 7.0) was added the ketoreductase enzyme as a predissolved solution in the same buffer. The reaction was initiated by addition of NADPH (1 mM final) and the course of reaction was followed by measurement of the decrease of absorbance at 340 nm. This absorbance corresponds to the NADPH concentration. The results were plotted as Absorbance units (NADPH) vs. time, and the slope of the plot determined (Absorbance units/min). The slope of the Absorbance vs. time plot was converted to concentration units using the extinction coefficient of NADPH, and the activity of the ketoreductase was determined in units of μmol (NADPH consumed)/min/mg (total ketoreductase catalyst). The measurement can also be performed using fluorescent detection utilizing an excitation of 340 nm for NADPH with emission measured at 455 nm. Other substrates of interest may be substituted for ethyl 4-chloro-3-keto-butyric acid ester to evaluate ketoreductase activity with respect to other substrates.

(2) Glucose Dehydrogenase (GDH)

To a solution of 50 mM glucose in 100 mM potassium phosphate buffer (pH 7.0) was added the glucose dehydrogenase enzyme as a predissolved solution in the same buffer. The reaction was initiated by addition of NADP (1 mM final) and the course of reaction was followed by measurement of the increase of absorbance at 340 nm or of the fluorescence (excitation 340 nm, emission 455 nm). The results were plotted as Absorbance units (NADPH) vs. time, and the slope of the plot determined (Absorbance units/min). The slope of the Absorbance vs. time plot was converted to concentration units using the extinction coefficient of NADPH (see (1) above), and the activity of the glucose dehydrogenase was determined in units of μmol (NADPH created)/min/mg (total glucose dehydrogenase catalyst).

(3) Halohydrin dehalogenase (HHDH)

To a solution of ethyl (S)-4-chloro-3-hydroxybutyrate (10 mM) in 300 mM potassium phosphate, 300 mM NaCN buffer (pH 8.0) was added the halohydrin dehalogenase enzyme as a predissolved solution in the same buffer. Over time, aliquots of the mixture were withdrawn and extracted with three volumes of ethyl acetate. The organic layer was then analyzed by gas chromatography (GC), as described hereinbelow in Example 6. Samples were taken at various time points, and the peak area of the product cyanohydrin, ethyl (R)-4-cyano-3-hydroxybutyrate, was plotted as a function of time. The peak areas were converted to concentration units using a standard curve that was prepared for the ethyl (R)-4-cyano-3-hydroxybutyrate. Activity of the halohydrin dehalogenase was determined in units of μmol (cyanohydrin produced)/min/mg (total halohydrin dehalogenase catalyst). Other nucleophiles and/or substrates of interest may be substituted to evaluate halohydrin dehalogenase activity with respect to other nucleophiles and/or substrates.

(4) Formate Dehydrogenase

To a solution of 150 mM formate in 100 mM triethanolamine buffer (pH 7.0) was added the formate dehydrogenase enzyme as a predissolved solution in the same buffer. The reaction was initiated by addition of NAD (2 mM final) and the course of reaction was followed by measurement of the increase of absorbance at 340 nm or of the fluorescence (excitation 340 nm, emission 455 nm). The results were plotted as Absorbance units (NADH) vs. time, and the slope of the plot determined (Absorbance units/min). The slope of the Absorbance vs. time plot was converted to concentration units using the extinction coefficient of NADH, and the activity of the formate dehydrogenase was determined in units of μmol (NADH created)/min/mg (total formate dehydrogenase catalyst).

Example 5: Preparation of ethyl (R)-4-cyano-3-hydroxybutyrate from ethyl 4-chloroacetoacetate (via ethyl (S)-4-chloro-3-hydroxybutyrate).

To a well-stirred solution of 100 mM potassium phosphate buffer, 500 mM NaCl, pH 7 (1 L) at room temperature was added glucose (160g, 830 mmoles, 1.1 equiv). To this was added ketoreductase SEQ ID NO: 2 (0.9g), glucose dehydrogenase S06 SEQ ID NO: 10 (0.5 g) and NADP (0.5g) as lyophilized powders. Once dissolved, butyl acetate (500 mL) was added to form an emulsion. To this emulsion was added a solution of ethyl 4-chloroacetoacetate (100g, 608 mmoles) in butyl acetate (500 mL), dropwise over 3 hours.

The pH was maintained between 6.8 and 7 by an automatic titrater that dispensed Na_2CO_3 (2M in water, about 160 mL total). After 40 hours the automated addition of the base had ceased and there was no residual starting material by gas chromatography. The layers were separated, and the aqueous phase was washed with ethyl acetate (500 mL). The combined
5 organics were dried over anhydrous sodium sulfate, filtered and evaporated on a rotary evaporator, to give essentially pure (~97%) ethyl (S)-4-chloro-3-hydroxybutyrate.

To a well stirred solution of ethyl (S)-4-chloro-3-hydroxybutyrate (8.25 g, 50 mmol) in 300 mM potassium phosphate buffer, 300 mM NaCN pH 8.0 (1L) at 30 °C was added halohydrin dehalogenase SEQ ID NO: 14 (9 g) as a lyophilized powder. After fifty seven
10 hours the mixture was washed with ethyl acetate (2 times 250 mL) and the combined organics dried over anhydrous sodium sulfate. The mixture was filtered and evaporated on a rotary evaporator to give essentially pure ethyl (R)-4-cyano-3-hydroxybutyrate, as determined using the gas chromatography method and elution time data described in Example 6, hereinbelow.

This example shows the process of the invention wherein a 4-cyano-3-hydroxybutyric acid ester (ethyl (R)-4-cyano-3-hydroxybutyrate) is produced by contacting a 4-halo-3-hydroxybutyric acid ester (ethyl (S)-4-chloro-3-hydroxybutyrate) with a halohydrin dehalogenase and cyanide (provided by a cyanide salt, NaCN). It further shows the process of the invention wherein the 4-halo-3-hydroxybutyric acid ester is provided by contacting a
20 4-halo-3-ketobutyric acid ester (ethyl 4-chloroacetoacetate) with a ketoreductase, a cofactor (NADPH, provided as NADP), and a cofactor regeneration system (glucose and glucose dehydrogenase). It further shows the overall production of nonracemic chiral ethyl (R)-4-cyano-3-hydroxybutyrate from achiral ethyl 4-chloroacetoacetate in high e.e. and in high purity without extensive purification procedures.

Example 6: Characterization of Ethyl (R)-4-cyano-3-hydroxybutyrate

The ethyl 4-cyano-3-(R)-hydroxybutyrate produced in Example 5 was analyzed using gas chromatography with flame ionization (FID) detection using an Agilent HP-5 column, 30 m long, 0.25 μm inner diameter, using the following program: 1 minute at 100°C,
30 5°C/minute for 10 minutes; 25°C/minute for 2 minutes; then 2 minutes at 200°C. Inlet and outlet temperatures were both 300°C, and the flow rate was 2 ml/minute. Under these

conditions, ethyl (R)-4-cyano-3-hydroxybutyrate elutes at 6.25 minutes, ethyl (S)-4-chloro-3-hydroxybutyrate elutes at 4.5 minutes, and ethyl 4-chloroacetoacetate elutes at 4.1 minutes.

Chemical purity of the species was measured using the integrated peak areas from the gas chromatography results.

5 Enantioselectivity of the halohydrin dehalogenase (HHDH) with respect to ethyl (R)-4-cyano-3-hydroxybutyrate was measured by gas chromatography and FID detection using a Restek gammaDex SA column (30 m long, 0.32 μ m inner diameter) using the following program: 25 minutes at 165°C and flow rate at 2 ml/min. Inlet and outlet temperatures were both at 230°C. Under these conditions ethyl (R)-4-cyano-3-
10 hydroxybutyrate elutes at 19.6 minutes and ethyl (S)-4-cyano-3-hydroxybutyrate elutes at 19.2 minutes.

Example 7: Preparation of Ethyl (S)-4-chloro-3-hydroxybutyrate from Ethyl 4-chloro-acetoacetate.

15 To a 3-necked jacketed 3L flask equipped with a mechanical stirrer and connected to an automatic titrator by a pH electrode and a feeding tube for addition of base, was charged triethanolamine (6.6 mL) and H₂O (492 mL) to make 100 mM triethanolamine solution. The pH was adjusted to 7 with 37% HCl. Then, D-Glucose (125 g) was added. The water circulating to the flask jacket was set to 30 °C. After 10 minutes, ketoreductase SEQ ID NO:
20 2 (5.7g) and glucose dehydrogenase S06 SEQ ID NO: 10 (3.1 g) powder were added. After 10 minutes, β -NAD (125 mg) was added and the resulting mixture was allowed to stir for 5 minutes. Then, butyl acetate (250 mL) was charged. Using an addition funnel, 2.4 M ethyl 4-chloroacetoacetate (250 mL, 100 g in 167 mL of butyl acetate) was slowly added over 3 hrs. The pH was maintained at 7 by the automatic titrator by the addition of 2 M Na₂CO₃ (152
25 mL) over 15 hrs. Subsequently, gas chromatography of a reaction sample showed complete conversion to product. Celite (16 g) was added and the reaction mixture was allowed to stir for 10 minutes. The solution was filtered through a celite pad and the organic layer was separated. The aqueous layer was extracted with butyl acetate (2x 200 mL). The organic layers were combined and the solvent removed under vacuum by rotary evaporation to obtain
30 87 g of the ethyl (S) 4-chloro-3-hydroxybutyrate. The enantiomeric excess was >99%, as determined after its conversion to ethyl (R)-4-cyano-3-hydroxybutyrate in Example 8.

Example 8: Preparation of Ethyl (R)-4-cyano-3-hydroxybutyrate from Ethyl (S)-4-chloro-3-hydroxybutyrate

To a 3-necked jacketed 3L flask equipped with a mechanical stirrer and connected to an automatic titrator by a pH electrode and a feeding tube for addition of base, was charged H₂O (1200 mL), NaCN (37.25 g) and NaH₂PO₄ (125 g) to bring the solution to pH 7. The water circulator was set to 40 °C. After 10 minutes, halohydrin dehalogenase SEQ ID NO: 32 as cell lysate (250 mL) was added. The reaction mixture was allowed to stir for 5 minutes. Using an addition funnel, ethyl (S)-4-chloro-3-hydroxybutyrate (45 g of the material from Example 7) was slowly added over 1 hour. The pH was maintained at 7 by the automatic titrator by the addition of 10 M NaOH (27 mL) over 17 hrs. Subsequently, gas chromatography of a reaction sample showed complete conversion to product. Celite (16 g) was added to the flask, which was then connected to a diaphragm, whose exhaust is bubbled into 5M NaOH (200 mL), to remove HCN. The mixture was heated to 60 °C under 100mm Hg pressure. After 1 hour a submerged air bubbler was added to the solution to aid the removal of the HCN. After 3 hours, an HCN detector indicated less than 5 ppm HCN in the off-gas. The mixture was allowed to cool to room temperature, then filtered through a celite pad. The filtrate was extracted with butyl acetate (3x 800 mL) and the combined organic layers filtered through a pad of activated charcoal. The solvent was removed under vacuum by rotary evaporation to provide 28.5 g of ethyl (R)-4-cyano-3-hydroxybutyrate. The purity was 98% (w/w) by HPLC and the enantiomeric excess was >99% (by chiral GC, the S enantiomer was undetectable).

Example 9: Preparation of Ethyl (S)-4-chloro-3-hydroxybutyrate from Ethyl 4-chloro-acetoacetate.

To a 100 mL vessel connected to an automatic titrator by a pH electrode and a feeding tube for addition of base was charged a solution of glucose (7.5 g) in 100 mM triethanolamine pH 7 buffer (25 mL). To this solution was charged ketoreductase SEQ ID NO: 42 (100 mg); 50 mg GDH SEQ ID NO: 66 and NADP (6.25 mg). Butyl acetate (10 ml) was then charged. Then, ethyl 4-chloroacetoacetate (6 g) in butyl acetate (10 mL) was charged. The pH was maintained at 7 by the automatic titrator by the addition of 4M NaOH (7.5 mL) over 7 hrs. A sample of the reaction mixture was extracted with an equal volume

of butyl acetate and the organic layer was analyzed by GC. The analysis showed 99% conversion of the ethyl 4-chloroacetoacetate to ethyl (S)-4-chloro-3-hydroxybutyrate.

Example 10: Preparation of Ethyl (S)-4-chloro-3-hydroxybutyrate from Ethyl 4-chloro-acetoacetate.

The procedure was identical to Example 9 with the exceptions that 400 mg of the ketoreductase SEQ ID NO: 42 was used and NAD⁺ (12.5 mg) was added in place of the NADP. The addition of the NaOH solution by the automatic titrator was complete in 11 hours and the GC analysis showed 99% conversion of the ethyl 4-chloroacetoacetate to ethyl (S)-4-chloro-3-hydroxybutyrate.

Example 11: Preparation of Ethyl (S)-4-chloro-3-hydroxybutyrate from Ethyl 4-chloro-acetoacetate.

To a 100 mL vessel connected to an automatic titrator by a pH electrode and a feeding tube for addition of base was charged a solution of glucose (12. g) in water (30 mL). To this solution was charged ketoreductase SEQ ID NO: 42 (100 mg); 50 mg GDH SEQ ID NO: 66 and NADP (6.25 mg). Butyl acetate (10 mL) was then charged. Ethyl 4-chloroacetoacetate (10 g) was then charged via syringe pump as follows: 1 mL was charged rapidly and the remainder was then charged at a rate of 1 mL/hr). The pH was maintained at 7 by the automatic titrator by the addition of 4M NaOH over 18 hours hrs. The stirring was stopped and the phases allowed to separate. The organic layer included some emulsion. The organic layer, including some emulsion, was separated and washed with 10 mL of water. The combined aqueous layers were extracted twice with 20 mL of butyl acetate. The organic extracts were combined and rotary evaporated under vacuum to remove water. Additional butyl acetate was added during the evaporation to help remove the water. When the water was removed the butyl acetate solution was decanted from solids in the flask. Evaporation of the solvent under vacuum then gave 8.85 g of ethyl (S)-4-chloro-3-hydroxybutyrate (87.4% yield) of very good purity.

Example 12: Preparation of Ethyl (R)-4-cyano-3-hydroxybutyrate from Ethyl (S)-4-chloro-3-hydroxybutyrate

To a 170mL vessel connected to an automatic titrator by a pH electrode and a feeding tube for addition of base was charged NaCN (1.5 g, 31 mmol) and water (50 mL). The vessel

was sealed and the headspace was deaerated with nitrogen. The pH was adjusted to 7 by the addition of conc. H_2SO_4 (0.9 mL). The reaction mixture was heated to 40 °C and treated with a solution of halohydrin dehalogenase SEQ ID NO: 32 (1.2 g in 10 mL water containing 42 μL of 14M β -mercaptoethanol). Then, ethyl (S)-4-chloro-3-hydroxybutyrate (1.8 g, 10.8 mmol) was added via syringe. The automatic titrator maintained the pH at 7 by the addition of 2M NaOH. After 15 hr the reaction was complete and a total of 4.6 mL 2M NaOH had been added. A sample of the reaction mixture was extracted with an equal volume of butyl acetate. GC analysis of the organic extract showed the conversion of the ethyl (S)-4-chloro-3-hydroxybutyrate to ethyl (R)-4-cyano-3-hydroxybutyrate was >99%.

Example 13: Preparation of Ethyl (R)-4-cyano-3-hydroxybutyrate from Ethyl (S)-4-chloro-3-hydroxybutyrate

The procedure was identical to Example 12 with the exception that 4M NaCN was used as the base instead of the 2M NaOH. After 8 hrs, the reaction was complete and a total of 2.3 mL 4M NaCN had been added. By GC analysis, the conversion of the ethyl (S)-4-chloro-3-hydroxybutyrate to ethyl (R)-4-cyano-3-hydroxybutyrate was >99%.

This example shows the process of the invention using an alkali cyanide as base to maintain both the pH and the cyanide concentration of the reaction mixture constant.

Example 14: Preparation of Ethyl (R)-4-cyano-3-hydroxybutyrate from Ethyl (S)-4-chloro-3-hydroxybutyrate

To a 250 mL vessel connected to an automatic titrator by a pH electrode and a feeding tube for addition of base (7.5 M NaOH) was charged water (83.5 mL) and 0.7 g of halohydrin dehalogenase SEQ ID NO: 24. The mixture was stirred for 30 minutes. The titrator was activated and set to maintain pH 7. Then, 25% aqueous HCN (9.26 mL, 8.6 g) was charged over 20 minute to make a 2.3% HCN solution. The mixture was heated at 40 °C for 10 minutes, then ethyl (S)-4-chloro-3-hydroxybutyrate (5 g) was charged over 1 hour. The automatic titrator maintained the pH at 7 by the addition of 2M NaOH. After 20 hrs, GC analysis of a butyl acetate extract of a reaction sample showed the conversion of the ethyl (S)-4-chloro-3-hydroxybutyrate to ethyl (R)-4-cyano-3-hydroxybutyrate was 95%.

This example shows the process of the invention using aqueous hydrocyanic acid as the source of cyanide.

Example 15: Preparation of Ethyl (R)-4-cyano-3-hydroxybutyrate from Ethyl (S)-4-chloro-3-hydroxybutyrate

To a 20 mL screw-cap vial was added NaCN (250 mg) and NaH₂PO₄ (830 mg).

- 5 Water (10 mL) was added followed by halohydrin dehalogenase SEQ ID NO: 32 as lyophilized powder (200 mg). Then ethyl (S)-4-chloro-3-hydroxybutyrate (300 mg) was added. The vial was capped and heated in an oil bath at 40 °C. After 4 hours, GC analysis of a butyl acetate extract of a reaction sample extract showed of 54% conversion of the ethyl (S)-4-chloro-3-hydroxybutyrate to ethyl (R)-4-cyano-3-hydroxybutyrate. After 72 hrs, the
10 GC analysis showed complete conversion.

Example 16: Preparation of Ethyl (S)-4-cyano-3-hydroxybutyrate from Ethyl (R)-4-chloro-3-hydroxybutyrate

- The procedure was identical to that of Example 15 with the exceptions that the
15 (R)-enantiomer of the Ethyl 4-chloro-3-hydroxybutyrate was reacted instead of the (S)-enantiomer and the quantities of all reaction components were halved. After 1 hour reaction time, the GC analysis showed 55% conversion of the ethyl (R)-4-chloro-3-hydroxybutyrate to ethyl (S)-4-cyano-3-hydroxybutyrate.

- This example in combination with preceding examples shows that the process of the
20 invention may be used to convert either enantiomer of the 4-halo-3-hydroxybutyric acid ester to the corresponding enantiomer of the 4-cyano-3-hydroxybutyric acid ester.

Example 17: Preparation of Methyl (S)-4-chloro-3-hydroxybutyrate from Methyl 4-chloro-acetoacetate

- 25 The procedure was identical to that of Example 9 with the exceptions that an equimolar amount of methyl 4-chloroacetoacetate was reacted instead of the ethyl 4-chloroacetoacetate and the enzymes used were ketoreductase SEQ ID NO: 50 and glucose dehydrogenase SEQ ID NO: 62. The reaction was completed in 11 hrs and the GC analysis showed >99% methyl (S)-4-chloro-3-hydroxybutyrate. The product was isolated by
30 extraction into butyl acetate and solvent evaporation and its identity confirmed by ¹H and ¹³C NMR.

Example 18: Preparation of Methyl (R)-4-cyano-3-hydroxybutyrate from Methyl (S)-4-chloro-3-hydroxybutyrate

The procedure was identical to that of Example 16 with the exception that an equimolar amount of methyl (S)-4-chloro-3-hydroxybutyrate (prepared by Example 17) was reacted instead of ethyl (R)-4-chloro-3-hydroxybutyrate. After 1 hour reaction time, the GC analysis showed 38% conversion of the methyl (R)-4-chloro-3-hydroxybutyrate to methyl (S)-4-cyano-3-hydroxybutyrate. The product was characterized by ^1H and ^{13}C NMR.

Example 19: Preparation of Ethyl (R)-4-cyano-3-hydroxybutyrate from Ethyl (S)-4-bromo-3-hydroxybutyrate.

The procedure was identical to that of Example 16 with the exception that an equimolar amount of ethyl (S)-4-bromo-3-hydroxybutyrate was reacted instead of ethyl (R)-4-chloro-3-hydroxybutyrate. After 1 hour reaction time, the GC analysis showed 90% conversion of the ethyl (S)-4-bromo-3-hydroxybutyrate to ethyl (S)-4-cyano-3-hydroxybutyrate. The product was characterized by ^1H and ^{13}C NMR.

This example shows that the process of the invention wherein the halo substituent of the 4-halo-3-hydroxybutyric acid ester is bromine.

Example 20: Preparation of Ethyl 3-hydroxybutyrate from Ethyl acetoacetate.

The procedure was identical to that of Example 17 with the exceptions that an equimolar amount of ethyl acetoacetate was reacted instead of the methyl 4-chloroacetoacetate and 200 mg of ketoreductase SEQ ID NO: 50 and 100 mg of glucose dehydrogenase SEQ ID NO: 62 were used. The reaction was completed in 6 hrs. The product was isolated by extraction into butyl acetate and solvent evaporation and characterized by ^1H and ^{13}C NMR.

In combination with preceding examples, this example demonstrates that ketoreductase enzymes that have activity for the reduction of ethyl acetoacetate to ethyl 3-hydroxybutyrate are useful for the reduction 4-halo-3-ketobutyric acid esters to 4-halo-3-hydroxybutyric acid esters in embodiments of this invention.

Example 21: pH profiles of enzymatic and nonenzymatic test reactions of ethyl 4-chloro-3-hydroxybutyrate with cyanide

Aqueous solutions containing 25 mg/mL sodium cyanide were prepared at pH 5.0, 6.0, 7.0, 7.5, 8.0, 8.5, and 9.0 by the addition of 85% phosphoric acid while monitoring with pH meter. 5 mL of each solution was charged to a separate 20 mL screw cap vial. Halohydrin dehalogenase SEQ ID NO: 38 (20 mg) was added to each vial, followed by ethyl (S)-4-chloro-3-hydroxybutyrate (50 mg, 0.30 mmol). For nonenzymatic reactions experiments, the procedure was identical with the exception that the enzyme was omitted. The vials were capped and heated in an oil bath at 55 °C for 3 hrs, then removed and cooled to room temperature. A 0.4 mL sample of each reaction mixture was extracted with 1 mL butyl acetate and the extracts were analyzed by gas chromatography.

The analyzed amounts of substrate and products in each vial are given in Table I, and graphed vs. pH in Figure 1. In both, chlorohydrin means ethyl (S)-4-chloro-3-hydroxybutyrate, cyanohydrin means ethyl (R)-4-cyano-3-hydroxybutyrate, and crotonate means ethyl 4-hydroxycrotonate. In the Table, ND means not detected.

Table I: Millimoles chlorohydrin, cyanohydrin and crotonate by-product analyzed in test reactions with and without halohydrin dehalogenase. See Example 21

PH	without halohydrin dehalogenase			with halohydrin dehalogenase		
	mmol chlorohydrin	mmol cyanohydrin	mmol crotonate	mmol chlorohydrin	mmol cyanohydrin	mmol crotonate
5.0	0.33	ND	ND	0.27	ND	ND
6.0	0.29	ND	ND	0.07	0.20	ND
7.0	0.30	ND	ND	0.01	0.28	ND
7.5	0.31	ND	ND	0.004	0.30	ND
8.0	0.30	0.01	ND	0.002	0.29	ND
8.5	0.21	0.05	0.001	0.001	0.24	ND
9.0	0.11	0.10	0.002	0.001	0.21	ND

The pHs of the final test reaction mixtures were remeasured. For the mixtures including halohydrin dehalogenase with initial pHs of 7 or above (being the mixtures in which near complete conversion of the chlorohydrin to the cyanohydrin occurred, the final mixture pHs were 0.4 to 0.6 pH units below the initial pHs. The other mixtures showed much lesser changes in pH from their initial values.

These data show that under these reaction conditions and time, no measurable nonenzymatic reaction of the ethyl 4-chloro-3-hydroxybutyrate with cyanide occurred at any tested pH less than 8. At pH 8 and above, increasing nonenzymatic reaction with cyanide to form ethyl 4-cyano-3-hydroxybutyrate occurred with increasing pH and was accompanied by increasing formation of ethyl 4-hydroxycrotonate by-product. In contrast, the enzymatic reaction with halohydrin dehalogenase occurred at all the tested pH's greater than 5 and with no detectable formation of ethyl 4-hydroxycrotonate at any tested pH. Additionally, for both enzymatic and nonenzymatic test reactions at pH greater than 8, the mole total of the GC-analyzed products decreased from the initial 0.30 mmoles provided (as ethyl 4-chloro-3-hydroxybutyrate reactant) indicating the increasing formation of non-analyzable by-products with increasing pH greater than 8. It was separately established that the ester group of the reactant and product are increasingly hydrolyzed to carboxylic acid groups at pHs greater than 8 and that the resulting carboxylic acids are not extracted in to the extracts of reaction mixture samples that are analyzed by GC. See Example 22.

Example 22: Nonenzymatic hydrolysis of ethyl 4-cyano-3-hydroxybutyrate.

Aqueous phosphate solutions were prepared at pH 7.0, 7.5, 8.0, 8.5, and 9.0 by dissolving 0.48 g of NaH_2PO_4 in 40 mL water and adjusting the pH by addition of 2M NaOH while monitoring with pH meter. 5 mL of each solution was charged to a separate 20 mL screw cap vial. Then, ethyl (R)-4-cyano-3-hydroxybutyrate (46 mg, 0.29 mmol) was added. The vials were capped and heated in an oil bath at 55 °C for 3 hrs, then cooled to room temperature. A 0.4 mL of each reaction mixture was extracted with 1 mL butyl acetate and the extracts were analyzed by GC. For an external standard a duplicate of the pH 7.0 mixture was freshly prepared and immediately extracted. The analyzed amounts of ethyl 4-cyano-3-hydroxybutyrate in each vial are given in Table II. No product of its hydrolysis was detected in the reaction sample extracts. It was separately established that the carboxylic acid product

of hydrolysis of this ester is not extracted into the extracts of the reaction samples that are analyzed by GC.

Table II: Millimoles chlorohydrin and cyanohydrin analyzed in test hydrolysis reactions. See Example 22

pH	mmol cyanohydrin
7.0	0.29
7.5	0.28
8.0	0.27
8.5	0.26
9.0	0.24

The pHs of the final test mixtures were remeasured. The mixtures with initial pHs of 8.0, 8.5, and 9.0 each had a final pH of 7.4. The mixture with an initial pH of 7.5 had a final pH of 7.3, and the mixture with an initial pH of 7 was unchanged. This evidences the production of carboxylic acid in the higher pH samples causing neutralization of the solutions into the phosphate buffering range.

This example in combination with Example 21 shows that ethyl 4-cyano-3-hydroxybutyrate is increasingly hydrolyzed with increasing pH at the pHs greater than 8 where it can be produced by nonenzymatic reaction of ethyl 4-chloro-3-hydroxybutyrate with cyanide.

Example 23: Preparation of ethyl (R)-4-cyano-3-hydroxybutyrate from ethyl 4-chloroacetoacetate (via ethyl (S)-4-chloro-3-hydroxybutyrate).

To a 100 mL vessel connected to an automatic titrator by a pH electrode and a feeding tube for addition of base (4M NaOH) was charged a solution (25 mL) of glucose (7.5 g) in 100 mM triethanolamine buffer, pH 7. To this solution was charged ketoreductase SEQ ID NO: 50 (50 mg), glucose dehydrogenase SEQ ID NO: 62 (20 mg) and NADP (1.5 mg). Butyl acetate (10 ml) and ethyl 4-chloroacetoacetate (6 g) in additional butyl acetate (10 mL) were then charged. The pH was maintained at 7 by the automatic titrator by the addition of 4M NaOH to the stirring mixture over 13 hrs. The phases were then allowed to separate for 30

minutes and the organic layer (25 mL), containing the ethyl (S)-4-chloro-3-hydroxybutyrate intermediate, was removed.

To a 170 mL vessel connected to an automatic titrator by a pH electrode and a feeding tube for addition of base (2M NaOH) was charged sodium cyanide (1.5 g) followed by water (50 mL). The vessel was sealed and the headspace was deaerated with nitrogen. The pH was adjusted to 7 using concentrated sulfuric acid (0.9 mL). The mixture was heated to 40 °C and treated with a solution of halohydrin dehalogenase SEQ ID NO: 32 (1.2 g) in 10 mL water containing 42 uL of 14M β -mercaptoethanol). Then, the organic layer (25 mL) containing ethyl (S)-4-chloro-3-hydroxybutyrate from the first step was added via syringe. The pH was maintained at 7 by the automatic titrator by the addition of 2M NaOH to the stirring mixture. After 15 hr, the conversion of ethyl (S)-4-chloro-3-hydroxybutyrate to ethyl (R)-4-cyano-3-hydroxybutyrate was 33% as indicated by the cumulative addition of 5 mL of the base (15 mL expected for complete conversion).

Example 24: Preparation of ethyl (R)-4-cyano-3-hydroxybutyrate from ethyl 4-chloroacetoacetate (via ethyl (S)-4-chloro-3-hydroxybutyrate).

To a 20 mL screw cap vial was added NaCN (125 mg, 2.55 mmol), NaH_2PO_4 (415 mg, 3.46 mmol) and glucose (750 mg, 3.8 mmol). Water (5 mL) was added followed by NADP (2 mg), ketoreductase SEQ ID NO: 56 (50 mg), glucose dehydrogenase SEQ ID NO: 62 (50 mg), and halohydrin dehalogenase SEQ ID NO: 32 (100 mg). Then ethyl 4-chloro-acetoacetate (24 mg, 0.15 mmol) in 0.5 mL butyl acetate was added. The vial was capped and heated in an oil bath at 30 °C. After 1 hr, GC analysis of a butyl acetate extract of a reaction sample showed 100% conversion of the ethyl 4-chloro-acetoacetate to ethyl (S)-4-chloro-3-hydroxybutyrate, at 96% selectivity, and ethyl (R)-4-cyano-3-hydroxybutyrate at 4% selectivity. Then, the reaction vial was heated to 40 °C for 15 hrs. GC analysis of a butyl acetate extract then showed 2% of the ethyl (S)-4-chloro-3-hydroxy-butyrate remaining, with overall 98% yield of ethyl (R)-4-cyano-3-hydroxybutyrate based on the starting ethyl 4-chloroacetate.

This example shows the process of the invention wherein a 4-cyano-3-hydroxybutyric acid ester (ethyl 4-cyano-3-(R)-hydroxybutyrate) is produced, via an intermediate 4-halo-3-hydroxybutyric acid ester (ethyl 4-chloro-3-(S)-hydroxybutyrate), by contacting a 4-halo-3-ketobutyric acid ester (ethyl 4-chloroacetoacetate) with a ketoreductase, a cofactor (NADPH,

provided as NADP) a cofactor regeneration system (glucose and glucose dehydrogenase), a halohydrin dehalogenase, and cyanide (provided by a cyanide salt, NaCN) with all the reactants simultaneously present in the reaction mixture.

5 Examples 25-29: Preparations of Ethyl (R)-4-cyano-3-hydroxybutyrate from Ethyl (S)-4-chloro-3-hydroxybutyrate

For each of Examples 25-29, to a 170mL vessel connected to an automatic titrator by a pH electrode and a feeding tube for addition of base was charged NaCN (1.5 g, 31 mmol) and water (50 mL). The vessel was sealed and the pH was adjusted to 7 by the addition of
10 conc. H₂SO₄ (0.9 mL). The reaction mixture was heated to 40 °C and treated with a solution of halohydrin dehalogenase (0.4 g in 10 mL water). The halohydrin dehalogenases used for these Examples had the polypeptide sequences given for the following SEQ ID NOs.:

Example 25 SEQ ID No. 32

Example 26 SEQ ID No. 94

15 Example 27 SEQ ID No. 96

Example 28 SEQ ID No. 98

Example 29 SEQ ID No. 100

Then, ethyl (S)-4-chloro-3-hydroxybutyrate (5.00 g, 30.1 mmol) was added via syringe. The automatic titrator maintained the pH at 7 by the addition of 4M NaCN. The progress of the
20 reactions were monitored by recording the cumulative volume of the NaCN solution added vs. time.

Figure 4 shows the percent conversion of ethyl (S)-4-chloro-3-hydroxybutyrate (calculated from the cumulative equivalents of NaCN added) vs. time for each of these Examples. Example 25 used a halohydrin dehalogenase having the amino acid sequence
25 SEQ ID NO. 32, which is the amino acid sequence of the native halohydrin dehalogenase from *Agrobacterium radiobacter* AD1 (*hheC*), expressed from novel nucleic acid corresponding to SEQ ID NO: 31. Comparison of the percent conversion vs. time for Examples 26 through 29 to that of Example 25 shows that novel halohydrin dehalogenases of the present invention have greater activity than the native halohydrin dehalogenase from
30 *Agrobacterium radiobacter* AD1 (*hheC*).

Example 30: Preparation of Ethyl (R)-4-cyano-3-hydroxybutyrate from Ethyl (S)-4-chloro-3-hydroxybutyrate

The procedure was identical to that of Examples 25-29 with the exception that halohydrin dehalogenase SEQ ID NO. 104 was used. After 12 hours, the reaction was complete based the addition of the NaCN solution, and GC analysis showed that conversion of the ethyl (S)-4-chloro-3-hydroxybutyrate to ethyl (R)-4-cyano-3-hydroxybutyrate was >99%. The reaction mixture was cooled and combined with five other similarly produced final reaction solutions in a 500 mL three-neck flask. The flask was equipped with a condenser and nitrogen dip tube extending into the liquid, and was connected to a diaphragm pump to apply vacuum (500 mmHg). A caustic trap was used to trap the HCN in the off gas. The reaction mixture was heated to 50 °C and a nitrogen bleed was used to facilitate the removal of HCN. After three hours, the HCN removal was complete. The mixture was cooled and partitioned into centrifuge bottles. 300 mL of butyl acetate was partitioned among the bottles, which were capped and shaken for extraction. The mixtures were centrifuged at 8000 rpm for 30 minutes. The layers were separated and the aqueous phase was likewise extracted two more times with 300 mL of butyl acetate. The combined butyl acetate extracts were evaporated under vacuum to give 19.6 g of ethyl R-4-cyano-3-hydroxybutyrate (83% yield) as a pale yellow liquid.

Example 31: Preparation of Ethyl (R)-4-cyano-3-hydroxybutyrate from Ethyl (S)-4-chloro-3-hydroxybutyrate.

To a 170mL vessel connected to an automatic titrator by a pH electrode and a feeding tube for addition of base was charged NaCN (1.5 g, 31 mmol) and water (50 mL). The vessel was sealed and the pH was adjusted to 7 by the addition of conc. H₂SO₄ (0.9 mL). The reaction mixture was heated to 40 °C and treated with a solution of halohydrin dehalogenase SEQ ID NO. 100 (0.4 g in 10 mL water). Then, ethyl (S)-4-chloro-3-hydroxybutyrate (10.0 g, 60.2 mmol) was added via syringe. The automatic titrator maintained the pH at 7 by the addition of 4M NaCN. After 18 hours, the reaction was complete based the addition of the NaCN solution (no more based being added, 14.6 mL cumulatively added) and GC analysis showed that conversion of the ethyl (S)-4-chloro-3-hydroxybutyrate to ethyl (R)-4-cyano-3-hydroxybutyrate was >99%. The reaction mixture was cooled and transferred to a 250 mL three-neck flask. The flask was equipped with a condenser and nitrogen dip tube extending

into the liquid, and was connected to a diaphragm pump to apply vacuum (500 mmHg). A caustic trap was used to trap the HCN in the off gas. The reaction mixture was heated to 50 °C and a nitrogen bleed was used to facilitate the removal of HCN. After three hours, the HCN removal was complete. The mixture was cooled and transferred to a centrifuge bottle. 60 mL of butyl acetate was added to the bottle, which was capped and shaken for extraction. The mixture was centrifuged at 10,000 rpm for 30 minutes. The layers were separated and the aqueous phase was likewise extracted two more times with 60 mL of butyl acetate. The combined butyl acetate extracts were evaporated under vacuum to give 7.7 g of ethyl R-4-cyano-3-hydroxybutrate (81% yield).

Examples 32-36: Preparations of t-Butyl (R)-6-cyano-5-hydroxy-3-oxohexanoate from t-Butyl (R)-6-chloro-5-hydroxy-3-oxohexanoate.

An aqueous solution containing 25 mg/mL sodium cyanide at pH 7.2 was prepared at by dissolving 1.25 g NaCN and 4.2 g NaH₂PO₄ in 50 mL of water. For each of Examples 32-36, 1 mL of the solution was charged to a 5 mL screw cap vial. Halohydrin dehalogenase powder (20 mg) was added to the vial, followed by 10 mg *tert*-butyl-(*S*)-6-chloro-5-hydroxy-3-oxo-hexanoate (Julich Fine Chemicals). The vial was capped and the reaction was stirred at room temperature for 12 hours. The reaction mixture was then extracted with 1 mL MTBE and the organic layer was analyzed by HPLC. In each Example, the *tert*-butyl (R)-6-chloro-5-hydroxy-3-oxohexanoate was completely reacted. The polypeptide sequence of the halohydrin dehalogenase used for each Examples and the analyzed reaction yield of *tert*-butyl (R)-6-cyano-5-hydroxy-3-oxohexanoate were as follows:

Example 32	SEQ ID No.106	25%
Example 33	SEQ ID No. 108	15%
Example 34	SEQ ID No. 32	15%
Example 35	SEQ ID No. 74	10%
Example 36	SEQ ID No. 110	10%

Examples 37-41: Preparations of t-Butyl (3R,5R)-6-cyano-3,5-dihydroxyhexanoate from t-Butyl (3R,5S)-6-chloro-3,5-dihydroxy-3-hexanoate.

An aqueous solution containing 28 mg/mL sodium cyanide at pH 6.7 was prepared at by dissolving 1.4 g NaCN and 6 g NaH₂PO₄ in 50 mL of water. For each of Examples 37-41, 1 mL of the solution was charged to a 5 mL screw cap vial. Halohydrin dehalogenase powder (20 mg) was added to the vial, followed by 20 mg *tert*-butyl (3R,5S)-6-chloro-3,5-dihydroxyhexanoate (Chemistry--A European Journal (2001), 7(21), 4562-4571). The vial was capped and the reaction was stirred at room temperature for 17 hours. The reaction mixture was then extracted with 1 mL ethyl acetate and the organic layer was analyzed by HPLC. In each Example, only t-butyl (3R,5R)-6-cyano-3,5-dihydroxyhexanoate and unreacted t-butyl (3R,5S)-6-chloro-3,5-dihydroxy-3-hexanoate were detected. The polypeptide sequence of the halohydrin dehalogenase used for each Examples and the reaction yield of t-butyl (3R,5R)-6-cyano-3,5-dihydroxyhexanoate were as follows:

Example 37	SEQ ID No. 100	83%
Example 38	SEQ ID No. 108	65%
Example 39	SEQ ID No. 32	64%
Example 40	SEQ ID No. 74	63%
Example 41	SEQ ID No. 102	81%

In a control reaction, omitting halohydrin dehalogenase, the conversion was 4%.

All publications, patents, patent applications, and other documents cited in this application are hereby incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application, or other document were individually indicated to be incorporated by reference for all purposes.

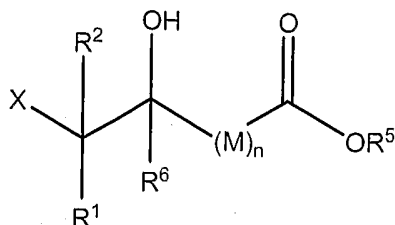
While preferred embodiments of the invention have been illustrated and described, it will be appreciated that various changes can be made therein without departing from the spirit and scope of the invention.

We claim:

1. A method for producing a vicinal cyano, hydroxy substituted carboxylic acid ester from a vicinal halo, hydroxy substituted carboxylic acid ester, the method comprising:
 - (a) providing a vicinal halo, hydroxy substituted carboxylic acid ester,
5 wherein the halo substituent is selected from the group consisting of chlorine, bromine, and iodine,
and wherein the vicinal halo, hydroxy substituted carboxylic acid ester is not a 4-halo-3-hydroxybutyric acid ester; and
 - (b) contacting the vicinal halo, hydroxy substituted carboxylic acid ester with a
10 halohydrin dehalogenase and cyanide under conditions suitable to form a reaction mixture for converting the vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted carboxylic acid ester.
2. The method of claim 1, wherein the vicinal cyano, hydroxy substituted
15 carboxylic acid ester is a non-racemic chiral vicinal cyano, hydroxy substituted carboxylic acid ester.
3. The method of claim 1, wherein the cyanide is provided by hydrocyanic acid.
- 20 4. The method of claim 1, wherein the cyanide is provided by a cyanide salt.
5. The method of claim 1, wherein the halo substituent of the vicinal halo, hydroxy substituted carboxylic acid ester is selected from chlorine and bromine.
- 25 6. The method of claim 1, wherein the vicinal halo, hydroxy substituted carboxylic acid ester is a vicinal chloro, hydroxy substituted carboxylic acid ester.
7. The method of claim 1, wherein the vicinal halo, hydroxy substituted carboxylic acid ester is a lower alkyl ester.

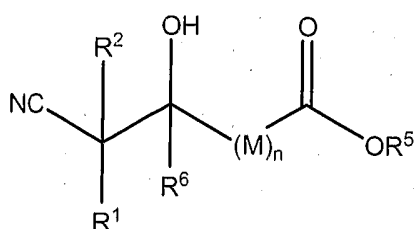
8. The method of claim 1, wherein

(1) the vicinal halo, hydroxy substituted carboxylic acid ester has the structure:



and

5 (2) the vicinal cyano, hydroxy substituted carboxylic acid ester has the structure:



wherein:

X is a halogen selected from the group consisting of chlorine, bromine, and iodine;

10 R^1 , R^2 , and R^6 are each independently selected from the group consisting of hydrogen, fluorine, an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted lower alkenyl, an optionally substituted aryl, an optionally substituted arylalkyl, amino, an optionally substituted lower alkylamino, an optionally substituted cycloalkylamino, an optionally substituted lower alkoxy, an optionally substituted cycloalkoxy, an optionally substituted aryloxy, and an optionally substituted arylalkoxy; and

15 R^5 is selected from the group consisting of an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted aryl, and an optionally substituted arylalkyl; and.

each M_n is independently selected from $-\text{C}(=\text{O})-$ (i.e., carbonyl) or $-\text{CR}^m\text{R}^n-$, wherein R^m and R^n are each independently selected from the group consisting of hydrogen, fluorine,

20 an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted lower alkenyl, an optionally substituted aryl, an optionally substituted arylalkyl, amino, an optionally substituted lower alkylamino, an optionally substituted cycloalkylamino, an optionally substituted lower alkoxy, an optionally substituted cycloalkoxy, an optionally substituted aryloxy, an optionally substituted aryl, hydroxyl, nitro, amino, cyano, carboxy

(i.e. a carboxylate or carboxylic acid group), carboalkoxy (i.e. an ester group), carbamide (i.e. an amide group), and acyl (i.e. forming a ketone); and

n is zero or an integer from 2 to 9, inclusive.

5

9. The method of claim 8, wherein n is an integer from 2 to 8, inclusive.

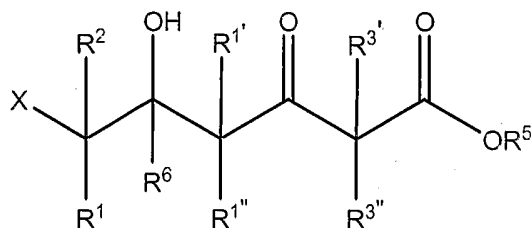
10. The method of claim 8, wherein n is 3.

10

11. The method of claim 1, wherein the vicinal cyano, hydroxy substituted carboxylic acid ester is a 6-halo-5-hydroxyhexanoic acid ester.

12. The method of claim 1, wherein

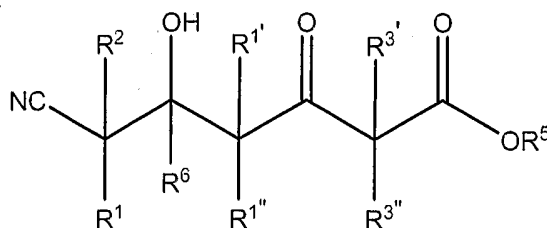
(1) the vicinal halo, hydroxy substituted carboxylic acid ester has the structure:



15

and

(2) the vicinal cyano, hydroxy substituted carboxylic acid ester has the structure:



wherein:

20

X is a halogen selected from the group consisting of chlorine, bromine, and iodine;

R^1 , R^2 , R^3 , R^4 , R^6 , $R^{1'}$, $R^{1''}$, $R^{3'}$, and $R^{3''}$ are each independently selected from the group consisting of hydrogen, fluorine, an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted lower alkenyl, an optionally substituted aryl, an optionally substituted arylalkyl, amino, an optionally substituted lower alkylamino, an optionally substituted cycloalkylamino, an optionally substituted lower alkoxy, an optionally

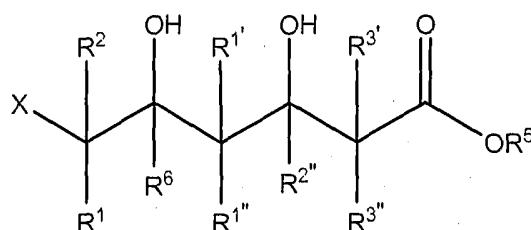
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substituted cycloalkoxy, an optionally substituted aryloxy, and an optionally substituted arylalkoxy; and

R^5 is selected from the group consisting of an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted aryl, and an optionally substituted arylalkyl.

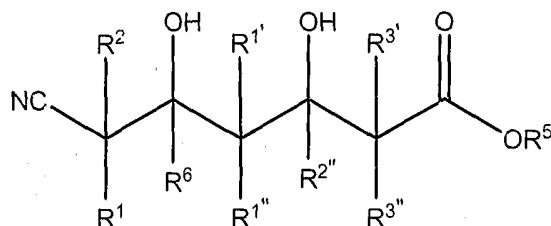
13. The method of claim 1, wherein

(1) the vicinal halo, hydroxy substituted carboxylic acid ester has the structure:



10 and

(2) the vicinal cyano, hydroxy substituted carboxylic acid ester has the structure:



wherein:

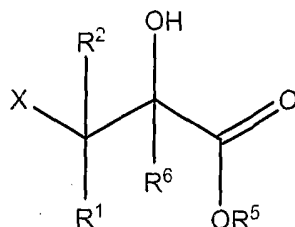
X is a halogen selected from the group consisting of chlorine, bromine, and iodine;

R^1 , R^2 , R^3 , R^4 , R^6 , $R^{1'}$, $R^{1''}$, $R^{2''}$, $R^{3'}$, and $R^{3''}$ are each independently selected from the group consisting of hydrogen, fluorine, an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted lower alkenyl, an optionally substituted aryl, an optionally substituted arylalkyl, amino, an optionally substituted lower alkylamino, an optionally substituted cycloalkylamino, an optionally substituted lower alkoxy, an optionally substituted cycloalkoxy, an optionally substituted aryloxy, and an optionally substituted arylalkoxy; and

R^5 is selected from the group consisting of an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted aryl, and an optionally substituted arylalkyl.

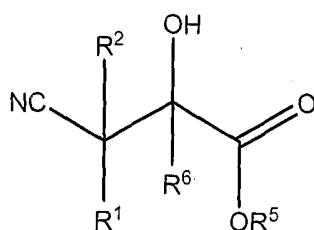
14. The method of claim 1, wherein

(1) the vicinal halo, hydroxy substituted carboxylic acid ester has the structure:



and

5 (2) the vicinal cyano, hydroxy substituted carboxylic acid ester has the structure:



wherein:

X is a halogen selected from the group consisting of chlorine, bromine, and iodine;

10 R^1 , R^2 , and R^6 are each independently selected from the group consisting of hydrogen, fluorine, an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted lower alkenyl, an optionally substituted aryl, an optionally substituted arylalkyl, amino, an optionally substituted lower alkylamino, an optionally substituted cycloalkylamino, an optionally substituted lower alkoxy, an optionally substituted cycloalkoxy, an optionally substituted aryloxy, and an optionally substituted arylalkoxy; and

15 R^5 is selected from the group consisting of an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted aryl, and an optionally substituted arylalkyl.

0 15. The method of claim 1, wherein the halohydrin dehalogenase is a naturally occurring halohydrin dehalogenase.

16. The method of claim 1, wherein the halohydrin dehalogenase is a non-naturally occurring halohydrin dehalogenase.

17. The method of claim 1, wherein the reaction mixture for converting the vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted carboxylic acid ester is maintained at a pH in the range of from about 5 to about 9.

5 18. The method of claim 17, wherein the reaction mixture for converting the vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted carboxylic acid ester is maintained at a pH in the range of from about 5 to about 8.

10 19. The method of claim 1, wherein the reaction mixture for converting the vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted carboxylic acid ester is maintained at a pH of about 8 or below.

15 20. The method of claim 1, wherein the reaction mixture for converting the vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted carboxylic acid ester further comprises a pH buffer.

21. The method of claim 1, further comprising:
(c) adding a base sufficient to maintain the reaction mixture for converting the vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted
20 carboxylic acid ester at a pH of about 5 or above.

22. The method of claim 21 wherein the base is selected from hydroxide salts, carbonate salts, and bicarbonate salts.

25 23. The method of claim 21 wherein the base is selected from a cyanide salt.

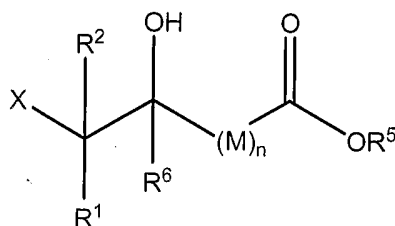
24. The method of claim 1, further comprising recovering the vicinal cyano, hydroxy substituted carboxylic acid ester from the reaction mixture for converting the vicinal halo, hydroxy substituted carboxylic acid ester to a vicinal cyano, hydroxy substituted
30 carboxylic acid ester.

25. The method of claim 22, further comprising purifying the vicinal cyano, hydroxy substituted carboxylic acid ester.

26. A composition comprising:

- 5 (a) a halohydrin dehalogenase;
 (b) cyanide; and
 (c) a vicinal halo, hydroxy substituted carboxylic acid ester,
 wherein the vicinal halo, hydroxy substituted carboxylic acid ester is not a 4-halo-3-hydroxybutyric acid ester.

10 27. The composition of claim 26, wherein the vicinal halo, hydroxy substituted carboxylic acid ester has the structure:



15 wherein:

X is a halogen selected from the group consisting of chlorine, bromine, and iodine;

20 R^1 , R^2 , and R^6 are each independently selected from the group consisting of hydrogen, fluorine, an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted lower alkenyl, an optionally substituted aryl, an optionally substituted arylalkyl, amino, an optionally substituted lower alkylamino, an optionally substituted cycloalkylamino, an optionally substituted lower alkoxy, an optionally substituted cycloalkoxy, an optionally substituted aryloxy, and an optionally substituted arylalkoxy; and

25 R^5 is selected from the group consisting of an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally substituted aryl, and an optionally substituted arylalkyl; and.

each M_n is independently selected from $-\text{C}(=\text{O})-$ (i.e., carbonyl) or $-\text{CR}^n\text{R}^m-$, wherein R^n and R^m are each independently selected from the group consisting of hydrogen, fluorine, an optionally substituted lower alkyl, an optionally substituted cycloalkyl, an optionally

substituted lower alkenyl, an optionally substituted aryl, an optionally substituted arylalkyl, amino, an optionally substituted lower alkylamino, an optionally substituted cycloalkylamino, an optionally substituted lower alkoxy, an optionally substituted cycloalkoxy, an optionally substituted aryloxy, an optionally substituted aryl, hydroxyl, nitro, amino, cyano, carboxy (i.e. a carboxylate or carboxylic acid group), carboalkoxy (i.e. an ester group), carbamide (i.e. an amide group), and acyl (i.e. forming a ketone); and

n is zero or an integer from 2 to 9, inclusive.

10

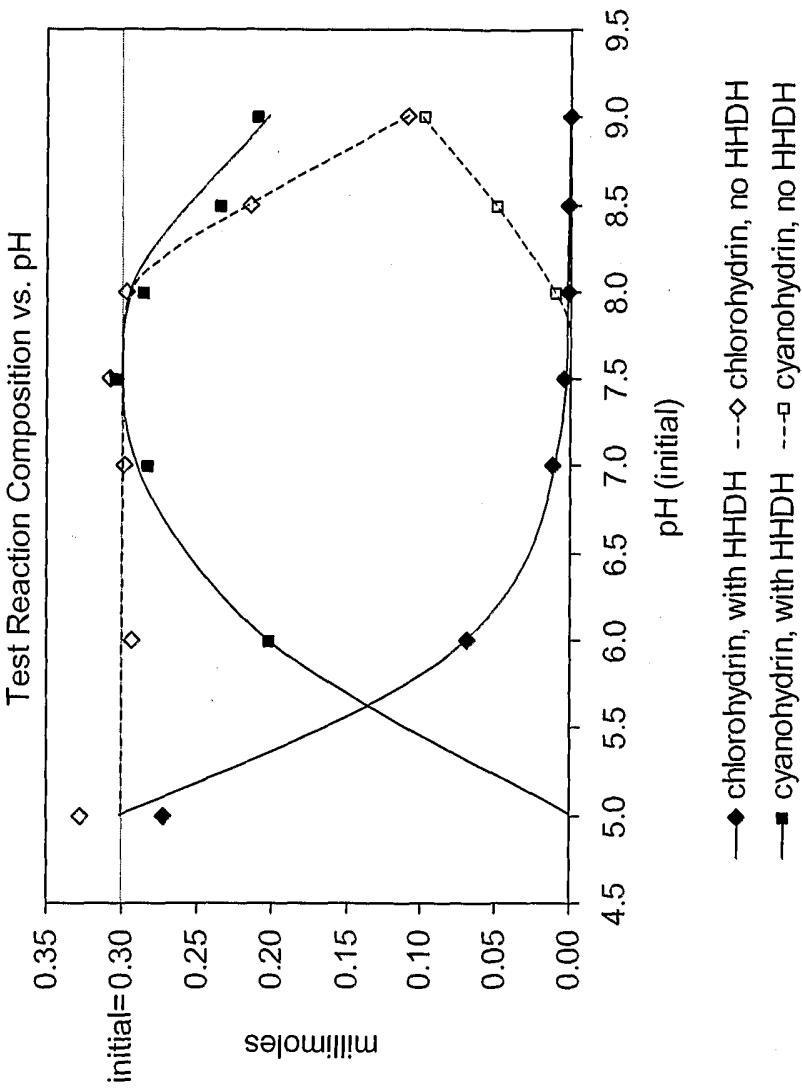


FIGURE 1

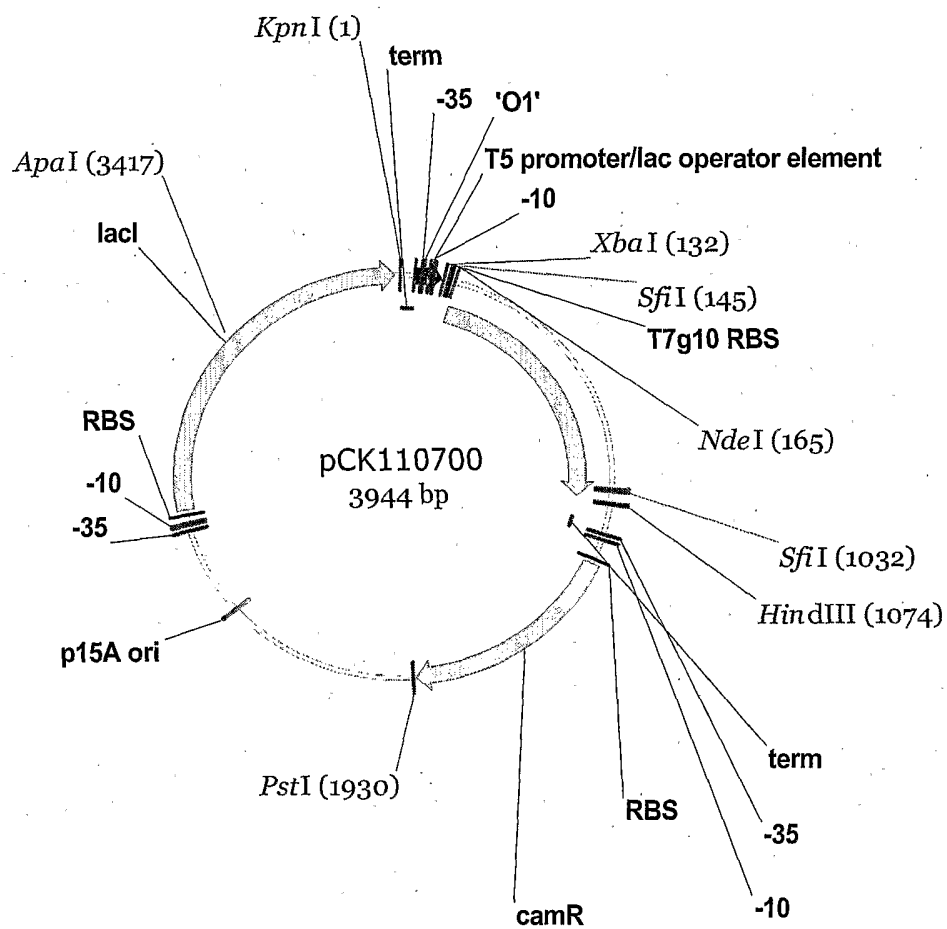


FIGURE 2

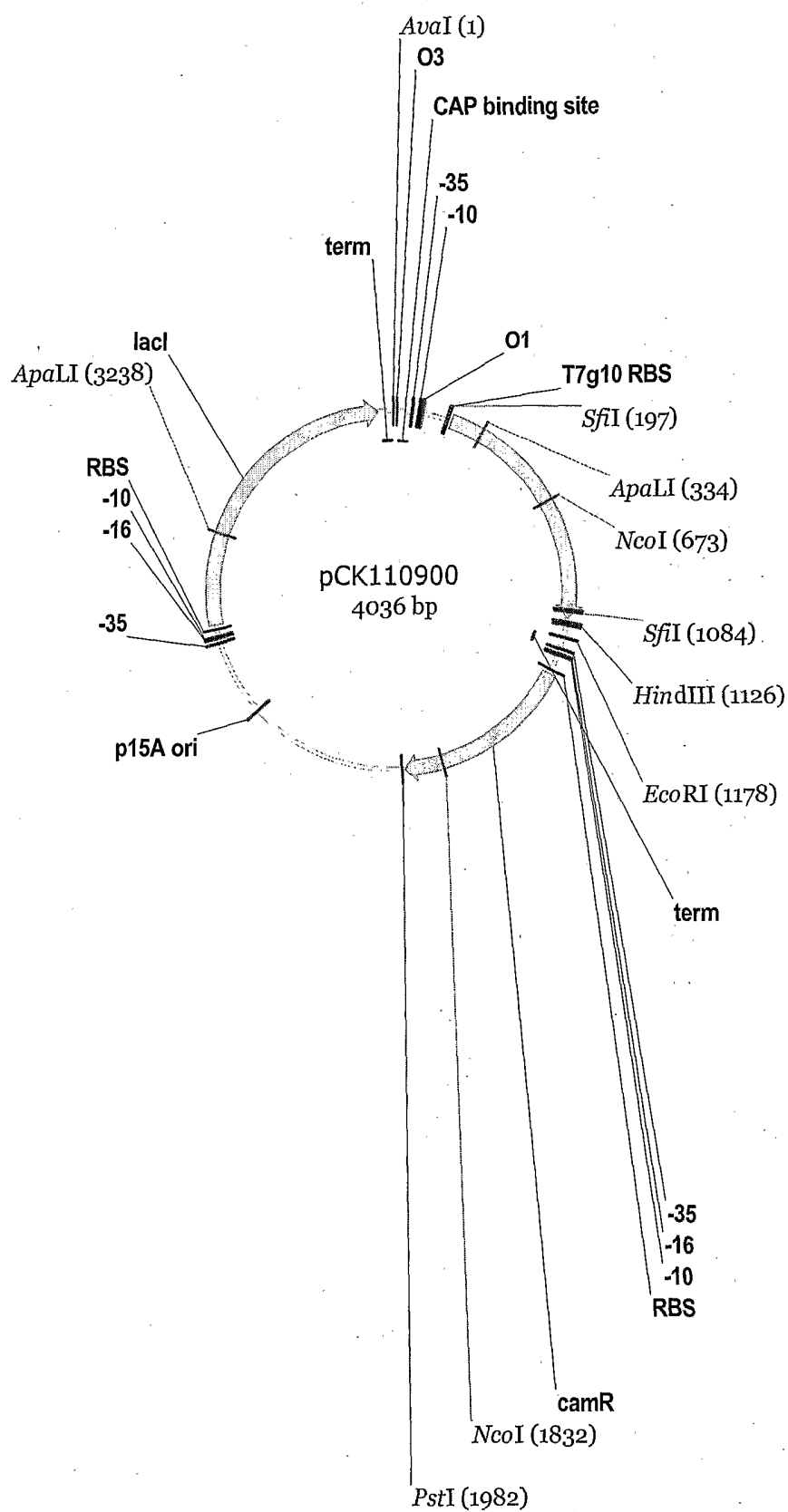


FIGURE 3

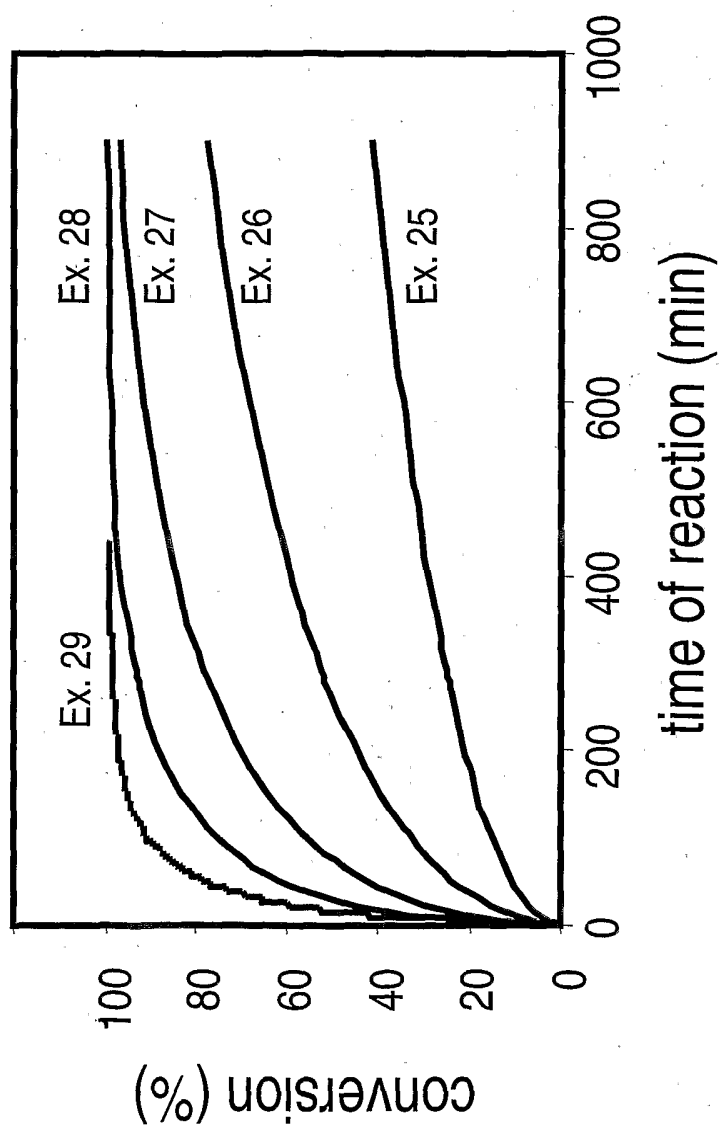


Figure 4

SEQUENCE LISTING

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 Gray, David R.
 Gruber, John M.
 Huisman, Gjalt W.
 Ma, Steven K.
 Newman, Lisa M. Sheldon, Roger
 Wang, Li A.

<120> Enzymatic Processes for the Production
 of 4-Substituted 3-Hydroxybutyric Acid Derivatives and
 Vicinal Cyano, Hydroxy-substituted Carboxylic Acid Esters

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<150> US Not yet assigned

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His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	

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Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
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Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
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Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
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Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
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Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
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Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	
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Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu	
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Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn	
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Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp	
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852

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

<210> 3
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 <212> DNA
 <213> Artificial Sequence

<220>
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 KRED CR1-2

<221> CDS

<222> (1)...(852)

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cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat      96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
          20          25          30

gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
          35          40          45

tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
          50          55          60

aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
          65          70          75          80

gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
          85          90          95

gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
          100          105          110

ata gta gca gca aat gca gga ata ccc tgg aca aag gga gca tat ata      384
Ile Val Ala Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
          115          120          125

gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
          130          135          140

aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
          145          150          155          160

agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
          165          170          175

atg agc gga cat ata gta aat gtc ccc caa ttc caa gca aca tat aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
          180          185          190

gca gca aag gca gga gta agg cat ttt gca aag agc tta gca gtc gag      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
          195          200          205

ttt gca ccc ttt gca agg gta aat agc gta agc ccc gga tat ata aat      672

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Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220
 aca gag ata agc gat ttc gtc ccc caa gag aca caa aat aag tgg tgg 720
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240
 agc tta gtc ccc tta gga agg gga gga gag aca gca gag tta gta gga 768
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255
 gca tat tta ttc tta gca agc gat gca gga agc tat gca aca gga aca 816
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270
 gat ata ata gta gat gga gga tat aca tta ccc taa 852
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *
 275 280

<210> 4
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 <213> Candida magnoliae

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

245 250 255
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 260 265 270
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
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<210> 5

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<212> DNA

<213> Artificial Sequence

<220>

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KRED CR1-3

<221> CDS

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cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala	
35 40 45	
tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	
ata gta gta gca aat gca gga ata ccc tgg aca aag gga gca tat ata	384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	
gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta	432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	
130 135 140	
aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa	480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	

145 150 155 160
 agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc 528
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
 165 170 175
 atg agc gga cat ata gta aat gtc ccc caa ttc caa gca aca tat aat 576
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
 180 185 190
 gca gca aag gca gga gta agg cat ttt gca aag agc tta gca gtc gag 624
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195 200 205
 ttt gca ccc ttt gca agg gta aat agc gta agc ccc gga tat ata aat 672
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220
 aca gag ata agc gat ttc gtc ccc caa gag aca caa aat aag tgg tgg 720
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240
 agc tta gtc ccc tta gga agg gga gga gag aca gca gag tta gta gga 768
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255
 gca tat tta ttc tta gca agc gat gca gga agc tat gca aca gga aca 816
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
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 gat ata ata gta gat gga gga tat aca tta ccc taa 852
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *
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<210> 6

<211> 283

<212> PRT

<213> Candida magnoliae

<400> 6

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 35 40 45
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125

Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
 130 135 140
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
 145 150 155 160
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
 165 170 175
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
 180 185 190
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195 200 205
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
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 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
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<210> 7

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<213> Artificial Sequence

<220>

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<221> CDS

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cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala	
35 40 45	
tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	

gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat 336
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110

ata gta gta gca aat gca gga ata ccc tgg aca aag gga gca tat ata 384
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125

gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta 432
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
 130 135 140

aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa 480
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
 145 150 155 160

agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc 528
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
 165 170 175

atg agc gga cat ata gta aat gtc ccc caa ttc caa gca aca tat aat 576
 Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
 180 185 190

gca gca aag gca gga gta agg cat ttt gca aag agc tta gca gtc gag 624
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195 200 205

ttt gca ccc ttt gca agg gta aat agc gta agc ccc gga tat ata aat 672
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220

aca gag ata agc gat ttc gtc ccc caa gag aca caa aat aag tgg tgg 720
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240

agc tta gtc ccc tta gga agg gga gga gag aca gca gag tta gta gga 768
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255

gca tat tta ttc tta gca agc gat gca gga agc tat gca aca gga aca 816
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270

gat ata ata gta gat gga gga tat act tta ccc taa 852
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *
 275 280

<210> 8

<211> 283

<212> PRT

<213> Candida magnoliae

<400> 8

Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala

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Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
35           40           45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
50           55           60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65           70           75           80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
85           90           95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
100          105          110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
115          120          125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
130          135          140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145          150          155          160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
165          170          175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
180          185          190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
195          200          205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
210          215          220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225          230          235          240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
245          250          255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
260          265          270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
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<210> 9

<211> 786

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1)...(786)

<223> Glucose dehydrogenase S06-3

<400> 9

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1           5           10           15

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48

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tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
20           25           30

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96

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aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val

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144

35	40	45	
aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Gln Gly 50 55 60			192
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile 65 70 75 80			240
aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu 85 90 95			288
aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val 100 105 110			336
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile 115 120 125			384
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser 130 135 140			432
agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala 145 150 155 160			480
agt aaa ggc ggg ata aag ctg atg aca gaa aca tta gcg ttg gaa tac Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr 165 170 175			528
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn 180 185 190			576
acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp 195 200 205			624
gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile 210 215 220			672
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr 225 230 235 240			720
ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe 245 250 255			768
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260			

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 <213> Bacillus sp.

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

<210> 11
 <211> 786
 <212> DNA
 <213> Bacillus sp.

<220>
 <221> CDS
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 Met Tyr Lys Asp Leu Glu Gly Lys Val Val Ile Thr Gly Ser Ser
 1 5 10 15

48

acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala 20 25 30	96
aaa gta gtt gtg aat tat cgt tgc aaa gaa gaa gaa gct aac agc gtt Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val 35 40 45	144
tta gaa gaa att aaa aaa gtc ggc gga gag gca att gcg gtt aaa ggt Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly 50 55 60	192
gac gta aca gtt gag tct gac gtg atc aat tta gtt caa tct gct att Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile 65 70 75 80	240
aaa gaa ttt gga aag tta gat gtt atg att aat aac gca gga atg gaa Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu 85 90 95	288
aat ccg gtt tca tct cat gaa atg tct tta agc gat tgg aat aaa gta Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val 100 105 110	336
att gat acg aac tta acg gga gca ttt tta gga agc cgt gaa gcg att Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile 115 120 125	384
aaa tat ttc gtg gaa aat gat att aag gga aca gtt att aat atg tgc Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser 130 135 140	432
agt gtt cat gag aaa att cct tgg cca tta ttt gtt cat tac gca gca Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala 145 150 155 160	480
agt aaa ggt ggc atg aag ctc atg act gaa aca ctt gca tta gaa tat Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr 165 170 175	528
gct cca aaa ggt att cgt gta aat aac att ggg ccg gga gcg att aat Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn 180 185 190	576
aca ccg att aac gct gag aaa ttt gct gat cct aag cag cgc gca gat Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Arg Ala Asp 195 200 205	624
gta gaa agc atg att cca atg gga tac atc gga gag ccg gaa gaa att Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile 210 215 220	672
gca gcg gtt gct gca tgg cta gct tct tca gaa gca agt tat gta aca Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr 225 230 235 240	720

ggg att acg ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc 768
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
 245 250 255

caa gca gga cgc gga taa 786
 Gln Ala Gly Arg Gly *
 260

<210> 12
 <211> 261
 <212> PRT
 <213> Bacillus sp.

<400> 12
 Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser
 1 5 10 15
 Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
 20 25 30
 Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
 35 40 45
 Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
 50 55 60
 Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
 65 70 75 80
 Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
 85 90 95
 Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
 100 105 110
 Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
 130 135 140
 Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
 145 150 155 160
 Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
 165 170 175
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
 180 185 190
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Arg Ala Asp
 195 200 205
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
 210 215 220
 Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr
 225 230 235 240
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
 245 250 255
 Gln Ala Gly Arg Gly
 260

<210> 13
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH.1

<221> CDS

<222> (1)...(765)

<400> 13

atg agc acc gct atc gtc acc aac gtc aaa cat ttt ggt ggt atg ggt	48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta ggg gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 14

<211> 254

<212> PRT

<213> Agrobacterium sp.

<400> 14

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

<210> 15

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH.2

<221> CDS

<222> (1)...(765)

<400> 15

atg	agc	acc	gct	atc	gtc	acc	aac	gtc	aaa	cat	ttt	ggt	ggt	atg	ggt	48
Met	Ser	Thr	Ala	Ile	Val	Thr	Asn	Val	Lys	His	Phe	Gly	Gly	Met	Gly	
1				5					10					15		

agc	gct	ctg	agg	ctg	agc	gaa	gct	ggt	cat	acc	gtc	gct	tgc	cat	gat	96
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp	
		20						25					30			

gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac	144
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr	
		35					40					45				

cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	atc	gaa	192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu	
		50				55					60					

gct	gtc	acc	agc	gct	tac	ggt	caa	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240
Ala	Val	Thr	Ser	Ala	Tyr	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp	
65				70					75					80		

atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat	288
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp	
			85						90					95		

tac	agg	ggt	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val	
		100						105					110			

aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile	
		115					120					125				

ttc	atc	act	tcg	gct	act	ccg	ttc	ggg	ccg	tgg	aag	gag	cta	tcg	act	432
Phe	Ile	Thr	Ser	Ala	Thr	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr	
	130					135					140					

tac	act	tcg	gct	cga	gct	ggg	gct	tgt	act	cta	gct	aat	gct	cta	tcg	480
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Thr	Leu	Ala	Asn	Ala	Leu	Ser	
145				150					155					160		

aag	gag	cta	ggg	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn	
			165						170					175		

tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg	576
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp	
		180						185					190			

aag	act	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta	624
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu	

195	200	205	
caa cga tta ggg act	caa aaa gag ttg ggg	gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr	Gln Lys Glu Leu Gly	Glu Leu Val Ala Phe Leu	
210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc	cag gtg ttt tgg ttg gca		720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly	Gln Val Phe Trp Leu Ala		
225	230	235	240
ggc ggc ttt ccc atg ata gaa cgt tgg ccc	ggc atg ccc gaa taa		765
Gly Gly Phe Pro Met Ile Glu Arg Trp	Pro Gly Met Pro Glu *		
245	250		

<210> 16
 <211> 254
 <212> PRT
 <213> Agrobacterium sp.

<400> 16
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 17
 <211> 765
 <212> DNA

<213> Artificial Sequence

<220>

<223> HHDH.16

<221> CDS

<222> (1)...(765)

<400> 17

atg agc acc gct atc gtc acc aac gtc aaa cat ttt ggt ggt atg ggt	48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta 624
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 18
 <211> 254
 <212> PRT
 <213> Agrobacterium sp.

<400> 18
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 19

<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 19
gaattcgccc atatgtatcc ggatttaaaa gg 32

<210> 20
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 20
tggccgcatc ctcattaacc gggcctgcc tggg 34

<210> 21
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 21
gaattcgccc atatgtataa agatttagaa gg 32

<210> 22
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 22
ggccgcatcc tcattatccg cgtoctgctt gga 33

<210> 23
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016013-B-03

<221> CDS
<222> (1)...(765)

<400> 23
atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt 48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly

1	5	10	15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat				96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp				
	20	25	30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac				144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr				
	35	40	45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa				192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu				
	50	55	60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat				240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp				
	65	70	75	80
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat				288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp				
	85	90	95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg				336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val				
	100	105	110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc				384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile				
	115	120	125	
ttc atc act tcg gct gct ccg ttc ggg cca tgg aaa gag cta tcg act				432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr				
	130	135	140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg				480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser				
	145	150	155	160
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat				528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn				
	165	170	175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg				576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp				
	180	185	190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta				624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu				
	195	200	205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ttg				672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu				
	210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca				720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala				
	225	230	235	240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 24
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH P016013-B-03

<400> 24
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 25
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH P016015-C-04

<221> CDS

<222> (1)...(765)

<400> 25

atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt	48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct ctg gcg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Ala	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	

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      210              215              220
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225              230              235              240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa      765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
      245              250

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<210> 26
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH P016015-C-04

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<400> 26
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
  1              5              10              15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
      20              25              30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
      35              40              45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
      50              55              60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
      65              70              75              80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
      85              90              95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Ala
      100              105              110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
      115              120              125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
      130              135              140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
      145              150              155              160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
      165              170              175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
      180              185              190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
      195              200              205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
      210              215              220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
      225              230              235              240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
      245              250

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<210> 27
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>

<223> HHDH P016014-E-01

<221> CDS

<222> (1)...(765)

<400> 27

atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt	48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gac ctg att gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gac	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aaa cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aaa gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624

Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ctg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 ggc ggc ttt ccc att ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 28
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH P016014-E-01

<400> 28
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 29
 <211> 768
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH P016014-G-08

<221> CDS
 <222> (1)...(765)

<400> 29
 atg agc acc gct att gtc acc aac gtc aaa cat ttt gga ggt atg ggt 48
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 agc gct ctg aaa ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96
 Ser Ala Leu Lys Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 ggt agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa gcc tac 144
 Gly Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Ala Tyr
 35 40 45
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg att gaa 192
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 gct gtc acc agc gct ttt ggt cat gtc gat gtc ctg gtc agc aac gat 240
 Ala Val Thr Ser Ala Phe Gly His Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat 288
 Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 aat gct gtg gct cca caa atg aag aag cga aag tcg ggg cac atc atc 384
 Asn Ala Val Ala Pro Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act 432
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg 480
 Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
 145 150 155 160
 aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat 528
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175

tac cta cac tcg gag gat tcg ccg ttc tat tac ccc act gag ccg tgg 576
 Tyr Leu His Ser Glu Asp Ser Pro Phe Tyr Tyr Pro Thr Glu Pro Trp
 180 185 190

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta 624
 Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240

ggc ggc ttt ccc gct ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Ala Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

tga 768

<210> 30
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH P016014-G-08

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

Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Ala Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 31
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH M₂1/2G5

<221> CDS
 <222> (1)...(765)

<400> 31
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 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa 192
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat 240
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat 288
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc 384
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act 432
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg 480
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser

145	150	155	160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat				528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn				
	165	170	175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg				576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp				
	180	185	190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta				624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu				
	195	200	205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg				672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu				
	210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca				720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala				
	225	230	235	240
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa				765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *				
	245	250		

<210> 32

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH Mz1/2G5

<400> 32

Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly				
1	5	10	15	
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp				
	20	25	30	
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr				
	35	40	45	
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu				
	50	55	60	
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp				
	65	70	75	80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp				
	85	90	95	
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val				
	100	105	110	
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile				
	115	120	125	
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr				
	130	135	140	
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser				
	145	150	155	160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn				

Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 165 170 175
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 33
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH Mz1.1A5

<221> CDS
 <222> (1)...(765)

<400> 33
 atg agc ccc gct atc gtc act aac gtc aaa cat ttt ggt ggt atg ggt 48
 Met Ser Pro Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 acc gct ctg agg ctg agc gaa gct ggt caa acc gtc gct tgc cat gat 96
 Thr Ala Leu Arg Leu Ser Glu Ala Gly Gln Thr Val Ala Cys His Asp
 20 25 30
 gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa 192
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat 240
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat 288
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc 384
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act 432

Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg 480
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat 528
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg 576
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta 624
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 34

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH Mz1.1A5

<400> 34

Met Ser Pro Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Thr Ala Leu Arg Leu Ser Glu Ala Gly Gln Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125

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

<210> 35
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH cys1.10

<221> CDS
 <222> (1)...(765)

<400> 35
 atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt 48
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15

 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30

 gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45

 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa 192
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60

 gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat 240
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80

 atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat 288
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95

 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc 384
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act 432
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140

tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg 480
 Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat 528
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg 576
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta 624
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 36

<211> 254

<212> PRT

<213> Artificial Sequence.

<220>

<223> HHDH cys1.10

<400> 36

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

```

      85              90              95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
      100              105              110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
      115              120              125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
      130              135              140
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145      150              155              160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
      165              170              175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
      180              185              190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
      195              200              205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
      210              215              220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225      230              235              240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
      245              250

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<210> 37
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH cys2.12

<221> CDS
 <222> (1)...(765)

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<400> 37
atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
  1              5              10              15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct gcg cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Ala His Asp
      20              25              30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
      35              40              45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
      50              55              60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
      65              70              75              80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
      85              90              95

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tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
                100                      105                      110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
                115                      120                      125

ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
                130                      135                      140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
                145                      150                      155                      160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                      170                      175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
                180                      185                      190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
                195                      200                      205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
                210                      215                      220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
                225                      230                      235                      240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa      765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
                245                      250

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<210> 38
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH cys2.12

<400> 38
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Ala His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45

```

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

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<210> 39
 <211> 855
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED krh133c

<221> CDS
 <222> (1)...(852)

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<400> 39
atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct      48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
  1          5          10          15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac      96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
      20          25          30

ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
      35          40          45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
      50          55          60

aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr

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65	70	75	80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg				288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala				
	85	90	95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac				336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp				
	100	105	110	
att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc				384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile				
	115	120	125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg				432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu				
	130	135	140	
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat tat cgt gaa				480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu				
	145	150	155	160
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc				528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser				
	165	170	175	
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat				576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn				
	180	185	190	
gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa				624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu				
	195	200	205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat				672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn				
	210	215	220	
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg				720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp				
	225	230	235	240
agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt				768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly				
	245	250	255	
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca				816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr				
	260	265	270	
gat atc att gtg gat ggc ggc tac acg ctg ccg taa tga				855
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *				
	275	280		

<210> 40

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh133c

<400> 40

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

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<210> 41

<211> 855

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED krh215

<221> CDS

<222> (1)...(855)

<400> 41

atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct

48

Met	Ala	Lys	Asn	Phe	Ser	Asn	Val	Glu	Tyr	Pro	Ala	Pro	Pro	Pro	Ala		
1				5					10						15		
cat	acc	aaa	aac	gaa	tca	ctg	cag	gta	ctg	gat	ctg	ttc	aaa	ctg	aac		96
His	Thr	Lys	Asn	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn		
			20					25					30				
ggc	aaa	gtc	gcg	tct	atc	acc	ggg	agc	agc	tca	ggc	att	ggg	tac	gcg		144
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Ser	Ser	Gly	Ile	Gly	Tyr	Ala		
		35					40					45					
ctg	gcc	gaa	gct	ttt	gcg	cag	gtt	ggc	gca	gac	gtt	gcg	atc	tgg	tat		192
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr		
	50					55					60						
aac	agc	cag	gat	gcc	acc	ggg	aaa	gca	gag	gcc	ctg	gct	aaa	aaa	tat		240
Asn	Ser	Gln	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr		
65					70				75						80		
ggc	gta	aaa	gtc	aag	gct	tat	aaa	gct	aat	gtc	agc	tcg	agt	gat	gcg		288
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala		
				85					90						95		
gtg	aaa	cag	act	att	gag	cag	cag	atc	aag	gat	ttt	ggc	cac	ctg	gac		336
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp		
			100					105					110				
att	gtt	gtg	gcg	aac	gca	ggc	atc	cca	tgg	act	aag	ggg	gca	tac	atc		384
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile		
		115					120					125					
gat	cag	gat	gac	gat	aaa	cat	ttt	gac	cag	gtg	att	gac	gtc	gac	ctg		432
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Ile	Asp	Val	Asp	Leu		
	130					135					140						
aaa	ggc	gta	ggc	tat	gta	gca	aaa	cat	gcg	ggg	cgc	cat	tat	cgt	gaa		480
Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Tyr	Arg	Glu		
145					150				155						160		
cgt	ttc	gaa	aaa	gaa	ggc	ata	aag	ggc	gcc	ttg	att	ttt	acg	gct	tcc		528
Arg	Phe	Glu	Lys	Glu	Gly	Ile	Lys	Gly	Ala	Leu	Ile	Phe	Thr	Ala	Ser		
				165				170						175			
gtg	tcg	ggg	cac	atc	gtt	aac	att	ccg	caa	ttt	cag	gcg	acc	tac	aat		576
Val	Ser	Gly	His	Ile	Val	Asn	Ile	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn		
			180					185					190				
gcg	gcc	aag	gca	ggc	gtg	cgt	cat	ttc	gca	aag	tcc	ctg	gcc	gtg	gaa		624
Ala	Ala	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu		
		195					200					205					
ttt	gct	cct	ttc	gca	cgt	gtt	aac	tct	gta	tct	cct	ggc	tat	att	aat		672
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn		
		210				215					220						
acc	gag	atc	tct	gat	ttc	gtc	ccg	caa	gaa	aca	caa	aat	aaa	tgg	tgg		720
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp		

225		230		235		240	
agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt							768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly							
		245		250		255	
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca							816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr							
		260		265		270	
gat atc att gtg gat ggc ggc tac acg ctg ccg taa tga							855
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro * *							
		275		280			

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<210> 42
<211> 283
<212> PRT
<213> Artificial Sequence
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<220>
<223> KRED krh215

<400>	42															
Met	Ala	Lys	Asn	Phe	Ser	Asn	Val	Glu	Tyr	Pro	Ala	Pro	Pro	Pro	Ala	
1				5					10					15		
His	Thr	Lys	Asn	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn	
			20					25					30			
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Ser	Ser	Gly	Ile	Gly	Tyr	Ala	
		35					40					45				
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr	
	50					55					60					
Asn	Ser	Gln	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr	
65					70						75				80	
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala	
				85					90					95		
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp	
			100					105					110			
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile	
		115				120						125				
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Ile	Asp	Val	Asp	Leu	
	130				135						140					
Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Tyr	Arg	Glu	
145					150					155					160	
Arg	Phe	Glu	Lys	Glu	Gly	Ile	Lys	Gly	Ala	Leu	Ile	Phe	Thr	Ala	Ser	
				165					170					175		
Val	Ser	Gly	His	Ile	Val	Asn	Ile	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn	
			180					185					190			
Ala	Ala	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu	
		195					200					205				
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn	
	210					215					220					
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp	
225					230					235					240	
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly	
				245					250					255		
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr	

260
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
 275 280 270

<210> 43
 <211> 855
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED krh267

<221> CDS
 <222> (1)...(855)

<400> 43
 atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct 48
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1 5 10 15
 cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30
 ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg 144
 Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
 35 40 45
 ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60
 aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240
 Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80
 ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95
 gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac 336
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110
 att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc 384
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125
 gat cag gat gac gat aag cat ttt gac cag gtg att gac gtc gac ctg 432
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu
 130 135 140
 aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ctt cgt gaa 480
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Leu Arg Glu
 145 150 155 160
 cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc 528

Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
 165 170 175

acg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat 576
 Thr Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
 180 185 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa 624
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195 200 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat 672
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg 720
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt 768
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca 816
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa tga 855
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro * *
 275 280

<210> 44

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh267

<400> 44

Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1 5 10 15

His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30

Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
 35 40 45

Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60

Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80

Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95

Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110

Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125

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

<210> 45
 <211> 855
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED krh287

<221> CDS
 <222> (1)...(855)

<400> 45
 atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct 48
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1 5 10 15
 cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30
 ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg 144
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
 35 40 45
 ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60
 aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80
 ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95

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gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
          100                      105                      110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
          115                      120                      125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
          130                      135                      140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
          145                      150                      155                      160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
          165                      170                      175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
          180                      185                      190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
          195                      200                      205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
          210                      215                      220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
          225                      230                      235                      240

agc tta gtt cca ttg ggc cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
          245                      250                      255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
          260                      265                      270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa tga      855
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro * *
          275                      280

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<210> 46

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh287

<400> 46

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

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<210> 47

<211> 855

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED krh320

<221> CDS

<222> (1)...(855)

<400> 47

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atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct      48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1          5          10          15
cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac      96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
          20          25          30

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ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala 35 40 45	144
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr 50 55 60	192
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr 65 70 75 80	240
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt tat gcg Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Tyr Ala 85 90 95	288
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp 100 105 110	336
att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile 115 120 125	384
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu 130 135 140	432
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu 145 150 155 160	480
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser 165 170 175	528
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn 180 185 190	576
gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu 195 200 205	624
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn 210 215 220	672
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp 225 230 235 240	720
agc tta gtt cca ttg ggc cgt ggt ggg gaa act gcg gaa tta gtt ggt Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly 245 250 255	768

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca 816
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa tga 855
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro * *
 275 280

<210> 48

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh320

<400> 48

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

<210> 49

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED krh326

<221> CDS

<222> (1)...(852)

<400> 49

atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct	48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala	
1 5 10 15	
cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	
att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc	384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg	432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	
130 135 140	
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa	480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	
145 150 155 160	
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc	528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	
165 170 175	
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat	576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn	
180 185 190	

gcg gtc aag gca ggc gtg cgt cac ttc gca aag tcc ctg gcc gtg gaa 624
 Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195 200 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat 672
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg 720
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt 768
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca 816
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa 852
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *
 275 280

<210> 50

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh326

<400> 50

Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1 5 10 15
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
 35 40 45
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
 130 135 140
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
 145 150 155 160
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
 165 170 175

Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
 180 185 190
 Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195 200 205
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
 275 280

<210> 51
 <211> 852
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED_krh408

<221> CDS
 <222> (1)...(852)

<400> 51
 atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct 48
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1 5 10 15

 cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30

 ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg 144
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
 35 40 45

 ctg gcc gaa gct ttt gcg cag gct ggc gca gac gtt gcg atc tgg tat 192
 Leu Ala Glu Ala Phe Ala Gln Ala Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60

 aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80

 ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95

 gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac 336
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110

 att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc 384
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile

115	120	125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg			432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu			
130	135	140	
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa			480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu			
145	150	155	160
cgt tcc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc			528
Arg Ser Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser			
165	170	175	
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aac			576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn			
180	185	190	
gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa			624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu			
195	200	205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat			672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn			
210	215	220	
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg			720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp			
225	230	235	240
agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt			768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly			
245	250	255	
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca			816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr			
260	265	270	
gat atc att gtg gac ggc ggc tac acg ctg ccg taa			852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *			
275	280		

<210> 52

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh408

<400> 52

Met	Ala	Lys	Asn	Phe	Ser	Asn	Val	Glu	Tyr	Pro	Ala	Pro	Pro	Pro	Ala
1				5				10						15	
His	Thr	Lys	Asn	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn
		20					25					30			
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Asn	Ser	Gly	Ile	Gly	Tyr	Ala

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

<210> 53

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED krh417

<221> CDS

<222> (1)...(852)

<400> 53

atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct 48
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1 5 10 15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg 144
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
 35 40 45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192

Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac 336
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc 384
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg 432
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
 130 135 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa 480
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
 145 150 155 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc 528
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
 165 170 175

atg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat 576
 Met Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
 180 185 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa 624
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195 200 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat 672
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg 720
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240

agc tta gtc cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt 768
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca 816
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa 852
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *

275

280

<210> 54
 <211> 283
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRED krh417

<400> 54
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1 5 10 15
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
 35 40 45
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
 130 135 140
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
 145 150 155 160
 Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
 165 170 175
 Met Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
 180 185 190
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195 200 205
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
 275 280

<210> 55
 <211> 852
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRED krh483

<221> CDS

<222> (1)...(852)

<400> 55

atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg ccg cca gct	48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala	
1 5 10 15	
cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac	96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	
ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc	384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg	432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	
130 135 140	
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa	480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	
145 150 155 160	
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc	528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	
165 170 175	
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat	576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn	
180 185 190	
gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa	624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu	
195 200 205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat	672

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Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
210                               215                               220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                               230                               235                               240

agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                               250                               255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
                260                               265                               270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *
                275                               280

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<210> 56

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh483

<400> 56

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

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Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
 275 280

<210> 57

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED krh476

<221> CDS

<222> (1)...(852)

<400> 57

atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg ccg cca gct 48
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1 5 10 15

cat acc aaa gac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96
 His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg 144
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
 35 40 45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac 336
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc 384
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg 432
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
 130 135 140

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aaa ggc gta ggc tat gta gcg aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                               150                               155                               160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                               165                               170                               175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
                               180                               185                               190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
                               195                               200                               205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
                               210                               215                               220

acc gag atc tct gat ttc gtc ccg caa gaa aca cag aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                               230                               235                               240

agc tta gtt cca ttg ggc cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                               245                               250                               255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
                               260                               265                               270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *
                               275                               280

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<210> 58

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh476

<400> 58

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

```

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      85              90              95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
      100              105              110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
      115              120              125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
      130              135              140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
      145              150              155              160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
      165              170              175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
      180              185              190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
      195              200              205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
      210              215              220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
      225              230              235              240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
      245              250              255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
      260              265              270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
      275              280

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<210> 59

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED:krh495

<221> CDS

<222> (1)...(852)

<400> 59

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atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg ccg cca gct      48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
  1              5              10              15

cat acc aaa gac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac      96
His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
      20              25              30

ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
      35              40              45

ctg gcc gaa gcc ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
      50              55              60

aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
      65              70              75              80

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ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac 336
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc 384
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125

gat cag gat gac gat aaa cat ttt gac cag gtg att gac gtc gac ctg 432
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu
 130 135 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat tat cgt gaa 480
 Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu
 145 150 155 160

cgt ttc gaa aaa gaa ggc ata aag ggc gcc ttg att ttt acg gct tcc 528
 Arg Phe Glu Lys Glu Gly Ile Lys Gly Ala Leu Ile Phe Thr Ala Ser
 165 170 175

gtg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat 576
 Val Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
 180 185 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa 624
 Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
 195 200 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat 672
 Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
 210 215 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg 720
 Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
 225 230 235 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt 768
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca 816
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa 852
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *
 275 280

<210> 60

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED krh495

<400> 60

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

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<210> 61

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<223> GDH 2313

<221> CDS

<222> (1)...(789)

<400> 61

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Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala

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48

1	5	10	15	
tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca				96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala	20	25	30	
aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta				144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val	35	40	45	
aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga				192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly	50	55	60	
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att				240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile	65	70	75	80
aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa				288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu	85	90	95	
aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc				336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val	100	105	110	
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att				384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	115	120	125	
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc				432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser	130	135	140	
agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca				480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	145	150	155	160
agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac				528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	165	170	175	
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac				576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	180	185	190	
acg acg atc aat gct gag aaa ttt gct gac cct aaa cag aaa gct gat				624
Thr Thr Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp	195	200	205	
gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc				672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	210	215	220	
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca				720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr	225	230	235	240

ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc 768
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
 245 250 255

cag gca ggc cgc ggt taa tga 789
 Gln Ala Gly Arg Gly * *
 260

<210> 62
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GDH 2313

<400> 62
 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1 5 10 15
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
 20 25 30
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
 35 40 45
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
 50 55 60
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65 70 75 80
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
 85 90 95
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
 100 105 110
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
 130 135 140
 Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
 145 150 155 160
 Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
 165 170 175
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
 180 185 190
 Thr Thr Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
 195 200 205
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
 210 215 220
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
 225 230 235 240
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
 245 250 255
 Gln Ala Gly Arg Gly
 260

<210> 63
 <211> 789
 <212> DNA

<213> Artificial Sequence

<220>

<223> GDH 2331

<221> CDS

<222> (1)...(789)

<400> 63

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Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala	
1 5 10 15	
tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca	96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala	
20 25 30	
aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta	144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val	
35 40 45	
aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga	192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly	
50 55 60	
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att	240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile	
65 70 75 80	
aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa	288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu	
85 90 95	
aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc	336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val	
100 105 110	
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att	384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	
115 120 125	
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc	432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser	
130 135 140	
agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca	480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac	528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	

acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat 624
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
 195 200 205

gcc gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc 672
 Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
 210 215 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca 720
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
 225 230 235 240

ggc gtc acg tta ttc gcg gac ggc ggt atg aca cta tat cct tca ttc 768
 Gly Val Thr Leu Phe Ala Asp Gly Gly Met Thr Leu Tyr Pro Ser Phe
 245 250 255

cag gca ggc cgc ggt taa tga 789
 Gln Ala Gly Arg Gly * *
 260

<210> 64
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GDH 2331

<400> 64
 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1 5 10 15
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
 20 25 30
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
 35 40 45
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
 50 55 60
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65 70 75 80
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
 85 90 95
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
 100 105 110
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
 130 135 140
 Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
 145 150 155 160
 Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
 165 170 175
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
 180 185 190
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
 195 200 205
 Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile

210 215 220
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
 225 230 235 240
 Gly Val Thr Leu Phe Ala Asp Gly Gly Met Thr Leu Tyr Pro Ser Phe
 245 250 255
 Gln Ala Gly Arg Gly
 260

<210> 65
 <211> 789
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GDH 2279

<221> CDS
 <222> (1)...(789)

<400> 65
 atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct gct 48
 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1 5 10 15
 tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca 96
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
 20 25 30
 aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta 144
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
 35 40 45
 aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga 192
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
 50 55 60
 gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att 240
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65 70 75 80
 aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa 288
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
 85 90 95
 aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc 336
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
 100 105 110
 atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att 384
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125
 aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc 432
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
 130 135 140
 agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca 480

Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
 145 150 155 160

agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac 528
 Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
 165 170 175

gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac 576
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
 180 185 190

acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat 624
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
 195 200 205

gcc gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc 672
 Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
 210 215 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca 720
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
 225 230 235 240

ggc gtc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc 768
 Gly Val Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
 245 250 255

cag gca ggc cgc ggt taa tga 789
 Gln Ala Gly Arg Gly * *
 260

<210> 66
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GDH 2279

<400> 66
 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1 5 10 15
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
 20 25 30
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
 35 40 45
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Gln Gly
 50 55 60
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65 70 75 80
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
 85 90 95
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
 100 105 110
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125

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

<210> 67

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<223> GDH 2379

<221> CDS

<222> (1)...(789)

<400> 67

atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct gct 48
 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1 5 10 15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca 96
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
 20 25 30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta 144
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
 35 40 45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga 192
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
 50 55 60

gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att 240
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65 70 75 80

aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa 288
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
 85 90 95

aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc 336
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val

100	105	110	
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att			384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile			
115	120	125	
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc			432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser			
130	135	140	
agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca			480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala			
145	150	155	160
agt aaa ggc ggg ctt aag ctg atg aca gaa aca tta gcg ttg gaa tac			528
Ser Lys Gly Gly Leu Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr			
165	170	175	
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac			576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn			
180	185	190	
acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat			624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp			
195	200	205	
gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc			672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile			
210	215	220	
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca			720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr			
225	230	235	240
ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc			768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe			
245	250	255	
cag gca ggc cgc ggt taa tga			789
Gln Ala Gly Arg Gly * *			
260			

<210> 68

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> GDH 2379

<400> 68

Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala

1 5 10 15

Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala

20 25 30

Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val

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

<210> 69
 <211> 1206
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> FDH FDHPS3
 <221> CDS
 <222> (1)...(1206)

<400> 69
 atg gca aaa gtt cta tgt gtt cta tat gat gat ccg gtt gat ggt tat 48
 Met Ala Lys Val Leu Cys Val Leu Tyr Asp Asp Pro Val Asp Gly Tyr
 1 5 10 15
 ccg aaa acc tat gca cgt gat gat cta ccg aaa att gat cat tat ccg 96
 Pro Lys Thr Tyr Ala Arg Asp Asp Leu Pro Lys Ile Asp His Tyr Pro
 20 25 30
 ggt ggt cag acc cta ccg acc ccg aaa gca att gat ttt acc ccg ggt 144
 Gly Gly Gln Thr Leu Pro Thr Pro Lys Ala Ile Asp Phe Thr Pro Gly
 35 40 45
 cag cta cta ggt agc gtt agc ggt gaa cta ggt cta cgt aaa tat cta 192
 Gln Leu Leu Gly Ser Val Ser Gly Glu Leu Gly Leu Arg Lys Tyr Leu
 50 55 60

gaa agc aac ggt cat acc cta gtt gtt acc agc gat aag gac ggc cct Glu Ser Asn Gly His Thr Leu Val Val Thr Ser Asp Lys Asp Gly Pro 65 70 75 80	240
gac agc gtg ttc gag cgc gag cta gtg gac gcc gac gtg gtg att agc Asp Ser Val Phe Glu Arg Glu Leu Val Asp Ala Asp Val Val Ile Ser 85 90 95	288
cag cct ttc tgg cct gcc tat cta acc cct gag cgc att gcc aag gcc Gln Pro Phe Trp Pro Ala Tyr Leu Thr Pro Glu Arg Ile Ala Lys Ala 100 105 110	336
aag aat cta aag cta gcc cta acc gcc ggc att ggc agc gac cat gtg Lys Asn Leu Lys Leu Ala Leu Thr Ala Gly Ile Gly Ser Asp His Val 115 120 125	384
gac cta cag agc gcc att gac cgc aat gtg acc gtg gcc gag gtg acc Asp Leu Gln Ser Ala Ile Asp Arg Asn Val Thr Val Ala Glu Val Thr 130 135 140	432
tat tgt aat agc att agc gtg gcc gag cat gtg gtg atg atg att cta Tyr Cys Asn Ser Ile Ser Val Ala Glu His Val Val Met Met Ile Leu 145 150 155 160	480
agc cta gtg cgc aat tat cta cct tcc cat gaa tgg gcg cgt aaa ggc Ser Leu Val Arg Asn Tyr Leu Pro Ser His Glu Trp Ala Arg Lys Gly 165 170 175	528
ggc tgg aac atc gcg gat tgc gtc tcc cat gcg tat gat ctg gaa gcg Gly Trp Asn Ile Ala Asp Cys Val Ser His Ala Tyr Asp Leu Glu Ala 180 185 190	576
atg cat gtc ggc acg gtc gcg gcg ggc cgt atc gcc ctg gcg gtc ctg Met His Val Gly Thr Val Ala Ala Gly Arg Ile Ala Leu Ala Val Leu 195 200 205	624
cgt cgt ctg gcg ccg ttt gat gtc cat ctg cat tat acg gat cgt cat Arg Arg Leu Ala Pro Phe Asp Val His Leu His Tyr Thr Asp Arg His 210 215 220	672
cgt ctg ccg gaa tcg gta gaa aaa gaa tta aac tta acg tgg cat gcg Arg Leu Pro Glu Ser Val Glu Lys Glu Leu Asn Leu Thr Trp His Ala 225 230 235 240	720
acg agg gaa gat atg tac cca gta tgt gat gta gta acg tta aac tgt Thr Arg Glu Asp Met Tyr Pro Val Cys Asp Val Val Thr Leu Asn Cys 245 250 255	768
cca tta cat cca gaa acg gaa cat atg att aac gat gaa acg tta aaa Pro Leu His Pro Glu Thr Glu His Met Ile Asn Asp Glu Thr Leu Lys 260 265 270	816
tta ttc aaa agg gga gcg tac att gtc aac acg gcg aga ggc aaa ttg Leu Phe Lys Arg Gly Ala Tyr Ile Val Asn Thr Ala Arg Gly Lys Leu 275 280 285	864

tgc gat aga gat gcg gtc gcg aga gcg ttg gaa tca ggc aga ttg gca 912
 Cys Asp Arg Asp Ala Val Ala Arg Ala Leu Glu Ser Gly Arg Leu Ala
 290 295 300
 ggc tat gcg ggc gat gtc tgg ttt ccg caa ccg gcg ccg aaa gat cat 960
 Gly Tyr Ala Gly Asp Val Trp Phe Pro Gln Pro Ala Pro Lys Asp His
 305 310 315 320
 ccg tgg aga acg atg ccg tat aac ggc atg acg ccg cat att tca ggc 1008
 Pro Trp Arg Thr Met Pro Tyr Asn Gly Met Thr Pro His Ile Ser Gly
 325 330 335
 acg acg ttg acg gcg caa gcg aga tat gct gcg ggc acg aga gaa att 1056
 Thr Thr Leu Thr Ala Gln Ala Arg Tyr Ala Ala Gly Thr Arg Glu Ile
 340 345 350
 ttg gaa tgc ttt ttt gaa ggc aga cca atc cgt gac gaa tat ctg atc 1104
 Leu Glu Cys Phe Phe Glu Gly Arg Pro Ile Arg Asp Glu Tyr Leu Ile
 355 360 365
 gtc cag ggt ggt gcc ctg gcc ggt acc ggt gcc cat tct tat tct aaa 1152
 Val Gln Gly Gly Ala Leu Ala Gly Thr Gly Ala His Ser Tyr Ser Lys
 370 375 380
 ggt aat gcc acc ggt ggt tct gaa gaa gcc aaa ttc aaa aaa gcc gtc 1200
 Gly Asn Ala Thr Gly Gly Ser Glu Glu Ala Lys Phe Lys Lys Ala Val
 385 390 395 400
 taa tga 1206
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<210> 70
 <211> 400
 <212> PRT
 <213> Pseudomonas sp. strain 101

<400> 70
 Met Ala Lys Val Leu Cys Val Leu Tyr Asp Asp Pro Val Asp Gly Tyr
 1 5 10 15
 Pro Lys Thr Tyr Ala Arg Asp Asp Leu Pro Lys Ile Asp His Tyr Pro
 20 25 30
 Gly Gly Gln Thr Leu Pro Thr Pro Lys Ala Ile Asp Phe Thr Pro Gly
 35 40 45
 Gln Leu Leu Gly Ser Val Ser Gly Glu Leu Gly Leu Arg Lys Tyr Leu
 50 55 60
 Glu Ser Asn Gly His Thr Leu Val Val Thr Ser Asp Lys Asp Gly Pro
 65 70 75 80
 Asp Ser Val Phe Glu Arg Glu Leu Val Asp Ala Asp Val Val Ile Ser
 85 90 95
 Gln Pro Phe Trp Pro Ala Tyr Leu Thr Pro Glu Arg Ile Ala Lys Ala
 100 105 110
 Lys Asn Leu Lys Leu Ala Leu Thr Ala Gly Ile Gly Ser Asp His Val
 115 120 125
 Asp Leu Gln Ser Ala Ile Asp Arg Asn Val Thr Val Ala Glu Val Thr
 130 135 140

Tyr Cys Asn Ser Ile Ser Val Ala Glu His Val Val Met Met Ile Leu
 145 150 155 160
 Ser Leu Val Arg Asn Tyr Leu Pro Ser His Glu Trp Ala Arg Lys Gly
 165 170 175
 Gly Trp Asn Ile Ala Asp Cys Val Ser His Ala Tyr Asp Leu Glu Ala
 180 185 190
 Met His Val Gly Thr Val Ala Ala Gly Arg Ile Ala Leu Ala Val Leu
 195 200 205
 Arg Arg Leu Ala Pro Phe Asp Val His Leu His Tyr Thr Asp Arg His
 210 215 220
 Arg Leu Pro Glu Ser Val Glu Lys Glu Leu Asn Leu Thr Trp His Ala
 225 230 235 240
 Thr Arg Glu Asp Met Tyr Pro Val Cys Asp Val Val Thr Leu Asn Cys
 245 250 255
 Pro Leu His Pro Glu Thr Glu His Met Ile Asn Asp Glu Thr Leu Lys
 260 265 270
 Leu Phe Lys Arg Gly Ala Tyr Ile Val Asn Thr Ala Arg Gly Lys Leu
 275 280 285
 Cys Asp Arg Asp Ala Val Ala Arg Ala Leu Glu Ser Gly Arg Leu Ala
 290 295 300
 Gly Tyr Ala Gly Asp Val Trp Phe Pro Gln Pro Ala Pro Lys Asp His
 305 310 315 320
 Pro Trp Arg Thr Met Pro Tyr Asn Gly Met Thr Pro His Ile Ser Gly
 325 330 335
 Thr Thr Leu Thr Ala Gln Ala Arg Tyr Ala Ala Gly Thr Arg Glu Ile
 340 345 350
 Leu Glu Cys Phe Phe Glu Gly Arg Pro Ile Arg Asp Glu Tyr Leu Ile
 355 360 365
 Val Gln Gly Gly Ala Leu Ala Gly Thr Gly Ala His Ser Tyr Ser Lys
 370 375 380
 Gly Asn Ala Thr Gly Gly Ser Glu Glu Ala Lys Phe Lys Lys Ala Val
 385 390 395 400

<210> 71
 <211> 1098
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> FDH FDHCh13
 <221> CDS
 <222> (1)...(1098)

<400> 71
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 Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp
 1 5 10 15
 gaa gaa aaa ctc tac ggc tgc acg gaa aat aag ctg ggc att gca aat 96
 Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala Asn
 20 25 30
 tgg ctg aag gat cag ggc cac gaa ctg att acg acg tca gat aag gaa 144
 Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
 35 40 45

ggc ggt aat tcc gtc ttg gat caa cac atc ccc gat gct gat atc atc Gly Gly Asn Ser Val Leu Asp Gln His Ile Pro Asp Ala Asp Ile Ile 50 55 60	192
atc aca aca ccc ttc cac ccc gct tac atc aca aaa gaa aga atc gat Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Ile Asp 65 70 75 80	240
aaa gct aaa aaa ttg aaa ttg gtc gtc gtc gct ggt gtc ggt tcc gat Lys Ala Lys Lys Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp 85 90 95	288
cac atc gat ttg gat tac atc aat caa aca ggt aaa aaa atc tcc gtc His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val 100 105 110	336
ttg gaa gtc aca ggt tcc aat gtc gtc tcc gtc gct gaa cac gtc gtc Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val 115 120 125	384
atg aca atg ttg gtc ttg gtc aga aat ttc gtc ccc gct cac gaa caa Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln 130 135 140	432
atc atc aat cac gat tgg gaa gtc gct gct atc gct aaa gat gct tac Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr 145 150 155 160	480
gat atc gaa ggt aaa aca atc gct aca atc ggt gct ggt aga atc ggt Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly 165 170 175	528
tac aga gtc ttg gaa aga ttg gtc ccc ttc aat ccc aaa gaa ttg ttg Tyr Arg Val Leu Glu Arg Leu Val Pro Phe Asn Pro Lys Glu Leu Leu 180 185 190	576
tac tac gat tac caa gct ttg ccc aaa gat gct gaa gaa aaa gtt ggt Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Asp Ala Glu Glu Lys Val Gly 195 200 205	624
gct cgt cgt gtt gaa aac ata gaa gaa ttg gtt gct cag gct gat ata Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile 210 215 220	672
gtt acc gtt aac gct ccg ttg cac gct ggt acc aaa ggt ttg ata aac Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn 225 230 235 240	720
aaa gaa ttg ttg tca aaa ttt aaa aaa ggt gct tgg ttg ctt aac acc Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Leu Asn Thr 245 250 255	768
gct cgt ggt gct ata tgc gtt gct gaa gat gtt gct gct gct ttg gaa Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu Glu 260 265 270	816
tca ggt cag ttg cgt ggt tac ggt ggt gat gtt tgg ttt ccg cag ccg	864

Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro
 275 280 285

gct ccg aaa gat cac ccg tgg cgt gat atg cgt aac aaa tac ggt gct 912
 Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala
 290 295 300

ggt aac gct atg acc ccg cac tac tca ggt acc acc ttg gat gct cag 960
 Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln
 305 310 315 320

acc cgt tac gct cag ggt acc aaa aac atc ctc gaa tcg ttt ttt acc 1008
 Thr Arg Tyr Ala Gln Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr
 325 330 335

ggt aaa ttt gat tat cgt cca cag gat atc atc ctc ctc aac ggt gaa 1056
 Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu
 340 345 350

tat gtt acc aaa gcc tat ggt aaa cac gat aaa aaa taa tga 1098
 Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys * *
 355 360

<210> 72

<211> 364

<212> PRT

<213> Candida boidinii

<400> 72

Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp
 1 5 10 15

Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala Asn
 20 25 30

Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
 35 40 45

Gly Gly Asn Ser Val Leu Asp Gln His Ile Pro Asp Ala Asp Ile Ile
 50 55 60

Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Ile Asp
 65 70 75 80

Lys Ala Lys Lys Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
 85 90 95

His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
 100 105 110

Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
 115 120 125

Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
 130 135 140

Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
 145 150 155 160

Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
 165 170 175

Tyr Arg Val Leu Glu Arg Leu Val Pro Phe Asn Pro Lys Glu Leu Leu
 180 185 190

Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Asp Ala Glu Glu Lys Val Gly
 195 200 205

Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile

210 215 220
 Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn
 225 230 235 240
 Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Leu Asn Thr
 245 250 255
 Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu Glu
 260 265 270
 Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro
 275 280 285
 Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala
 290 295 300
 Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln
 305 310 315 320
 Thr Arg Tyr Ala Gln Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr
 325 330 335
 Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu
 340 345 350
 Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys
 355 360

<210> 73
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH P016514-B-12

<221> CDS
 <222> (1)...(765)

<400> 73
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 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa 192
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat 240
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat 288
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
 85 90 95
 tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg 336

Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc 384
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act 432
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 tac act tcg gct cga gct ggg gct tgt tcc cta gct aat gct cta tcg 480
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser
 145 150 155 160
 aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat 528
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg 576
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta 624
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 74

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH P016514-B-12

<400> 74

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

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

<210> 75

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH Mz1/4H6

<221> CDS

<222> (1)...(765)

<400> 75

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1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	

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atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                        85                        90                        95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
                        100                        105                        110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
                        115                        120                        125

ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
                        130                        135                        140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                        150                        155                        160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                        165                        170                        175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
                        180                        185                        190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
                        195                        200                        205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
210                        215                        220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                        230                        235                        240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa      765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
                        245                        250

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<210> 76

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH Mz1/4H6

<400> 76

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
1           5           10           15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp

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

<210> 77
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH P016229-F-04

<221> CDS
 <222> (1)...(765)

<400> 77
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 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 agt gct ctg agg ctg tgc gag gct ggt cac acc gtc gct tgc cat gat 96
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 gaa agc ttt aaa cag aaa gat gaa ctg gag gct ttt gct gaa acc tac 144
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 cca cag ctg aaa cca atg agc gaa cag gaa cca gct gga ctg att gaa 192
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Gly Leu Ile Glu
 50 55 60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

<210> 78
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH P016229-F-04

<400> 78
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 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Gly Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 79
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH P016230-A-08

<221> CDS
 <222> (1)...(765)

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 1 5 10 15
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp 20 25 30
 20 25 30
 gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr

35	40	45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa			192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu			
50	55	60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat			240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp			
65	70	75	80
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat			288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp			
85	90	95	
tat cgt ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg			336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val			
100	105	110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc			384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile			
115	120	125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act			432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr			
130	135	140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg			480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser			
145	150	155	160
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat			528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn			
165	170	175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg			576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp			
180	185	190	
aag act aat ccg gaa cac gtg gct cac gtg aag aag gtg act gct cta			624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu			
195	200	205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg			672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu			
210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca			720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala			
225	230	235	240
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa			765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *			
245	250		

<210> 80

<211> 254

<212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH P016230-A-08

<400> 80
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 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 81
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH P016096-G9

<221> CDS
 <222> (1)...(765)

<400> 81
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 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96

Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp		
			20					25					30				
gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac	144	
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr		
		35					40					45					
cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	atc	gaa	192	
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu		
		50				55					60						
gct	gtc	acc	agc	gct	tac	ggc	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240	
Ala	Val	Thr	Ser	Ala	Tyr	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp		
	65				70				75						80		
atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat	288	
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp		
				85				90						95			
tac	agg	ggc	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336	
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val		
			100					105					110				
aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384	
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile		
		115					120					125					
ttc	atc	act	tcg	gct	act	ccg	ttc	ggg	cca	tgg	aaa	gag	cta	tcg	act	432	
Phe	Ile	Thr	Ser	Ala	Thr	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr		
	130					135					140						
tac	act	tcg	gct	cga	gct	ggg	gct	tgt	act	cta	gct	aat	gct	cta	tcg	480	
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Thr	Leu	Ala	Asn	Ala	Leu	Ser		
	145				150					155				160			
aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528	
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn		
			165					170					175				
tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg	576	
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp		
			180					185					190				
aag	act	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta	624	
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu		
		195					200					205					
caa	cga	cta	ggg	act	caa	aaa	gag	ttg	ggg	gaa	ttg	gtg	gca	ttc	ctg	672	
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu		
	210					215					220						
gca	tct	ggc	tct	tgt	gat	tat	ttg	act	ggc	cag	gtg	ttt	tgg	ttg	gca	720	
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala		
	225				230				235					240			
ggc	ggc	ttt	ccc	att	atc	gaa	cgt	tgg	ccc	ggc	atg	ccc	gaa	taa		765	
Gly	Gly	Phe	Pro	Ile	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu	*			

245

250

<210> 82
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH P016096-G9

<400> 82
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 83
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH P016097-F9

<221> CDS
 <222> (1)...(765)

<400> 83

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agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp 20 25 30	96
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr 35 40 45	144
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu 50 55 60	192
gct gtc acc agc gct tac ggt cag gtc gat atc ctg gtc agc aac gat Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp 65 70 75 80	240
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp 85 90 95	288
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val 100 105 110	336
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile 115 120 125	384
ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr 130 135 140	432
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser 145 150 155 160	480
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn 165 170 175	528
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp 180 185 190	576
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu 195 200 205	624
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Val Ala Phe Leu 210 215 220	672
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720

Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 84
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH P016097-F9

<400> 84
 Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 85
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH P016097-H10

<221> CDS

<222> (1)...(765)

<400> 85

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1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg got tgt tcc cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 86
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH P016097-H10

<400> 86
 Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
 115 120 125
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser
 145 150 155 160
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 87
 <211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH P016099-A1

<221> CDS

<222> (1)...(765)

<400> 87

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Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat atc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp	
180 185 190	

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta 624
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 88

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH P016099-A1

<400> 88

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

Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 89

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH P016231-A-03

<221> CDS

<222> (1)...(765)

<400> 89

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agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct tca gaa ttt cag cca atc gat aaa tac gcc gtc gaa gat	288
Ile Phe Ala Ser Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	

	165		170		175	
tat cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg						576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp						
	180		185		190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta						624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu						
	195		200		205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg						672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu						
	210		215		220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca						720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala						
	225		230		235	240
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa						765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *						
	245		250			

<210> 90

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH P016231-A-03

<400> 90

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

	195		200		205										
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu
	210					215					220				
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala
225					230					235					240
Gly	Gly	Phe	Pro	Met	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu		
			245						250						

<210> 91
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH P016231-E-03

<221> CDS
 <222> (1)...(765)

<400> 91	
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1 5 10 15	
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg	480

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Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                      150                      155                      160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                      165                      170                      175

tac cta cac tcg gag gat tcg ccg tac tat tat ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
                      180                      185                      190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
                      195                      200                      205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
                      210                      215                      220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                      230                      235                      240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa      765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
                      245                      250

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<210> 92

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH P016231-E-03

<400> 92

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
  1                      5                      10                      15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
                      20                      25                      30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
                      35                      40                      45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
                      50                      55                      60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                      70                      75                      80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                      85                      90                      95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
                      100                      105                      110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
                      115                      120                      125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
                      130                      135                      140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                      150                      155                      160

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Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
 180 185 190
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 93

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH S00827801

<221> CDS

<222> (1)...(765)

<400> 93

atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt	48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly	
1 5 10 15	
agc gct ctg agg ctg agc gaa ggt ggt cat acc gtc gct tgc cat gat	96
Ser Ala Leu Arg Leu Ser Glu Gly Gly His Thr Val Ala Cys His Asp	
20 25 30	
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat	288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act 432
 Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
 130 135 140
 tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg 480
 Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
 145 150 155 160
 aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat 528
 Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
 165 170 175
 tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg 576
 Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
 180 185 190
 aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta 624
 Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

<210> 94
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HHDH S00827801

<400> 94
 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 Ser Ala Leu Arg Leu Ser Glu Gly Gly His Thr Val Ala Cys His Asp
 20 25 30
 Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45
 Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
 50 55 60
 Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65 70 75 80
 Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
 85 90 95
 Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
 100 105 110
 Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile

```

      115              120              125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
130              135              140
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145              150              155              160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
      165              170              175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
      180              185              190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
      195              200              205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
      210              215              220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225              230              235              240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
      245              250

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<210> 95
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH S00890554

<221> CDS
 <222> (1)...(765)

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
1              5              10              15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
      20              25              30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
      35              40              45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
      50              55              60

gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
      65              70              75              80

atc ttt gct cta gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
      85              90              95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
      100              105              110

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aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
      115                      120                      125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
      130                      135                      140

tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
      145                      150                      155                      160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
      165                      170                      175

tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
      180                      185                      190

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
      195                      200                      205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
      210                      215                      220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
      225                      230                      235                      240

ggc ggc ttt ccc acg ata gaa cgt tgg ccc ggc atg ccc gaa taa      765
Gly Gly Phe Pro Thr Ile Glu Arg Trp Pro Gly Met Pro Glu *
      245                      250

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<210> 96

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH S00890554

<400> 96

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

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Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
      85      90      95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
      100     105     110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
      115     120     125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
      130     135     140
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
      145     150     155     160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
      165     170     175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Pro Thr Glu Pro Trp
      180     185     190
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
      195     200     205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
      210     215     220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
      225     230     235     240
Gly Gly Phe Pro Thr Ile Glu Arg Trp Pro Gly Met Pro Glu
      245     250

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<210> 97

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH S00994580

<221> CDS

<222> (1)...(765)

<400> 97

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
  1              5              10              15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
      20              25              30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
      35              40              45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg att gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
      50              55              60

gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
      65              70              75              80

atc ttt gct cta gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp

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	85	90	95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg				336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val				
	100	105	110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc				384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile				
	115	120	125	
ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act				432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr				
	130	135	140	
tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg				480
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser				
	145	150	155	160
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat				528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn				
	165	170	175	
tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg				576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp				
	180	185	190	
aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta				624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu				
	195	200	205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg				672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu				
	210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca				720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala				
	225	230	235	240
ggc ggc ttt ccc acg ata gaa cgt tgg ccc ggc atg ccc gaa taa				765
Gly Gly Phe Pro Thr Ile Glu Arg Trp Pro Gly Met Pro Glu *				
	245	250		

<210> 98

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH S00994580

<400> 98

Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly

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5

10

15

Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp

20

25

30

Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr

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

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<210> 99
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HHDH S01018044

<221> CDS
 <222> (1)...(765)

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<400> 99
atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
  1              5              10              15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
      20              25              30

gaa agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
      35              40              45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
      50              55              60

gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat      240

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Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65          70          75          80

atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat      288
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
          85          90          95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
          100          105          110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
          115          120          125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
          130          135          140

tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg      480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145          150          155          160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
          165          170          175

tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
          180          185          190

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
          195          200          205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
          210          215          220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225          230          235          240

ggc ggc ttt ccc gtc ata gaa cgt tgg ccc ggc atg ccc gaa taa      765
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu *
          245          250

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<210> 100

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH S0108044

<400> 100

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

<210> 101

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH S01035939

<221> CDS

<222> (1)...(765)

<400> 101

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 Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15
 agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96
 Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
 20 25 30
 gaa agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa acc tac 144
 Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
 35 40 45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg att gaa	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat	240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat	288
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val	
100 105 110	
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg	480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta	624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggc ggc ttt ccc gtc ata gaa cgt tgg ccc ggc atg ccc gaa taa	765
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

<210> 102

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH S01035939

<400> 102

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

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<210> 103

<211> 768

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH S01009684

<221> CDS

<222> (1)...(765)

<400> 103

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atg agc act gcg att gtt act aac gtc aaa cat ttc ggt ggt atg ggg      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1           5           10           15

agt gcg ctg aaa ctg tcg gag gcc ggt cat aca gta gcg tgt cac gat      96
Ser Ala Leu Lys Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
           20           25           30

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gaa agt ttc aaa caa aag gac gaa ttg gaa gcc ttt gcg gaa act tac	144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr	
35 40 45	
cca cag ctg aaa ccg atg tca gaa cag gag cca gcg gag tta att gag	192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu	
50 55 60	
gcg gtc acc agt gcc ttc ggc cag gtg gat gtc ctg gtt agc aac gac	240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp	
65 70 75 80	
atc ttt gct ctg gaa ttc cag ccg att gac aag tat gcc gtc gaa gac	288
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp	
85 90 95	
tac cgt ggt gcg gta gaa gca ctg cag atc aag ccg ttc gcg ttg gtt	336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Lys Pro Phe Ala Leu Val	
100 105 110	
aat gcc gta gct agt caa atg aaa aaa cgt aaa tca ggt cat att atc	384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile	
115 120 125	
ttc att act agc gcg gct ccg ttt ggt cca tgg aag gag ctg tcg act	432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr	
130 135 140	
tat agt agt gcg cgc gcc ggg gcc tcc gcg ttg gct aac gca ctg agt	480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser	
145 150 155 160	
aaa gaa tta ggt gag tat aat atc cct gtt ttc gcc att ggg cca aac	528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn	
165 170 175	
tat ctg cac tca gaa gat agc cca tac tat tac cca acg gaa ccg tgg	576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp	
180 185 190	
aag atc aac cct gaa cat gtg gcg cat gtt aaa aaa gta aca gcc tta	624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu	
195 200 205	
caa cgt ctg ggt act caa aaa gaa ott ggc gag ctg gtt gcg ttt ctc	672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu	
210 215 220	
gct tct ggt agc tgc gat tac ttg acc ggc caa gtc ttc tgg tta gcc	720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala	
225 230 235 240	
ggg ggc ttt ccg gtg att gag cgc tgg cca ggt atg ccg gaa taa	765
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu *	
245 250	

tga

768

<210> 104

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH S01009684

<400> 104

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

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<210> 105

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH S00817219

<221> CDS

<222> (1)...(765)

<400> 105

atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt

48

Met	Ser	Thr	Ala	Ile	Val	Thr	Asn	Val	Lys	His	Phe	Gly	Gly	Met	Gly		
1				5					10					15			
agc	gct	ctg	agg	ctg	agc	gaa	gct	ggc	cat	acc	gtc	gct	tgc	cat	gat		96
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp		
			20					25					30				
gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac		144
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr		
		35					40					45					
cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	atc	gaa		192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu		
		50				55					60						
gct	gtc	acc	agc	gct	tac	ggc	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat		240
Ala	Val	Thr	Ser	Ala	Tyr	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp		
65					70				75						80		
atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat		288
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp		
				85				90					95				
tac	agg	ggc	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg		336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val		
			100					105					110				
aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc		384
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile		
		115					120					125					
ttc	atc	act	tcg	gct	gct	ccg	ttc	ggg	cca	tgg	aag	gag	cta	tcg	act		432
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr		
		130				135					140						
tac	act	tcg	gct	cga	gct	ggg	gct	tgt	tcc	cta	gct	aat	gct	cta	tcg		480
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Ser	Leu	Ala	Asn	Ala	Leu	Ser		
145					150				155					160			
aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat		528
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn		
			165					170					175				
tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg		576
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp		
			180					185					190				
aag	act	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta		624
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu		
		195					200					205					
caa	cga	cta	ggg	act	caa	aaa	gag	ttg	ggg	gaa	ttg	gtg	gca	ttt	ttg		672
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu		
		210				215					220						
gca	tct	ggc	tct	tgt	gat	tat	ttg	act	ggc	cag	gtg	ttt	tgg	ttg	gca		720
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala		

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225          230          235          240
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa      765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *
                245                250

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tgaggatcc 774

<210> 106

<211> 254

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> HHDH S00817219

<400> 106

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

 $\langle 210 \rangle \quad 10^7$

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH S00708827

<221> CDS

<222> (1)...(765)

<400> 107

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Met	Ser	Thr	Ala	Ile	Val	Thr	Asn	Val	Lys	His	Phe	Gly	Gly	Met	Gly	
1				5					10					15		

agc	gct	ctg	agg	ctg	agc	gaa	gct	ggt	cat	acc	gtc	gct	tgc	cat	gat	96
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp	
			20					25					30			

gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac	144
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr	
		35					40					45				

cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gac	ctg	att	gaa	192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Asp	Leu	Ile	Glu	
	50					55					60					

gct	gtc	acc	agc	gct	tac	ggt	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240
Ala	Val	Thr	Ser	Ala	Tyr	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp	
	65				70				75						80	

atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat	288
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp	
				85					90					95		

tac	agg	ggt	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val	
			100					105					110			

aat	gct	gtg	gct	tcg	caa	atg	aag	aaa	cga	aag	tcg	ggg	cac	atc	atc	384
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile	
		115					120					125				

ttc	atc	act	tcg	gct	act	ccg	ttc	ggg	cca	tgg	aaa	gag	cta	tcg	act	432
Phe	Ile	Thr	Ser	Ala	Thr	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr	
	130					135					140					

tac	act	tcg	gct	cga	gct	ggg	gct	tgt	act	cta	gct	aat	gct	cta	tcg	480
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Cys	Thr	Leu	Ala	Asn	Ala	Leu	Ser	
	145				150					155					160	

aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn	
			165						170				175			

tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg	576
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp	
			180					185					190			

aag	act	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta	624
Lys	Thr	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu	
		195					200					205				

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ctg 672
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca 720
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240

ggc ggc ttt ccc ata ata gaa cgt tgg ccc ggc atg ccc gaa taa 765
 Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu *
 245 250

tgaggatcc 774

<210> 108

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH S00708827

<400> 108

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

<210> 109

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> HHDH S00772501

<221> CDS

<222> (1)...(765)

<400> 109

atg	agc	acc	gct	atc	gtc	acc	aac	gtc	aaa	cat	ttt	gga	ggg	atg	ggg	48
Met	Ser	Thr	Ala	Ile	Val	Thr	Asn	Val	Lys	His	Phe	Gly	Gly	Met	Gly	
1				5					10					15		

agc	gct	ctg	agg	ctg	agc	gaa	gct	ggg	cat	acc	gtc	gct	tgc	cat	gat	96
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp	
			20					25					30			

gaa	agc	ttt	aaa	cag	aaa	gat	gaa	ctg	gaa	gct	ttt	gct	gaa	acc	tac	144
Glu	Ser	Phe	Lys	Gln	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr	
		35					40					45				

cca	cag	ctg	aaa	cca	atg	agc	gaa	cag	gaa	cca	gct	gaa	ctg	atc	gaa	192
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu	
	50					55				60						

gct	gtc	acc	agc	gct	ttt	ggg	cag	gtc	gat	gtc	ctg	gtc	agc	aac	gat	240
Ala	Val	Thr	Ser	Ala	Phe	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp	
65					70				75					80		

atc	ttt	gct	cca	gaa	ttt	cag	cca	atc	gat	aaa	tac	gct	gtc	gaa	gat	288
Ile	Phe	Ala	Pro	Glu	Phe	Gln	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp	
			85					90						95		

tac	agg	ggg	gct	gtc	gaa	gct	ctg	cag	atc	agg	cca	ttt	gct	cta	gtg	336
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val	
			100				105						110			

aat	gct	gtg	gct	tcg	caa	atg	aag	aag	cga	aag	tcg	ggg	cac	atc	atc	384
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile	
		115					120					125				

ttc	atc	act	tcg	gct	gcc	ccg	ttc	ggg	cca	tgg	aag	gag	cta	tcg	act	432
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr	
	130					135				140						

tac	act	tcg	gct	cga	gct	ggg	gct	agt	act	cta	gct	aat	gct	cta	tcg	480
Tyr	Thr	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Thr	Leu	Ala	Asn	Ala	Leu	Ser	
145					150					155				160		

aag	gag	cta	gga	gag	tac	aat	atc	ccg	gtg	ttc	gct	atc	ggg	ccg	aat	528
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn	
			165					170					175			

tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	ttc	tac	ccg	act	gag	ccg	tgg	576
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Phe	Tyr	Pro	Thr	Glu	Pro	Trp	

180	185	190	
aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta			624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu			
195	200	205	
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg			672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu			
210	215	220	
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca			720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala			
225	230	235	240
ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa			765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu *			
245	250		

<210> 110

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> HHDH S00772501

<400> 110

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

225	230	235	240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu			
245	250		
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<211> 762			
<212> DNA			
<213> Artificial Sequence			
 <220>			
<223> HHDH S01035968			
 <221> CDS			
<222> (1)...(765)			
 <400> 111			
atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt			48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly			
1 5 10 15			
agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat			96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp			
20 25 30			
gaa agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa acc tac			144
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr			
35 40 45			
cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa			192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu			
50 55 60			
gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat			240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp			
65 70 75 80			
atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat			288
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp			
85 90 95			
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg			336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val			
100 105 110			
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc			384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile			
115 120 125			
ttc atc act tcg gct gcc cgg ttc ggg cca tgg aag gag cta tcg act			432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr			
130 135 140			
tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg			480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser			
145 150 155 160			
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat			528

Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn		
				165					170						175		
tac	cta	cac	tcg	gag	gat	tcg	ccg	tac	tat	tac	ccc	act	gag	ccg	tgg		576
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Tyr	Tyr	Pro	Thr	Glu	Pro	Trp		
			180					185					190				
aag	att	aat	ccg	gag	cac	gtg	gct	cac	gtg	aag	aag	gtg	act	gct	cta		624
Lys	Ile	Asn	Pro	Glu	His	Val	Ala	His	Val	Lys	Lys	Val	Thr	Ala	Leu		
		195					200					205					
caa	cga	cta	ggg	act	caa	aaa	gag	ttg	ggg	gaa	ttg	gtg	gca	ttt	ttg		672
Gln	Arg	Leu	Gly	Thr	Gln	Lys	Glu	Leu	Gly	Glu	Leu	Val	Ala	Phe	Leu		
	210					215					220						
gca	tct	ggc	tct	tgt	gat	tat	ttg	act	ggc	cag	gtg	ttt	tgg	ttg	gca		720
Ala	Ser	Gly	Ser	Cys	Asp	Tyr	Leu	Thr	Gly	Gln	Val	Phe	Trp	Leu	Ala		
225				230					235					240			
ggc	ggc	ttt	ccc	gtc	ata	gaa	cgt	tgg	ccc	ggc	atg	ccc	gaa				762
Gly	Gly	Phe	Pro	Val	Ile	Glu	Arg	Trp	Pro	Gly	Met	Pro	Glu				
			245						250								

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<210> 112
<211> 254
<212> PRT
<213> Artificial Sequence
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<220>
<223> HHDH S01035968

<400> 112																
Met	Ser	Thr	Ala	Ile	Val	Thr	Asn	Val	Lys	His	Phe	Gly	Gly	Met	Gly	
1				5					10					15		
Ser	Ala	Leu	Arg	Leu	Ser	Glu	Ala	Gly	His	Thr	Val	Ala	Cys	His	Asp	
			20					25					30			
Glu	Ser	Phe	Lys	His	Lys	Asp	Glu	Leu	Glu	Ala	Phe	Ala	Glu	Thr	Tyr	
		35					40					45				
Pro	Gln	Leu	Lys	Pro	Met	Ser	Glu	Gln	Glu	Pro	Ala	Glu	Leu	Ile	Glu	
	50					55					60					
Ala	Val	Thr	Ser	Ala	Phe	Gly	Gln	Val	Asp	Val	Leu	Val	Ser	Asn	Asp	
65					70					75					80	
Ile	Phe	Ala	Leu	Glu	Phe	Arg	Pro	Ile	Asp	Lys	Tyr	Ala	Val	Glu	Asp	
				85					90					95		
Tyr	Arg	Gly	Ala	Val	Glu	Ala	Leu	Gln	Ile	Arg	Pro	Phe	Ala	Leu	Val	
			100					105					110			
Asn	Ala	Val	Ala	Ser	Gln	Met	Lys	Lys	Arg	Lys	Ser	Gly	His	Ile	Ile	
		115					120					125				
Phe	Ile	Thr	Ser	Ala	Ala	Pro	Phe	Gly	Pro	Trp	Lys	Glu	Leu	Ser	Thr	
	130					135					140					
Tyr	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Ser	Ala	Leu	Ala	Asn	Ala	Leu	Ser	
145					150					155				160		
Lys	Glu	Leu	Gly	Glu	Tyr	Asn	Ile	Pro	Val	Phe	Ala	Ile	Gly	Pro	Asn	
				165					170					175		
Tyr	Leu	His	Ser	Glu	Asp	Ser	Pro	Tyr	Tyr	Tyr	Pro	Thr	Glu	Pro	Trp	
			180					185					190			

Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
 195 200 205
 Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
 210 215 220
 Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
 225 230 235 240
 Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu
 245 250

<210> 113

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED S01040430

<221> CDS

<222> (1)...(852)

<400> 113

atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg gcg cca gct 48
 Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala
 1 5 10 15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96
 His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg 144
 Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
 35 40 45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat 192
 Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
 50 55 60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat 240
 Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65 70 75 80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg 288
 Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
 85 90 95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac 336
 Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
 100 105 110

ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc 384
 Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
 115 120 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtt gac gtc gac ctg 432
 Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
 130 135 140

```

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                      150                      155                      160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                      165                      170                      175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg gcc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Ala Tyr Asn
                      180                      185                      190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
                      195                      200                      205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
                      210                      215                      220

acc gag atc tct gat ttc gtc ccg caa gaa aca cag aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                      230                      235                      240

agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                      245                      250                      255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc acg      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
                      260                      265                      270

gat atc att gtg gac ggc ggc tac acg ctg ccg tag      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *
275                      280

```

<210> 114

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED S01040430

<400> 114

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

```

```

      85              90              95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
      100              105              110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
      115              120              125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
      130              135              140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
      145              150              155
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
      165              170              175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Ala Tyr Asn
      180              185              190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
      195              200              205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
      210              215              220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
      225              230              235
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
      245              250              255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
      260              265              270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
      275              280

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<210> 115

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED S01091361

<221> CDS

<222> (1)...(852)

<400> 115

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atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg gcg cca gct      48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala
  1              5              10              15

```

```

cat acc aaa gac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac      96
His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
      20              25              30

```

```

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
      35              40              45

```

```

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
      50              55              60

```

```

aac agt cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
      65              70              75              80

```

```

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                        85                        90                        95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
                        100                        105                        110

ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
                        115                        120                        125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
                        130                        135                        140

aaa ggc gca ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Ala Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
                        145                        150                        155                        160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                        165                        170                        175

atg tcg ggt cac att gtt aat gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
                        180                        185                        190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
                        195                        200                        205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
                        210                        215                        220

acc gag atc tct gat ttc gtc ccg cag gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
                        225                        230                        235                        240

agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                        245                        250                        255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc acg      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
                        260                        265                        270

gat atc gtt gtg gac ggc ggc tac acg ctg ccg tag      852
Asp Ile Val Val Asp Gly Gly Tyr Thr Leu Pro *
                        275                        280

```

<210> 116

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED S01091361

<400> 116

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

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<210> 117

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED S01091625

<221> CDS

<222> (1)...(852)

<400> 117

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atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg gcg cca gct
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala

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48

1	5	10	15	
cat acc aag aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac				96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	20	25	30	
ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg				144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	35	40	45	
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat				192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	50	55	60	
aac agt cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat				240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	65	70	75	80
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg				288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	85	90	95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac				336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	100	105	110	
ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc				384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	115	120	125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg				432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	130	135	140	
aaa ggc gca ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa				480
Lys Gly Ala Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	145	150	155	160
cgt ttc gag aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc				528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	165	170	175	
atg tcg ggt cac atc gtt aat gtg ccg caa ttt cag gcg acc tac aat				576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn	180	185	190	
gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa				624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu	195	200	205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat				672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn	210	215	220	
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aga tgg tgg				720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Arg Trp Trp	225	230	235	240

agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt 768
 Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
 245 250 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca 816
 Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
 260 265 270

gat atc att gtg gac ggc ggc tac acg ctg ccg tag 852
 Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *
 275 280

<210> 118

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED S01091625

<400> 118

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

Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
275 280

<210> 119

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> KRED S01094648

<221> CDS

<222> (1)...(852)

<400> 119

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Met Ala Lys Asn Phe Ser Asn Val Gly Tyr Pro Ala Pro Ala Pro Ala	
1 5 10 15	
cat acc aaa agc gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac	96
His Thr Lys Ser Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn	
20 25 30	
ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg	144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala	
35 40 45	
ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat	192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr	
50 55 60	
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat	240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr	
65 70 75 80	
ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg	288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala	
85 90 95	
gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac	336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp	
100 105 110	
ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc	384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile	
115 120 125	
gat cag gat gac gat aaa cat ttt gac cag gtg gtt gac gtc gac ctg	432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu	
130 135 140	
aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa	480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu	
145 150 155 160	
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc	528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser	

165	170	175	
atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg gcc tac aat			576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Ala Tyr Asn			
180	185	190	
gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa			624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu			
195	200	205	
ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat			672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn			
210	215	220	
acc gag atc tct gat ttc gtc ccg caa gga aca cag aat aaa tgg tgg			720
Thr Glu Ile Ser Asp Phe Val Pro Gln Gly Thr Gln Asn Lys Trp Trp			
225	230	235	240
agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt			768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly			
245	250	255	
gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc acg			816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr			
260	265	270	
gat atc att gtg gac ggc ggc tac acg ctg ccg tag			852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro *			
275	280		

<210> 120

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRED S01094648

<400> 120

Met	Ala	Lys	Asn	Phe	Ser	Asn	Val	Gly	Tyr	Pro	Ala	Pro	Ala	Pro	Ala
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His	Thr	Lys	Ser	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn
			20				25					30			
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Asn	Ser	Gly	Ile	Gly	Tyr	Ala
		35				40					45				
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr
	50				55				60						
Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr
65			70						75				80		
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala
			85				90						95		
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp
		100				105						110			
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile
	115				120							125			
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu

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

<210> 121

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<223> GDH S01024744

<221> CDS

<222> (1)...(789)

<400> 121

atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct gct 48
 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1 5 10 15
 tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca 96
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
 20 25 30
 aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta 144
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
 35 40 45
 aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga 192
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
 50 55 60
 gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att 240
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65 70 75 80
 aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa 288
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
 85 90 95
 aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc 336

Asn	Pro	Val	Pro	Ser	His	Glu	Met	Pro	Leu	Lys	Asp	Trp	Asp	Lys	Val		
			100					105					110				
atc	ggc	acg	aac	tta	acg	ggt	gcc	ttt	tta	gga	agc	cgt	gaa	gcg	att		384
Ile	Gly	Thr	Asn	Leu	Thr	Gly	Ala	Phe	Leu	Gly	Ser	Arg	Glu	Ala	Ile		
			115				120					125					
aaa	tat	ttc	gta	gaa	aac	gat	atc	aag	gga	aat	gtc	att	aac	atg	tcc		432
Lys	Tyr	Phe	Val	Glu	Asn	Asp	Ile	Lys	Gly	Asn	Val	Ile	Asn	Met	Ser		
			130				135				140						
agt	gtg	cac	gaa	gtg	att	cct	tgg	cca	tta	ttt	gtc	cac	tat	gcg	gca		480
Ser	Val	His	Glu	Val	Ile	Pro	Trp	Pro	Leu	Phe	Val	His	Tyr	Ala	Ala		
			145			150				155					160		
agt	aaa	ggc	ggg	atg	aag	ctg	atg	aca	gaa	aca	tta	gcg	ttg	gaa	tac		528
Ser	Lys	Gly	Gly	Met	Lys	Leu	Met	Thr	Glu	Thr	Leu	Ala	Leu	Glu	Tyr		
				165					170					175			
gcg	ccg	aag	ggc	att	cgc	gtc	aat	aat	att	ggg	cca	ggt	gcg	atc	aac		576
Ala	Pro	Lys	Gly	Ile	Arg	Val	Asn	Asn	Ile	Gly	Pro	Gly	Ala	Ile	Asn		
			180					185					190				
acg	acg	atc	aat	aag	gag	aaa	ttt	gct	gac	cct	gaa	cag	aga	gct	gat		624
Thr	Thr	Ile	Asn	Lys	Glu	Lys	Phe	Ala	Asp	Pro	Glu	Gln	Arg	Ala	Asp		
			195				200					205					
gta	gaa	agc	atg	att	cca	atg	gga	tat	atc	ggc	gaa	ccg	gag	gag	atc		672
Val	Glu	Ser	Met	Ile	Pro	Met	Gly	Tyr	Ile	Gly	Glu	Pro	Glu	Glu	Ile		
			210				215					220					
gcc	gca	gta	gca	gcc	tgg	ctt	gct	tcg	aag	gaa	gcc	agc	tac	gtc	aca		720
Ala	Ala	Val	Ala	Ala	Trp	Leu	Ala	Ser	Lys	Glu	Ala	Ser	Tyr	Val	Thr		
					230					235					240		
ggc	atc	acg	tta	ttc	gcg	gac	ggc	ggt	atg	aca	caa	tat	cct	tca	ttc		768
Gly	Ile	Thr	Leu	Phe	Ala	Asp	Gly	Gly	Met	Thr	Gln	Tyr	Pro	Ser	Phe		
				245					250						255		
cag	gca	ggc	cgc	ggt	taa	tga											789
Gln	Ala	Gly	Arg	Gly	*	*											
				260													

<210> 122

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> GDH S01024744

<400> 122

Met	Tyr	Pro	Asp	Leu	Lys	Gly	Lys	Val	Val	Ala	Ile	Thr	Gly	Ala	Ala		
1				5				10					15				
Ser	Gly	Leu	Gly	Lys	Ala	Met	Ala	Ile	Arg	Phe	Gly	Lys	Glu	Gln	Ala		
			20					25					30				

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

<210> 123

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<223> GDH S01052992

<221> CDS

<222> (1)...(789)

<400> 123

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 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1 5 10 15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca 96
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
 20 25 30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta 144
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
 35 40 45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga 192
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly

50	55	60	
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile 65 70 75 80			240
aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu 85 90 95			288
aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val 100 105 110			336
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile 115 120 125			384
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser 130 135 140			432
agt gtg cac gaa gtg att cct tgg cca tta ttt gtc cac tat gcg gca Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala 145 150 155 160			480
agt aaa ggt ggg atg aag ctg atg aca aaa aca tta gcg ttg gaa tac Ser Lys Gly Gly Met Lys Leu Met Thr Lys Thr Leu Ala Leu Glu Tyr 165 170 175			528
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aat Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn 180 185 190			576
acg acg atc aat aag gag aaa ttt gct gac cct gaa cag aga gct gat Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp 195 200 205			624
gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gat gag atc Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Asp Glu Ile 210 215 220			672
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc tgc tac gtc aca Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Cys Tyr Val Thr 225 230 235 240			720
ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe 245 250 255			768
cag gca ggc cgc ggt taa tga Gln Ala Gly Arg Gly * * 260			789

<210> 124

<211> 261

<212> PRT
<213> Artificial Sequence

<220>
<223> GDH S01052992

<400> 124
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
1 5 10 15
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
20 25 30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
35 40 45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
50 55 60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65 70 75 80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
85 90 95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
100 105 110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
115 120 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
130 135 140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145 150 155 160
Ser Lys Gly Gly Met Lys Leu Met Thr Lys Thr Leu Ala Leu Glu Tyr
165 170 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
180 185 190
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
195 200 205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Asp Glu Ile
210 215 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Cys Tyr Val Thr
225 230 235 240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
245 250 255
Gln Ala Gly Arg Gly
260

<210> 125
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> GDH S01063714

<221> CDS
<222> (1)...(789)

<400> 125
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Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Thr
1 5 10 15

48

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala 20 25 30	96
aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val 35 40 45	144
aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly 50 55 60	192
gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile 65 70 75 80	240
aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu 85 90 95	288
aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val 100 105 110	336
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile 115 120 125	384
aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser 130 135 140	432
agt gtg cac gaa gtg att cct tgg cca tta ttt gtc cac tat gcg gca Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala 145 150 155 160	480
agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr 165 170 175	528
gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn 180 185 190	576
acg acg atc aat aag gag aaa ttt gct gac cct gaa cag aga gct gat Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp 195 200 205	624
gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile 210 215 220	672
gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr 225 230 235 240	720

ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc 768
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
 245 250 255

cag gca ggc cgc ggt taa tga 789
 Gln Ala Gly Arg Gly * *
 260

<210> 126

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> GDH S01063714

<400> 126

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