DESCRIPTION

METHOD OF PRODUCING HETEROGENEOUS PROTEINS

TECHNICAL FIELD

The present invention relates to a method of producing a heterogenous protein, more specifically, a method of producing a polypeptide using a cell which strongly expresses alanine aminotransferase.

BACKGROUND ART

When proteins useful as pharmaceuticals are produced with the recombinant DNA technique, use of animal cells enables complicated post-translational modification and folding which prokaryotic cells can not perform. Therefore, animal cells are frequently used as host cells for producing recombinant proteins.

Recently, a large number of biopharmaceuticals, such as antibodies and physiologically active proteins, have been developed. Techniques that permit efficient production of recombinant proteins by animal cells lead to cost reduction of biopharmaceuticals and promise their stable supply to patients.

Under these circumstances, a method of protein production with higher production efficiency is desired.

Alanine is one of the proteinogenic amino acids, and is a non-essential amino acid. In a living body, it is biosynthesized by transfer of an amino group from glutamate to pyruvate, and is degraded by a reverse reaction.

As an alanine degrading enzyme, alanine aminotransferase (EC 2.6.1.2.) (Non-patent document 1) has been known. This enzyme transfers an amino group from alanine to 2-oxoglutarate to synthesize glutamate. Alanine aminotransferase is also called glutamic-pyruvic transaminase, which is abbreviated as GPT (Non-patent document 2). GPT and GOP (aspartate aminotransferase) are enzymes found in the liver. Since GPT and GOP are released into the blood when hepatic cells are destroyed, the liver is diagnosed to have some kind of disorder when abnormally high levels of GPT and GOT are observed.

As shown above, alanine aminotransferase is used as a marker of hepatic function. However, it has not been known how host cells such as CHO cells behave if alanine aminotransferase is strongly expressed in them.

[Non-Patent Document 1]

Sanjay B. J., et. al., Hepatology (2004) 39(5), 1297-1302

[Non-Patent Document 2]

Melanie M. S., et. al., Genomics (1997) 40, 247-252

DISCLOSURE OF THE INVENTION

PROBLEM FOR SOLUTION BY THE INVENTION

It is an object of the present invention to provide a method which is capable of producing a natural or recombinant protein in high yield.

MEANS TO SOLVE THE PROBLEM

As a result of extensive and intensive researches toward the solution of the above problem, the present inventors have found that it is possible to increase the yield of a desired polypeptide by using a cell that strongly expresses alanine aminotransferase (hereinafter sometimes referred to as "ALT"). Thus, the present invention has been achieved. Moreover, the desired polypeptide could be produced in an even greater amount by using cells capable of co-expressing ALT and a taurine transporter. Since alanine is produced in large amount over time in cell culture, alanine accumulated in cells is secreted in the medium. If the reaction of biosynthesizing pyruvate and glutamate from alanine can be promoted by strongly expressing ALT, the products are utilized in metabolism during a TCA cycle and glucose production by glycogenesis. This will improve cell culture behavior, and thus high-yield production of the desired polypeptide is anticipated.

The present invention may be summarized as follows.

(1) A method of producing a polypeptide, comprising culturing a cell which strongly expresses alanine aminotransferase and has a transferred DNA encoding a desired polypeptide and thereby allowing the cell to produce said polypeptide.

(2) The method of (1) above, wherein the cell which strongly expresses alanine aminotransferase is a cell into which a DNA encoding the alanine aminotransferase has been transferred.

(3) The production method of (1) or (2) above, wherein the cells that strongly express alanine aminotransferase further express a taurine transporter strongly.

(4) The production method of (3) above, wherein the cells that strongly express a taurine transporter are cells into which DNA encoding a taurine transporter has been transferred.

(5) The method of (2) or (4) above, wherein the cell is Chinese hamster ovary cells.

(6) The method of any one of (1) to (5) above, wherein the desired polypeptide is an antibody.

(7) The method of any one of (2) to (6) above, wherein the DNA encoding the alanine aminotransferase is any one of the following (a) to (e):

(a) a DNA encoding a polypeptide having the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60;

(b) a DNA encoding a polypeptide which has an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60 by substitution, deletion, addition and/or insertion of one or more amino acid residues and yet has alanine aminotransferase activity;

(c) a DNA encoding a polypeptide having 70% or more amino acid sequence homology with the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60 and yet having alanine aminotransferase activity;

(d) a DNA having the nucleotide sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59;

(e) a DNA which hybridizes to a DNA complementary to a DNA having the nucleotide sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59 under stringent conditions and yet encodes a polypeptide having alanine aminotransferase activity.

(8) A method of preparing a pharmaceutical containing a polypeptide prepared by the method of any one of (1) to (7) above.

(9) A cell which has a transferred DNA encoding alanine aminotransferase and a transferred DNA encoding a desired polypeptide.

(10) The cell according to (9) above, which further has a transferred DNA encoding a taurine transporter.

(11) A cell which has a transferred DNA encoding alanine aminotransferase and a transferred DNA encoding a taurine transporter.

(12) A method of producing a polypeptide, comprising culturing in an α-ketoglutarate-containing medium a cell which strongly expresses alanine aminotransferase and has a transferred DNA encoding a desired polypeptide and thereby allowing the cell to produce said polypeptide.

EFFECT OF THE INVENTION

According to the present invention, it has become possible to increase the yield of a desired polypeptide.

The present specification encompasses the contents disclosed in the specification and/or the drawings of Japanese Patent Application No. 2007-205158 based on which the present patent application claims priority.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows a plasmid for Puromycin selection which was used for expressing human ALT1 (496 amino acids).

Fig. 2 shows a plasmid for Hygromycin selection which was used for expressing human ALT1 (496 amino acids).

Fig. 3 shows anti-glypican-3 antibody yield plots on day 17 of 50 ml shaker flask fed-batch culture. The antibody yield in pPur-ALT1-transferred cell (n=4) was superior to that in pPur-transferred cell (n=3) ($P<0.01$).

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Fig. 4 is a graph showing the antibody yields of A72, which is an ALT1 expressing strain, and P41 as a control strain, in 1 L jar fed-batch culture. The anti-glypican-3 antibody yield of A72 was 2.9 g/L on day 19 of the culture, which was higher than that of P41.

Fig. 5 is a graph showing the survival ratios of A72, which is an ALT1 expressing strain, and P41 as a control strain. The survival ratio of A72 at the late stage of the culture was higher than that of P41.

Fig. 6 shows anti-glypican-3 antibody yield plots on day 4 of 50 ml shaker flask fed-batch culture. The antibody yield in pHyg-TauT/pPur-ALT1-cotransferred cell (n=6) was superior to that in pHyg-TauT/pPur-cotransferred cell (n=8) ($P<0.01$).

Fig. 7 is a graph showing the antibody yield of TA41, which is a TauT/ALT1 co-expressing strain, in 1 L jar fed-batch culture. The anti-glypican-3 antibody yield was 5.3 g/L on day 21 of the culture.

Fig. 8 shows the nucleotide sequence of a newly cloned, CHO cell-derived hamster taurine transporter gene and the amino acid sequence deduced therefrom.

Fig. 9 is a taurine transporter membrane topology of a newly cloned, CHO cell-derived TauT.

Fig. 10 shows a plasmid which was used for expressing hamster TauT (622 amino acids).

Fig. 11 shows viable cell density plots on day 7 of 50 ml shaker flask batch culture. The viable cell density in pHyg/TauT-transferred cell was superior to that in pHyg-transferred cell.

Fig. 12 shows lactate yield plots on day 7 of 50 ml shaker flask batch culture. pHyg/TauT-transferred cell produced less lactate, and was superior to pHyg-transferred cell.

Fig. 13 shows anti-glypican-3 antibody yield plots on day 7 of 50 ml shaker flask batch culture. Four out of the 7 strains of pHyg/TauT-transferred cell showed antibody yields higher than the highest yield in pHyg-transferred cell.

Fig. 14 shows anti-glypican-3 antibody yield plots on day 7 of 50 ml shaker flask fed-batch culture. The antibody yield in pHyg/TauT-transferred cell was superior to that in pHyg-transferred cell.

Fig. 15 is a graph showing the survival ratio of a pHyg/TauT-transferred cell T10 (which showed high growth ability) in 1 L jar fed-batch culture. The survival ratio of T10 was 80% or more even on day 32 of the culture.

Fig. 16 is a graph showing the antibody yield of a pHyg/TauT-transferred cell T10 (which showed high growth ability during the expansion process in static culture) in 1 L jar fed-batch culture. The anti-glypican-3 antibody yield of T10 was 2.9 g/L on day 35 of the culture.

Fig. 17 shows the results of flow cytometric analysis indicating that TauT-transferred T10 cell is expressing TauT molecules on its cell membrane.

Fig. 18 is a graph showing intracellular ammonia contents (concentration ratios) in 1 L jar fed-batch culture. The ammonia inhibition in pHyg/TauT-transferred strains was remarkable compared to the parent strain.

Fig. 19 is a graph showing that taurine is taken into cells depending on the taurine concentration in the medium. No difference was observed in taurine uptake between pHyg/TauT-transferred strains and the parent strain.

Fig. 20 is a graph showing the consumption of glutamine in the medium. Compared to the parent strain, pHyg/TauT-transferred strains showed a remarkably high glutamine consumption/cell without depending on the taurine concentration in the medium.

Fig. 21 is a graph showing that the anti-glypican-3 antibody yields of pHyg/TauT-transferred strains are almost equal without depending on the initial taurine concentration in the medium.

Fig. 22 shows the anti-glypican-3 antibody yield of TA41, a TauT/ALT co-expressing strain, on day 14 of fed-batch culture in a shaker. The antibody yield was increased by addition of α-ketoglutarate.

BEST MODE FOR CARRYING OUT THE INVENTION

Hereinbelow, embodiments of the present invention will be described in more detail.

The present invention provides a method of producing a polypeptide, comprising culturing a cell which strongly expresses ALT and has a transferred DNA encoding a desired polypeptide and thereby allowing the cell to produce the polypeptide.

In the method of the present invention, the cell may be either a natural cell capable of producing the desired polypeptide or a transformed cell into which a DNA encoding the desired polypeptide has been transferred. Preferably, a transformed cell into which a DNA encoding the desired polypeptide has been transferred is used.

In the method of the present invention, the desired polypeptide is not particularly limited. The polypeptide may be any polypeptide such as an antibody (e.g., anti-IL-6 receptor antibody, anti-IL-6 antibody, anti-glypican-3 antibody, anti-CD3 antibody, anti-CD20 antibody, anti-GPIIb/IIIa antibody, anti-TNF antibody, anti-CD25 antibody, anti-EGFR antibody, anti-Her2/neu antibody, anti-RSV antibody, anti-CD33 antibody, anti-CD52 antibody, anti-IgE antibody, anti-CD11a antibody, anti-VEGF antibody, anti-VLA4 antibody, and the like) or a physiologically active protein (e.g., granulocyte-colony stimulating factor (G-CSF), granulocyte macrophage-colony stimulating factor (GM-CSF), erythropoietin, interferon, interleukin such as IL-1 or IL-6, t-PA, urokinase, serum albumin, blood coagulation factor, PTH, and the like). An antibody is particularly preferred, and may be any antibody such as a natural antibody, a low molecular sized antibody (e.g., Fab, scFv, sc(Fv)2), a chimeric antibody, a humanized antibody, etc.

By using strongly ALT expressing cells, the amount of a polypeptide produced by cells can be increased.

ALT is fundamentally known as an enzyme that produces glutamate by transferring an amino group from alanine to 2-oxoglutarate. The present inventors considered that if the reaction of biosynthesizing pyruvate and glutamate from alanine could be promoted by strongly expressing ALT in host cells such as CHO cells, the products might be utilized in metabolism during a TCA cycle and glucose production by glycogenesis, and this might improve cell culture behavior, leading to high-yield production of the desired polypeptide.

The strongly ALT expressing cells are not particularly limited as long as they are capable of ALT expression at higher levels than natural cells. Natural cells include, but are not particularly limited to, cells that are used as hosts in the production of recombinant proteins and may be exemplified by CHO cells.

A cell which strongly expresses ALT is not particularly limited as long as the cell

has an increased expression level of ALT compared to a corresponding natural cell. The natural cell is not particularly limited. A cell which is used as a host in the production of a recombinant protein (e.g., CHO cells) may be used.

As a cell which strongly expresses ALT, a cell into which an ALT gene has been artificially transferred may be given. A cell into which an ALT gene has been artificially transferred can be prepared by methods known to those skilled in the art. For example, such a cell may be prepared by incorporating an ALT gene into a vector and transforming the vector into a cell. Furthermore, the concept of "cells into which an ALT gene has been artificially transferred" encompasses herein cells in which an endogenous ALT gene has been activated by gene activation technology (see, for example, International Publication WO94/12650) so that ALT is strongly expressed.

As ALT to be strongly expressed in a cell, ALT derived from any organism may be used. Specifically, ALTs derived from human, mouse, rat, dog, African clawed frog, fruit fly, nematode, Japanese rice, Cyanidioschyzon merolae, Saccharomyces cerevisiae, Ashbya gossypii, Candida albicans, Schizosaccharomyces pombe, Aspergillus nidulans, Aspergillus fumigatus, Aspergillus oryzae, Cryptococcus neoformans, Dictyostelium discoideum, Trypanosoma brucei, Leishmania major, Entamoeba histolytica and Trypanosoma cruzi are known and can be used. Preferably, ALT derived from human, a rodent or the same species as the host cell may be used. For example, when the cell which is allowed to strongly express ALT is Chinese hamster ovary cells (CHO cells), ALT is preferably derived from human or hamster. For ALT in humans, mice, and yeast, variants (ALT1 and ALT2) exist. ALT2 has 80% or greater homology to ALT1 at the amino acid level. ALT1 was forcedly expressed in the Examples described later.

Further, as an ALT gene to be strongly expressed in a cell, any one of the following DNAs (a) to (e) encoding ALT may be used.

(a) a DNA encoding a polypeptide having the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60;

(b) a DNA encoding a polypeptide which has an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60 by substitution, deletion, addition and/or insertion of one or more amino acid residues and yet has alanine aminotransferase activity;

(c) a DNA encoding a polypeptide having 70% or more amino acid sequence homology with the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16,

18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60 and yet having alanine aminotransferase activity;

(d) a DNA having the nucleotide sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59;

(e) a DNA which hybridizes to a DNA complementary to a DNA having the nucleotide sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59 under stringent conditions and yet encodes a polypeptide having alanine aminotransferase activity.

The cell which strongly expresses ALT may be any cell, for example, eukaryotic cell such as animal, plant and yeast cells, prokaryotic cell such as *E. coli* and B. subtilis, etc. Preferably, animal cells such as CHO and COS cells are used, CHO cells are particularly preferred. In order to prepare a desired polypeptide, cells suitable for transfer of a gene encoding the desired polypeptide such as CHO-dhfr- cells are preferred.

Preferably, the cell of the present invention which strongly expresses ALT further expresses a taurine transporter strongly in order to prepare a desired polypeptide. By transferring a gene encoding the desired polypeptide into the cell and culturing the resultant cell in a medium, the desired polypeptide can be produced in a greater amount.

When a desired polypeptide is produced using a cell into which an ALT gene has been artificially transferred, the order of the transfer of an ALT gene and the transfer of a gene encoding a desired polypeptide is not particularly limited. A gene encoding a desired polypeptide may be transferred after the transfer of an ALT gene. Alternatively, an ALT gene may be transferred after the transfer of a gene encoding a desired polypeptide. It is also possible to transfer an ALT gene and a gene encoding a desired polypeptide simultaneously.

An ALT gene and a gene encoding a desired polypeptide may be transferred simultaneously in a single vector. Alternatively, they may be transferred separately using a plurality of vectors.

By using a cell which strongly expresses ALT and a taurine transporter, an intracellular ammonia concentration can decline.

It is known that taurine transporter is a membrane protein having the osmoregulatory function of taking up amino acids (such as taurine and β-alanine) into cells.

A cell which strongly expresses a taurine transporter is not particularly limited as long as the cell has an increased expression level of a taurine transporter compared to a corresponding natural cell. The natural cell is not particularly limited. A cell which is

used as a host in the production of a recombinant protein (e.g., CHO cells) may be used.

As a cell which strongly expresses a taurine transporter, a cell into which a taurine transporter gene has been artificially transferred may be given. A cell into which a taurine transporter gene has been artificially transferred can be prepared by methods known to those skilled in the art. For example, such a cell may be prepared by incorporating a taurine transporter gene into a vector and transforming the vector into a cell.

As a taurine transporter to be strongly expressed in a cell, a taurine transporter derived from any organism may be used. Specifically, a taurine transporter derived from human or a rodent (such as mouse, rat or hamster) may be used. Preferably, a taurine transporter derived from human, a rodent or the same species as the host cell may be used. For example, when the cell which is allowed to strongly express a taurine transporter is Chinese hamster ovary cells (CHO cells), the taurine transporter is preferably derived from human or hamster.

Further, as a taurine transporter gene to be strongly expressed in a cell, any one of the following DNAs (a_1) to (e_1) encoding a taurine transporter may be used.

(a_1) a DNA encoding a polypeptide having the amino acid sequence as shown in SEQ ID NO: 62, 64, 66 or 68;

(b_1) a DNA encoding a polypeptide which has an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 62, 64, 66 or 68 by substitution, deletion, addition and/or insertion of one or more amino acid residues and yet has taurine transporter activity;

(c_1) a DNA encoding a polypeptide having 70% or more amino acid sequence homology with the amino acid sequence as shown in SEQ ID NO: 62, 64, 66 or 68 and yet having taurine transporter activity;

(d_1) a DNA having the nucleotide sequence as shown in SEQ ID NO: 61, 63, 65 or 67;

(e_1) a DNA which hybridizes to a DNA complementary to a DNA having the nucleotide sequence as shown in SEQ ID NO: 61, 63, 65 or 67 under stringent conditions and yet encodes a polypeptide having taurine transporter activity.

Production of a desired polypeptide may be performed by transferring a gene encoding the desired polypeptide into a cell which strongly expresses a taurine transporter gene and an ALT gene and culturing the resultant cell in a medium. Furthermore, a desired polypeptide can be prepared by using a cell in which an endogenous gene has been activated by gene activation technology (see, for example, International Publication WO94/12650) so that a desired polypeptide has been produced.

When a desired polypeptide is produced using a cell into which a taurine

transporter gene and an ALT gene have been artificially transferred, the order of the transfer of a taurine transporter gene, the transfer of an ALT gene and the transfer of a gene encoding a desired polypeptide is not particularly limited. A gene encoding a desired polypeptide may be transferred after the transfer of a taurine transporter gene and an ALT gene. Alternatively, a taurine transporter gene and an ALT gene may be transferred after the transfer of a gene encoding a desired polypeptide. It is also possible to transfer a taurine transporter gene, an ALT gene and a gene encoding a desired polypeptide simultaneously.

A taurine transporter gene, an ALT gene and a gene encoding a desired polypeptide may be transferred simultaneously in a single vector. Alternatively, they may be transferred separately using a plurality of vectors.

For culturing the cell which strongly expresses ALT (and which may strongly express a taurine transporter), media used in conventional cell culture (preferably, animal cell culture) may be used. These media usually contain amino acids, vitamins, lipid factors, energy sources, osmotic regulators, iron sources and pH regulators. The contents of these components are usually as follows: amino acids 0.05-1500 mg/L, vitamins 0.001-10 mg/L, lipid factors 0-200 mg/L, energy sources 1-20 g/L, osmotic regulators 0.1-10000 mg/L, iron sources 0.1-500 mg/L, pH regulators 1-10000 mg/L, trace metal elements 0.00001-200 mg/L, surfactants 0-5000 mg/L, growth cofactors 0.05-10000 μg/L and nucleosides 0.001-50 mg/L. However, the contents are not limited to these ranges and may be appropriately selected depending on the type of the cell to be cultured, the type of the desired polypeptide, and so on.

In addition to these components, trace metal elements, surfactants, growth cofactors, nucleosides, and the like may be added.

Specific examples of such components include amino acids, such as L-alanine, L-arginine, L-asparagine, L-aspartic acid, L-cysteine, L-cystine, L-glutamine, L-glutamic acid, glycine, L-histidine, L-isoleucine, L-leucine, L-lysine, L-methionine, L-ornithine, L-phenylalanine, L-proline, L-serine, L-threonine, L-tryptophan, L-tyrosine, and L-valine, preferably, L-alanine, L-arginine, L-asparagine, L-aspartic acid, L-cystine, L-glutamine, L-glutamic acid, glycine, L-histidine, L-isoleucine, L-leucine, L-lysine, L-methionine, L-phenylalanine, L-proline, L-serine, L-threonine, L-tryptophan, L-tyrosine and L-valine; vitamins, such as i-inositol, biotin, folic acid, lipoic acid, nicotinamide, nicotinic acid, p-aminobenzoic acid, calcium pantothenate, pyridoxal hydrochloride, pyridoxine hydrochloride, riboflavin, thiamine hydrochloride, vitamin B_{12} and ascorbic acid, preferably, biotin, folic acid, lipoic acid, nicotinamide, calcium pantothenate, pyridoxal hydrochloride, riboflavin, thiamine hydrochloride, vitamin B_{12} and ascorbic acid; lipid factors, such as

choline chloride, choline tartrate, linoleic acid, oleic acid and cholesterol, preferably, choline chloride; energy sources, such as glucose, galactose, mannose, and fructose, preferably, glucose; osmotic regulators, such as sodium chloride, potassium chloride, and potassium nitrate, preferably, sodium chloride; iron sources, such as iron EDTA, ferric citrate, ferrous chloride, ferric chloride, ferrous sulfate, ferric sulfate, and ferric nitrate, preferably, ferric chloride, iron EDTA, and ferric citrate; and pH regulators, such as sodium hydrogencarbonate, calcium chloride, sodium dihydrogen-phosphate, HEPES and MOPS, preferably, sodium hydrogencarbonate. Culture media containing any of these components may be given as examples.

Besides the above components, there may be added trace metal elements, such as copper sulfate, manganese sulfate, zinc sulfate, magnesium sulfate, nickel chloride, tin chloride, magnesium chloride and sodium subsilicate, preferably, copper sulfate, zinc sulfate and magnesium sulfate; surfactants, such as Tween 80 and Pluronic F68; growth cofactors, such as recombinant insulin, recombinant IGF-1, recombinant EGF, recombinant FGF, recombinant PDGF, recombinant TGF-α, ethanolamine hydrochloride, sodium selenite, retinoic acid and putrescine dihydrochloride, preferably, sodium selenite, ethanolamine hydrochloride, recombinant IGF-1 and putrescine dihydrochloride; and nucleosides, such as deoxyadenosine, deoxycytidine, deoxyguanosine, adenosine, cytidine, guanosine and uridine. In preferable examples of above media, antibiotics, such as streptomycin, penicillin-G potassium and gentamicin, and pH-indicators, such as Phenol Red, may be contained.

Further, α-ketoglutarate, serving as a substrate for ALT, can be added to the medium. The yield of the desired polypeptide (for example, an antibody) can be increased by addition of α-ketoglutarate. In this case, the amount of α-ketoglutarate to be added is normally in the range of 0.01 to 1000 mM, preferably 0.1 to 100 mM, and more preferably 1 to 10 mM.

The pH of the medium varies depending on the cell to be cultured. Generally, pH 6.8-7.6 is appropriate. In many cases, pH 7.0-7.4 is appropriate.

It is also possible to use a commercial medum for animal cell culture, e.g., D-MEM (Dulbecco's Modified Eagle Medium), D-MEM/F-12 1:1 Mixture (Dulbecco's Modified Eagle Medium: Nutrient Mixture F-12), RPMI1640, CHO-S-SFMII (Invitrogen), CHO-SF (Sigma-Aldrich), EX-CELL 301 (JRH Biosciences), CD-CHO (Invitrogen), IS CHO-V (Irvine Scientific), PF-ACF-CHO (Sigma-Aldrich) or the like.

Alternatively, the medium may be a serum-free medium such as CD-CHO (Invitrogen).

When the cell which strongly expresses ALT (and which may strongly express a

taurine transporter) is CHO cells, CHO cells may be cultured by methods known to those skilled in the art. For example, CHO cells may be cultured usually in an atmosphere with a CO_2 concentration in the gas phase of 0 to 40%, preferably 2 to 10%, at 30 to 39°C, preferably about 37°C.

Moreover, in the case where the desired polypeptide such as an antibody is produced by cell culture, cells become highly confluent at the late stage of the culture (approximately 1×10^7 cells/ml), and the effect of waste products such as lactate becomes extremely high. If the desired polypeptide is produced by strongly ALT expressing cells, a high survival ratio is maintained even at the late stage of the culture, and an improvement in the yield of the desired polypeptide can also be anticipated.

An appropriate culture period for producing a desired polypeptide using the cell which strongly expresses ALT is usually 1 day to 3 months, preferably 1 day to 2 months, more preferably 1 day to 1 month.

With respect to various culture devices for animal cell culture, a fermentor type tank culture device, an air lift type culture device, a culture flask type culture device, a spinner flask type culture device, a microcarrier type culture device, a fluidized bed type culture device, a hollow fiber type culture device, a roller bottle type culture device, a packed bed type culture device, or the like may be used.

Culture may be performed by any culture method such as batch culture, fed-batch culture or continuous culture. Preferably, fed-batch culture or continuous culture is used. Fed-batch culture is more preferred.

When the cell which strongly expresses ALT (and which may strongly express a taurine transporter) is cultured, taurine may be added to the medium in order to promote taurine uptake into cells. The concentration of taurine to be added to the medium is not specifically limited, but is normally in the range of 0 g/L to 100 g/L, preferably 0 g/L to 20 g/L, and more preferably 0 g/L to 10 g/L.

When the polypeptide produced according to the method of the present invention has a biological activity useful as a pharmaceutical, it is possible to produce a pharmaceutical by mixing this polypeptide with pharmaceutically acceptable carriers or additives and formulating into a preparation.

Specific examples of pharmaceutically acceptable carriers and additives include water, organic solvents that are pharmaceutically acceptable, collagen, polyvinyl alcohol, polyvinylpyrrolidone, carboxyvinyl polymer, carboxymethylcellulose sodium, sodium polyacrylate, sodium alginate, water-soluble dextran, carboxymethyl starch sodium, pectin, methylcellulose, ethyl cellulose, xanthan gum, gum Arabic, casein, agar-agar, polyethylene

glycol, diglycerin, glycerin, propylene glycol, petrolatum, paraffin, stearyl alcohol, stearic acid, human serum albumin (HSA), mannitol, sorbitol, lactose, and surfactants that are acceptable as pharmaceutical additives.

Actual additives may be selected from the above-mentioned additives singly or in combination according to the dosage form of the therapeutic of the present invention, but are not limited to those listed above. For example, when a polypeptide is used in an injectable formulation, the purified polypeptide may be dissolved in a solvent such as physiological saline, buffer or a glucose solution, and then an adsorption inhibitor such as Tween 80, Tween 20, gelatin or human serum albumin may be added to the solution. Alternatively, a freeze-dried agent may be used to prepare a dosage form which is dissolved and reconstituted prior to use. Examples of the excipient useful for freeze-drying include sugar alcohols and saccharides such as mannitol and glucose.

Effective doses of the polypeptide may be appropriately selected depending on the type of the polypeptide, the type of the disease to be treated or prevented, the age of the patient, the severity of the disease, etc. For example, when the polypeptide is anti-glypican antibody, the effective dose of anti-glypican antibody is selected within a range of 0.001 mg to 1000 mg per kg of body weight per administration. Alternatively, a dose of 0.01-100000 mg/body may be selected per patient. However, effective dose is not limited to these ranges.

The polypeptide may be administered either orally or parenterally, but parenteral administration is preferred. Specifically, injection (e.g., systemic or local administration by intravenous injection, intramuscular injection, intraperitoneal injection, subcutaneous injection, etc.), transnasal administration, transpulmonary administration, transdermal administration and the like may be enumerated.

In the present invention, as a gene encoding ALT, a DNA encoding a polypeptide having the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60 may be used. Alternatively, a DNA encoding a polypeptide which has an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60 by substitution, deletion, addition and/or insertion of one or more amino acid residues and yet has alanine aminotransferase activity may be used.

The polypeptide which has an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60 by substitution, deletion, addition and/or

insertion of one or more amino acid residues and yet has alanine aminotransferase activity is functionally equivalent to ALT derived from human, mouse, rat, dog, African clawed frog, fruit fly, nematode, Japanese rice, Cyanidioschyzon merolae, Saccharomyces cerevisiae, Ashbya gossypii, Candida albicans, Schizosaccharomyces pombe, Aspergillus nidulans, Aspergillus fumigatus, Aspergillus oryzae, Cryptococcus neoformans, Dictyostelium discoideum, Trypanosoma brucei, Leishmania major, Entamoeba histolytica or Trypanosoma cruzi (hereinafter sometimes referred to as "ALT derived from human or the like"). Such a polypeptide encompasses, for example, mutants of ALT derived from human or the like. In Example described below, a mutant in which four out of 496 amino acids were replaced (R53S, Q72R, F286S and M332K) was used.

As methods well-known to those skilled in the art for preparing polypeptides functionally equivalent to a specific polypeptide, methods of introducing mutations into polypeptides may be given. For example, those skilled in the art could prepare polypeptides functionally equivalent to ALT derived from human or the like by appropriately introducing mutations into amino acids of ALT derived from human or the like by site-directed mutagenesis (Hashimoto-Gotoh, T. et al. (1995) Gene 152, 271-275; Zoller, MJ, and Smith, M.(1983) Methods Enzymol. 100, 468-500; Kramer, W. et al. (1984) Nucleic Acids Res. 12, 9441-9456; Kramer W, and Fritz HJ (1987) Methods. Enzymol. 154, 350-367; Kunkel, TA (1985) Proc Natl Acad Sci USA. 82, 488-492; Kunkel (1988) Methods Enzymol. 85, 2763-2766). Mutations in amino acids may also occur in nature.

Specific examples of polypeptides functionally equivalent to the ALT derived from human or the like include, but are not limited to, a polypeptide having an amino acid sequence derived from the amino acid sequence (e.g., SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60) of the ALT derived from human or the like by deletion of one or more amino acids, preferably 1-30 amino acids, more preferably 1-10 amino acids; a polypeptide having an amino acid sequence derived from the amino acid sequence of the ALT derived from human or the like by addition of one or more amino acids, preferably 1-30 amino acids, more preferably 1-10 amino acids; and a polypeptide having an amino acid sequence derived from the amino acid sequence of the ALT derived from human or the like by substitution of one or more amino acids, preferably 1-30 amino acids, more preferably 1-10 amino acids, with other amino acids.

Amino acid residues to be mutated are not particularly limited. Preferably, amino acid residues are mutated to other amino acids in which the nature of the initial amino acid side chain is conserved. Specific examples of the nature of amino acid side chain include

hydrophobic amino acids (A, I, L, M, F, P, W, Y and V), hydrophilic amino acids (R, D, N, C, E, Q, G, H, K, S and T), amino acids with an aliphatic side chain (G, A, V, L, I and P), amino acids with a hydroxyl group-containing side chain (S, T and Y), amino acids with a sulfur atom-containing side chain (C and M), amino acids with a carboxylic acid and amide-containing side chain (D, N, E and Q), amino acids with a base-containing side chain (R, K and H) and amino acids with an aromatic-containing side chain (H, F, Y and W) (In parentheses are one-letter codes for amino acids).

It has been reported that a polypeptide having an amino acid sequence derived from an original amino acid sequence by modification (such as deletion, addition and/or substitution of one or more amino acids) maintains the biological activity of the original polypeptide (Mark, D. F. et al., Proc. Natl. Acad. Sci. USA (1984) 81, 5662-5666; Zoller, M. J. & Smith, M. Nucleic Acids Research (1982) 10, 6487-6500; Wang, A. et al., Science 224, 1431-1433; Dalbadie-McFarland, G et al., Proc. Natl. Acad. Sci. USA (1982) 79, 6409-6413).

As one example of the polypeptide in which one or more amino acid residues are added to the ALT derived from human or the like, a fusion polypeptide comprising the ALT derived from human or the like may be given. Such a fusion polypeptide is composed of the ALT derived from human or the like and other polypeptide fused thereto. Such a fusion polypeptide may be prepared by linking a gene encoding the ALT derived from human or the like in frame with a gene encoding the other polypeptide, transferring the resultant DNA into an expression vector and expressing the DNA in a host cell. Techniques known to those skilled in the art may be used. There is no limitation on the polypeptide to be fused to the ALT derived from human or the like.

Examples of polypeptides to be fused to the ALT derived from human or the like include, but are not limited to, FLAG (Hopp, T. P. et al., BioTechnology (1988) 6, 1204-1210), 6xHis comprising six histidine (His) residues, 10xHis, influenza hemagglutinin (HA), human c-myc fragment, VSV-GP fragment, p18HIV fragment, T7-tag, HSV-tag, E-tag, SV40T antigen fragment, lck tag, α-tubulin fragment, B-tag, protein C fragment, glutathione-S-transferase (GST), influenza hemagglutinin (HA), immunoglobulin constant region, β-galactosidase and maltose-binding protein (MBP).

A commercially available gene encoding such polypeptide is fused to the gene encoding the ALT derived from human or the like. The fused gene thus prepared is expressed to prepare a fused polypeptide.

An alternative method known to those skilled in the art for preparing polypeptides functionally equivalent to a specific polypeptide is a method using the hybridization

technique (Sambrook, J et al., Molecular Cloning 2nd ed., 9.47-9.58, Cold Spring Harbor Lab. Press, 1989). Those skilled in the art could routinely isolate a DNA highly homologous to the DNA sequence (e.g., SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59) of the ALT derived from human or the like based on that DNA sequence or a part thereof, and isolate polypeptides functionally equivalent to the ALT derived from human or the like from that DNA.

Hybridization conditions for isolating a DNA encoding a polypeptide functionally equivalent to the ALT derived from human or the like can be appropriately selected by those skilled in the art. For example, low stringent hybridization conditions may be given. Low stringent hybridization conditions are, for example, 42°C, 2 x SSC and 0.1% SDS, preferably 50°C, 2 x SSC and 0.1% SDS. More preferably, high stringent conditions may be given. For example, high stringent conditions are 65°C, 2 x SSC and 0.1% SDS. Under these conditions, as the hybridization temperature is lowered, not only DNAs with high homology but also DNAs with only low homology are obtained. Conversely, it is expected that only those DNAs with high homology are obtained as the hybridization temperature is elevated. However, not only the temperature but also a plurality of factors (such as salt concentrations) affect the stringency of hybridization. Those skilled in the art could appropriately select these factors to realize similar stringency.

The polypeptide encoded by a DNA isolated by these hybridization techniques may have 70% or more homology and usually has high homology with the ALT derived from human or the like in the amino acid sequence. The term "high homology" refers to usually 97% or more homology, preferably 98% or more homology, more preferably 99% or more homology. For determination of the homology of polypeptides, the algorithm described in Wilbur, W. J. and Lipman, D. J., Proc. Natl. Acad. Sci. USA (1983) 80, 726-730 may be followed.

The polypeptide may vary in amino acid sequence, molecular weight, isoelectric point, presence or absence of sugar chains, morphology, etc. depending on the cell or host that produce the polypeptide or the purification method that will be described later. However, as long as the resultant polypeptide has functions equivalent to the functions of the ALT derived from human or the like, DNA encoding the polypeptide can be used in the present invention. For example, when the polypeptide of the present invention is expressed in a prokaryote (e.g., *Escherichia coli*), a methionine reside is added to the N-terminus of the initial amino acid sequence of the polypeptide. When the polypeptide is expressed in a eukaryote (e.g., a mammalian cell), the N-terminal signal sequence is removed. These

polypeptides can be used in the present invention.

The polypeptide may be prepared as a recombinant polypeptide or a natural polypeptide by methods known to those skilled in the art. A recombinant polypeptide may be prepared by incorporating a DNA encoding the polypeptide in an appropriate expression vector, introducing the vector into an appropriate host cell, collecting the resultant transformant, extracting a crude polypeptide, and then purifying the polypeptide by chromatography (such as ion exchange, reversed phase or gel filtration chromatography, or affinity chromatography in which an antibody to the polypeptide prepared by the method of the present invention is fixed in a column) or a combination of these chromatographic techniques.

When the polypeptide is expressed in a host cell (e.g., animal cell or *E. coli*) as a fusion polypeptide with glutathione-S-transferase polypeptide or as a recombinant polypeptide with histidine residues added thereto, the expressed polypeptide may be purified with a glutathione column or a nickel column.

After purification of a fusion polypeptide, regions other than the polypeptide of interest may be cut off by thrombin or factor Xa and removed from the fusion polypeptide.

When the polypeptide is a natural polypeptide, the polypeptide may be isolated by purification methods known to those skilled in the art. For example, an extract from tissues or cells expressing the polypeptide functionally equivalent to the ALT derived from human or the like may be applied to an affinity column to which an antibody to the ALT derived from human or the like is bound. The antibody may be either a polyclonal antibody or a monoclonal antibody.

In the present invention, as DNA encoding ALT, a DNA having the nucleotide sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59 may be used. Alternatively, a DNA which hybridizes to a DNA complementary to a DNA having the nucleotide sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59 under stringent conditions and yet encodes a polypeptide having alanine aminotransferase activity, may be used.

The DNA encoding ALT can be used in the *in vivo* or *in vitro* production of a desired polypeptide as described above. Further, the DNA encoding ALT may be used in the creation of a cell which strongly expresses ALT. The DNA encoding ALT may take any form as long as it is capable of encoding ALT. That is, the DNA may be, for example, a cDNA synthesized from mRNA, a genomic DNA or a chemically synthesized DNA. It should be noted that, as long as the DNA is capable of encoding ALT, the DNA may have

any nucleotide sequence based on the degeneracy of genetic codes.

The DNA encoding ALT may be prepared by methods known to those skilled in the art. For example, the DNA may be prepared by preparing a cDNA library from a cell expressing ALT and performing hybridization using a part of the DNA sequence of ALT (e.g., SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59) as a probe. The cDNA library may be prepared, for example, by the method described in Sambrook, J. et al., Molecular Cloning, Cold Spring Harbor Laboratory Press (1989). Alternatively, a commercial cDNA library may be used. It is also possible to prepare the DNA encoding ALT by preparing RNA from a cell expressing ALT, synthesizing oligo DNA molecules based on the DNA sequence of ALT (e.g., SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59), and performing PCR using the oligo DNA molecules as primers to thereby amplify a cDNA encoding ALT.

Further, by determining the nucleotide sequence of the resultant cDNA, it is possible to determine the translation region encoding ALT and to obtain the amino acid sequence of ALT. Further, by screening a genomic library using the resultant cDNA as a probe, it is possible to isolate a genomic DNA.

Specifically, the following procedures may be used. First, mRNA is isolated from cells, tissues or the like expressing ALT. For the isolation of mRNA, the total RNA is prepared by known methods, for example, the guanidine ultracentrifugation method (Chirgwin, J. M. et al., Biochemistry (1979) 18, 5294-5299), the AGPC method (Chomczynski, P. and Sacchi, N., Anal. Biochem. (1987) 162, 156-159) or the like, and then mRNA is purified from the total RNA using mRNA Purification Kit (Pharmacia), etc. Alternatively, mRNA may be prepared directly using QuickPrep mRNA Purification Kit (Pharmacia).

From the resultant mRNA, cDNA is synthesized using a reverse transcriptase. Alternatively, cDNA may be synthesized using a kit such as AMV Reverse Transcriptase First-Strand cDNA Synthesis Kit (SEIKAGAKU CORPORATION). It is also possible to synthesize and amplify cDNA according to the 5'-RACE method (Frohman, M. A. et al., Proc. Natl. Acad. Sci. USA (1988) 85, 8998-9002; Belyavsky, A. et al., Nucleic Acids Res. (1989) 17, 2919-2932) using 5'-Ampli FINDER RACE Kit (Clontech) and polymerase chain reaction (PCR) with primers.

A DNA fragment of interest is prepared from the resultant PCR product and ligated to a vector DNA to thereby prepare a recombinant vector. The vector is introduced into a host (e.g., *E. coli*), followed by selection of resultant colonies to thereby obtain a desired

recombinant vector. The nucleotide sequence of the DNA of interest may be confirmed by a known method such as the dideoxynucleotide chain termination method.

Further, a nucleotide sequence of higher expression efficiency can be designed for the DNA encoding ALT by considering the frequency of codon usage in the host to be used for expression (Grantham, R. et al., Nucleic Acids Research (1981) 9, p. 43-74). Further, the DNA encoding ALT can be modified using commercially available kits or known methods. Examples of such modifications include, but are not limited to, digestion with restriction enzymes, insertion of synthetic oligonucleotides or appropriate DNA fragments, addition of linkers, and insertion of an initiation codon (ATG) and/or a termination codon (TAA, TGA or TAG).

The DNA encoding ALT also includes a DNA which hybridizes to a DNA having the nucleotide sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59 under stringent conditions and encodes a polypeptide functionally equivalent to ALT.

Stringent conditions can be appropriately selected by those skilled in the art, including, for example, low stringent conditions. Low stringent conditions refer to, for example, 42° C, 2 x SSC and 0.1% SDS, preferably 50° C, 2 x SSC and 0.1% SDS. More preferably, high stringent conditions may be selected. High stringent conditions refer to, for example, 65° C, 2 x SSC and 0.1% SDS. Under these conditions, as the hybridization temperature is elevated, DNAs with a higher homology can be obtained. The above-described DNA which hybridizes is preferably a DNA derived from nature, e.g., cDNA or chromosomal DNA.

These DNAs isolated by hybridization techniques usually have a high nucleotide sequence identity with a DNA encoding the ALT derived from human or the like. The DNA encoding ALT also includes a DNA which encodes a polypeptide functionally equivalent to the ALT derived from human or the like and has high identity with a DNA encoding the ALT derived from human or the like. The term "high identity" refers to usually 96% or more homology, preferably 98% or more homology, more preferably 99% or more identity. The identity of nucleotide sequences may be determined by algorithm BLAST (Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Based on this algorithm, programs such as BLASTN and BLASTX have been developed (Altschul et al. J. Mol. Biol. 215:403-410, 1990). When nucleotide sequences are analyzed by BLASTN based on BLAST, parameters may be set as score = 100 and wordlength = 12, for example. Specific procedures for these analysis methods are known (http://www.ncbi.nlm.nih.gov.).

The DNA encoding ALT may be inserted into a vector.

When the host cell to be used is *E. coli*, it is preferable that the vector has a replication origin ("ori") so that the vector is largely amplified in *E. coli* (e.g., JM109, DH5α, HB101 and XL1-Blue) and prepared in large quantity, and also genes for selecting transformed *E. coli* (e.g., drug resistance genes that enable discrimination of transformant with some drugs such as ampicillin, tetracycline, kanamycin or chloramphenicol). Examples of preferable vectors include, but are not limited to, M13 vectors, pUC vectors, pBR322, pBluescript and pCR-Script. In addition to these vectors, pGEM-T, pDIRECT, pT7, etc. may be enumerated when the vector is used for the purpose of subcloning a cDNA and cutting off the subcloned cDNA. When the vector is used for the purpose of producing the polypeptide of the present invention, an expression vector is especially useful. When expression in *E. coli* is intended, the expression vector preferably has the above-described features so that the vector is amplified in *E. coli*, and it also preferably has a promoter which allows efficient expression in *E. coli* such as JM109, DH5α, HB101 or XL1-Blue, e.g., lacZ promoter (Ward et al, Nature (1989) 341, 544-546; FASEB J. (1992) 6, 2422-2427), araB promoter (Better et al, Science (1988) 240, 1041-1043) or T7 promoter. Specific examples of such vector include, in addition to those listed above, pGEX-5X-1 (Pharmacia), QIAexpress system (Qiagen), pEGFP, or pET (for its host, T7 RNA polymerase-expressing BL21 is preferred).

The vector may comprise signal sequences for polypeptide secretion. When the polypeptide is to be produced in the periplasm of *E. coli*, pelB signal sequence (Lei, S. P. et al., J. Bacteriol. (1987) 169, 4379) may be used as a signal sequence for polypeptide secretion. Introduction of the vector into a host cell may be performed, for example, by the calcium chloride method or electroporation.

In cases where a host cell other than *E. coli* is used, vectors useful for producing a desired polypeptide include, but are not limited to, mammal-derived expression vectors [e.g., pcDNA3 from Invitrogen; pEGF-BOS (Nucleic Acids. Res. 1990, 18(17), p. 5322); pEF, pCDM8], insect cell-derived expression vectors (e.g., Bac-to-BAC baculovairus expression system from GIBCO BRL; pBacPAK8), plant-derived expression vectors (e.g., pMH1, pMH2), animal virus-derived expression vectors (e.g., pHSV, pMV, pAdexLcw), retrovirus-derived expression vectors (e.g., pZIpneo), yeast-derived expression vectors (e.g., Pichia Expression Kit fron Invitrogen; pNV11; SP-Q01), and *Bacillus subtilis*-derived expression vectors (e.g., pPL608, pKTH50).

When expression of the polypeptide in animal cells (such as CHO cells, COS cells, NIH3T3 cells, etc.) is intended, the vector preferably has a promoter necessary for

expressing the polypeptide in those cells. Examples of such promoter include, but are not limited to, SV40 promoter (Mulligan et al, Nature (1979) 277, 108), MMLV-LTR promoter, EF1α promoter (Mizushima et al., Nucleic Acids Res. (1990) 18, 5322) and CMV promoter. More preferably, the vector also has genes for selecting transformed cells (e.g., drug resistance genes that enable discrimination with drugs such as neomycin or G418). Examples of vectors having such properties include, but are not limited to, pMAM, pDR2, pBK-RSV, pBK-CMV, pOPRSV and pOP13.

Further, when stable expression of a gene of interest and intracellular amplification of the copy number of the gene are indented, the following method may be used. Briefly, into CHO cells lacking a nucleic acid synthesis pathway, a vector having DHFR gene that complements the lack (e.g., pCHOI) is introduced, followed by amplification with methotrexate (MTX). On the other hand, when tentative expression of a gene of interest is intended, a method may be used in which COS cells carrying a gene expressing SV40T antigen on the chromosome is transformed with a vector having the replication origin of SV40 (e.g., pcD). As the replication origin, a replication origin derived from polyomavirus, adenovirus or bovine papillomavirus (BPV) may also be used. Further, the expression vector may contain selectable markers for amplifying the copy number of the gene in a host cell system. Examples of such selectable markers include, but are not limited to, aminoglycoside phosphotransferase (APH) gene, thymidine kinase (TK) gene, *E. coli* xanthine-guanine phosphoribosyl transferase (Ecogpt) gene and dihydrofolate reductase (dhfr) gene.

The host cell into which the DNA encoding ALT (which may be incorporated in a vector) is transferred is not particularly limited. For example, *E. coli* or various animal cells may be used. If DNA encoding a desired polypeptide is transferred into a host cell into which DNA encoding ALT is transferred, this host cell can express ALT strongly, which leads to an increased production of the desired polypeptide. DNA encoding a taurine transporter (which may be incorporated into a vector) may be further transferred into the host cell into which DNA encoding ALT is transferred. By transferring DNA encoding a desired polypeptide and DNA encoding a taurine transporter into a host cell into which DNA encoding ALT is transferred, the yield of the desired polypeptide can be increased. For the production of the polypeptide, there are *in vivo* and *in vitro* production systems. Examples of *in vitro* production systems include systems using eukaryotes and systems using prokaryotes.

In the present invention, as DNA encoding a taurine transporter, a DNA encoding a polypeptide having the amino acid sequence as shown in SEQ ID NO: 62, 64, 66 or 68 may

be used. Alternatively, a DNA encoding a polypeptide which has an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 62, 64, 66 or 68 by substitution, deletion, addition and/or insertion of one or more amino acid residues and yet has taurine transporter activity may be used.

The polypeptide which has an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 62, 64, 66 or 68 by substitution, deletion, addition and/or insertion of one or more amino acid residues and yet has taurine transporter activity is functionally equivalent to a hamster, rat, mouse or human tanrine transporter (hereinafter sometimes referred to as "taurine transporter derived from hamster or the like"). Such a polypeptide encompasses, for example, mutants of the taurine transporter derived from hamster or the like.

As methods well-known to those skilled in the art for preparing polypeptides functionally equivalent to a specific polypeptide, methods of introducing mutations into polypeptides may be given. For example, those skilled in the art could prepare polypeptides functionally equivalent to hamster taurine transporter by appropriately introducing mutations into amino acids of hamster taurine transporter by site-directed mutagenesis (Hashimoto-Gotoh, T. et al. (1995) Gene 152, 271-275; Zoller, MJ, and Smith, M.(1983) Methods Enzymol. 100, 468-500; Kramer, W. et al. (1984) Nucleic Acids Res. 12, 9441-9456; Kramer W, and Fritz HJ (1987) Methods. Enzymol. 154, 350-367; Kunkel, TA (1985) Proc Natl Acad Sci USA. 82, 488-492; Kunkel (1988) Methods Enzymol. 85, 2763-2766). Mutations in amino acids may also occur in nature.

Specific examples of polypeptides functionally equivalent to the taurine transporter derived from hamster or the like include, but are not limited to, a polypeptide having an amino acid sequence derived from the amino acid sequence of the taurine transporter derived from hamster or the like by deletion of one or more amino acids, preferably 2-30 amino acids, more preferably 2-10 amino acids; a polypeptide having an amino acid sequence derived from the amino acid sequence of the taurine transporter derived from hamster or the like by addition of one or more amino acids, preferably 2-30 amino acids, more preferably 2-10 amino acids; and a polypeptide having an amino acid sequence derived from the amino acid sequence of the taurine transporter derived from hamster or the like by substitution of one or more amino acids, preferably 2-30 amino acids, more preferably 2-10 amino acids, with other amino acids.

Amino acid residues to be mutated are not particularly limited. Preferably, amino acid residues are mutated to other amino acids in which the nature of the initial amino acid side chain is conserved. Specific examples of the nature of amino acid side chain include

hydrophobic amino acids (A, I, L, M, F, P, W, Y and V), hydrophilic amino acids (R, D, N, C, E, Q, G H, K, S and T), amino acids with an aliphatic side chain (G, A, V, L, I and P), amino acids with a hydroxyl group-containing side chain (S, T and Y), amino acids with a sulfur atom-containing side chain (C and M), amino acids with a carboxylic acid and amide-containing side chain (D, N, E and Q), amino acids with a base-containing side chain (R, K and H) and amino acids with an aromatic-containing side chain (H, F, Y and W) (In parentheses are one-letter codes for amino acids).

As one example of the polypeptide in which one or more amino acid residues are added to the taurine transporter derived from hamster or the like, a fusion polypeptide comprising the taurine transporter derived from hamster or the like may be given. Such a fusion polypeptide is composed of the taurine transporter derived from hamster or the like and other polypeptide fused thereto. Such a fusion polypeptide is included in the present invention. Such a fusion polypeptide may be prepared by linking a gene encoding the taurine transporter derived from hamster or the like in frame with a gene encoding the other polypeptide, transferring the resultant DNA into an expression vector and expressing the DNA in a host cell. Techniques known to those skilled in the art may be used. There is no limitation on the polypeptide to be fused to the taurine transporter derived from hamster or the like.

Examples of polypeptides to be fused to the taurine transporter derived from hamster or the like include, but are not limited to, FLAG (Hopp, T. P. et al., BioTechnology (1988) 6, 1204-1210), 6xHis comprising six histidine (His) residues, 10xHis, influenza hemagglutinin (HA), human c-myc fragment, VSV-GP fragment, p18HIV fragment, T7-tag, HSV-tag, E-tag, SV40T antigen fragment, lck tag, α-tubulin fragment, B-tag, protein C fragment, glutathione-S-transferase (GST), influenza hemagglutinin (HA), immunoglobulin constant region, β-galactosidase and maltose-binding protein (MBP).

A commercially available gene encoding such polypeptide is fused to the gene encoding the taurine transporter derived from hamster or the like. The fused gene thus prepared is expressed to prepare a fused polypeptide.

An alternative method known to those skilled in the art for preparing polypeptides functionally equivalent to a specific polypeptide is a method using the hybridization technique (Sambrook, J et al., Molecular Cloning 2nd ed., 9.47-9.58, Cold Spring Harbor Lab. Press, 1989). Those skilled in the art could routinely isolate a DNA highly homologous to the DNA sequence of the taurine transporter derived from hamster or the like based on that DNA sequence or a part thereof, and isolate polypeptides functionally equivalent to the taurine transporter derived from hamster or the like from that DNA.

Hybridization conditions for isolating a DNA encoding a polypeptide functionally equivalent to the taurine transporter derived from hamster or the like can be appropriately selected by those skilled in the art. For example, low stringent hybridization conditions may be given. Low stringent hybridization conditions are, for example, 42°C, 2 x SSC and 0.1% SDS, preferably 50°C, 2 x SSC and 0.1% SDS. More preferably, high stringent conditions may be given. For example, high stringent conditions are 65°C, 2 x SSC and 0.1% SDS. Under these conditions, as the hybridization temperature is lowered, not only DNAs with high homology but also DNAs with only low homology are obtained. Conversely, it is expected that only those DNAs with high homology are obtained as the hybridization temperature is elevated. However, not only the temperature but also a plurality of factors (such as salt concentrations) affect the stringency of hybridization. Those skilled in the art could appropriately select these factors to realize similar stringency.

The polypeptide encoded by a DNA isolated by these hybridization techniques may have 70% or more homology and usually has high homology with the taurine transporter derived from hamster or the like in the amino acid sequence. The polypeptide also include those polypeptides which are functionally equivalent to the taurine transporter derived from hamster or the like and have high homology with the amino acid sequence of the taurine transporter derived from hamster or the like. The term "high homology" refers to usually 97% or more homology, preferably 98% or more homology, more preferably 99% or more homology. For determination of the homology of polypeptides, the algorithm described in Wilbur, W. J. and Lipman, D. J., Proc. Natl. Acad. Sci. USA (1983) 80, 726-730 may be followd.

The polypeptide may vary in amino acid sequence, molecular weight, isoelectric point, presence or absence of sugar chains, morphology, etc. depending on the cell or host that produce the polypeptide or the purification method that will be described later. However, as long as the resultant polypeptide has functions equivalent to the functions of the taurine transporter derived from hamster or the like, a DNA encoding the polypeptide can be used in the present invention. For example, when the polypeptide is expressed in a prokaryote (e.g., *Escherichia coli*), a methionine reside is added to the N-terminus of the initial amino acid sequence of the polypeptide. When the polypeptide is expressed in a eukaryote (e.g., a mammalian cell), the N-terminal signal sequence is removed. DNAs encoding such polypeptides can be used in the present invention.

The polypeptide may be prepared as a recombinant polypeptide or a natural polypeptide by methods known to those skilled in the art. A recombinant polypeptide may be prepared by incorporating a DNA encoding the polypeptide in an appropriate expression

vector, introducing the vector into an appropriate host cell, collecting the resultant transformant, extracting a crude polypeptide, and then purifying the polypeptide by chromatography (such as ion exchange, reversed phase or gel filtration chromatography, or affinity chromatography in which an antibody to the polypeptide is fixed in a column) or a combination of these chromatographic techniques.

When the polypeptide is expressed in a host cell (e.g., animal cell or *E. coli*) as a fusion polypeptide with glutathione-S-transferase polypeptide or as a recombinant polypeptide with histidine residues added thereto, the expressed polypeptide may be purified with a glutathione column or a nickel column.

After purification of a fusion polypeptide, regions other than the polypeptide of interest may be cut off by thrombin or factor Xa and removed from the fusion polypeptide.

When the polypeptide is a natural polypeptide, the polypeptide may be isolated by purification methods known to those skilled in the art. For example, an extract from tissues or cells expressing the polypeptide may be applied to an affinity column to which an antibody to the taurine transporter derived from hamster or the like described later is bound. The antibody may be either a polyclonal antibody or a monoclonal antibody.

In the present invention, as DNA encoding a taurine transporter, a DNA having the nucleotide sequence as shown in SEQ ID NO: 61, 63, 65 or 67 may be used. Alternatively, a DNA which hybridizes to a DNA complementary to a DNA having the nucleotide sequence as shown in SEQ ID NO: 61, 63, 65 or 67 under stringent conditions and yet encodes a polypeptide having taurine transporter activity may be used.

The DNA encoding a taurine transporter can be used in the *in vivo* or *in vitro* production of a desired polypeptide as described above. Further, the DNA encoding a taurine transporter may be used in the creation of a cell which strongly expresses a taurine transporter. The DNA encoding a taurine transporter may take any form as long as it is capable of encoding a taurine transporter. That is, the DNA may be, for example, a cDNA synthesized from mRNA, a genomic DNA or a chemically synthesized DNA. It should be noted that, as long as the DNA is capable of encoding a taurine transporter, the DNA may have any nucleotide sequence based on the degeneracy of genetic codes.

The DNA encoding a taurine transporter may be prepared by methods known to those skilled in the art. For example, the DNA may be prepared by preparing a cDNA library from a cell expressing a taurine transporter and performing hybridization using a part of the DNA sequence encoding a taurine transporter (e.g., SEQ ID NO: 61, 63, 65 or 67) as a probe. The cDNA library may be prepared, for example, by the method described in Sambrook, J. et al., Molecular Cloning, Cold Spring Harbor Laboratory Press (1989).

Alternatively, a commercial cDNA library may be used. It is also possible to prepare the DNA encoding a taurine transporter by preparing RNA from a cell expressing the taurine transporter, synthesizing oligo DNA molecules based on the DNA sequence of the taurine transporter (e.g., SEQ ID NO: 61, 63, 65 or 67), and performing PCR using the oligo DNA molecules as primers to thereby amplify a cDNA encoding the taurine transporter.

Further, by determining the nucleotide sequence of the resultant cDNA, it is possible to determine the translation region encoding a taurine transporter and to obtain the amino acid sequence of the taurine transporter. Further, by screening a genomic library using the resultant cDNA as a probe, it is possible to isolate a genomic DNA.

Specifically, the following procedures may be used. First, mRNA is isolated from cells, tissues or the like expressing a taurine transporter. For the isolation of mRNA, the total RNA is prepared by known methods, for example, the guanidine ultracentrifugation method (Chirgwin, J. M. et al., Biochemistry (1979) 18, 5294-5299), the AGPC method (Chomczynski, P. and Sacchi, N., Anal. Biochem. (1987) 162, 156-159) or the like, and then mRNA is purified from the total RNA using mRNA Purification Kit (Pharmacia), etc. Alternatively, mRNA may be prepared directly using QuickPrep mRNA Purification Kit (Pharmacia).

From the resultant mRNA, cDNA is synthesized using a reverse transcriptase. Alternatively, cDNA may be synthesized using a kit such as AMV Reverse Transcriptase First-Strand cDNA Synthesis Kit (SEIKAGAKU CORPORATION). It is also possible to synthesize and amplify cDNA according to the 5'-RACE method (Frohman, M. A. et al., Proc. Natl. Acad. Sci. USA (1988) 85, 8998-9002; Belyavsky, A. et al., Nucleic Acids Res. (1989) 17, 2919-2932) using 5'-Ampli FINDER RACE Kit (Clontech) and polymerase chain reaction (PCR) with primers.

A DNA fragment of interest is prepared from the resultant PCR product and ligated to a vector DNA to thereby prepare a recombinant vector. The vector is introduced into a host (e.g., *E. coli*), followed by selection of resultant colonies to thereby obtain a desired recombinant vector. The nucleotide sequence of the DNA of interest may be confirmed by a known method such as the dideoxynucleotide chain termination method.

Further, a nucleotide sequence of a higher expression efficiency can be designed for the DNA encoding a taurine transporter by considering the frequency of codon usage in the host to be used for expression (Grantham, R. et al., Nucleic Acids Research (1981) 9, p. 43-74). Further, the DNA encoding a taurine transporter can be modified using commercially available kits or known methods. Examples of such modifications include, but are not limited to, digestion with restriction enzymes, insertion of synthetic

oligonucleotides or appropriate DNA fragments, addition of linkers, and insertion of an initiation codon (ATG) and/or a termination codon (TAA, TGA or TAG).

The DNA encoding a taurine transporter also includes a DNA which hybridizes to a DNA complementary to a DNA having the nucleotide sequence as shown in SEQ ID NO: 61, 63, 65 or 67 under stringent conditions and encodes a polypeptide functionally equivalent to a taurine transporter.

Stringent conditions can be appropriately selected by those skilled in the art, including, for example, low stringent conditions. Low stringent conditions refer to, for example, 42° C, 2 x SSC and 0.1% SDS, preferably 50° C, 2 x SSC and 0.1% SDS. More preferably, high stringent conditions may be selected. High stringent conditions refer to, for example, 65° C, 2 x SSC and 0.1% SDS. Under these conditions, as the hybridization temperature is elevated, DNAs with a higher homology can be obtained. The above-described DNA which hybridizes is preferably a DNA derived from nature, e.g., cDNA or chromosomal DNA.

These DNAs isolated by hybridization techniques usually have a high nucleotide sequence identity with a DNA encoding the taurine transporter derived from hamster, *etc.* The DNA also includes a DNA which encodes a polypeptide functionally equivalent to the taurine transporter derived from hamster, *etc.* and has high identity with a DNA encoding the taurine transporter derived from hamster, *etc.* The term "high identity" refers to usually 96% or more homology, preferably 98% or more homology, more preferably 99% or more identity. The identity of nucleotide sequences may be determined by algorithm BLAST (Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Based on this algorithm, programs such as BLASTN and BLASTX have been developed (Altschul et al. J. Mol. Biol. 215:403-410, 1990). When nucleotide sequences are analyzed by BLASTN based on BLAST, parameters may be set as expect value = 100 and word size = 12, for example. Specific procedures for these analysis methods are known (http://www.ncbi.nlm.nih.gov.).

The DNA encoding a taurine transporter may be inserted into a vector.

When the host cell to be used is *E. coli*, it is preferable that the vector has a replication origin ("ori") so that the vector is largely amplified in *E. coli* (e.g., JM109, DH5α, HB101 and XL1-Blue) and prepared in large quantity, and also genes for selecting transformed *E. coli* (e.g., drug resistance genes that enable discrimination of transformant with some drugs such as ampicillin, tetracycline, kanamycin or chloramphenicol). Examples of preferable vectors include, but are not limited to, M13 vectors, pUC vectors, pBR322, pBluescript and pCR-Script. In addition to these vectors, pGEM-T, pDIRECT,

pT7, etc. may be enumerated when the vector is used for the purpose of subcloning a cDNA and cutting off the subcloned cDNA. When the vector is used for the purpose of producing the polypeptide of the present invention, an expression vector is especially useful. When expression in *E. coli* is intended, the expression vector preferably has the above-described features so that the vector is amplified in *E. coli*, and it also preferably has a promoter which allows efficient expression in *E. coli* such as JM109, DH5α, HB101 or XL1-Blue, e.g., lacZ promoter (Ward et al, Nature (1989) 341, 544-546; FASEB J. (1992) 6, 2422-2427), araB promoter (Better et al, Science (1988) 240, 1041-1043) or T7 promoter. Specific examples of such vector include, in addition to those listed above, pGEX-5X-1 (Pharmacia), QIAexpress system (Qiagen), pEGFP, or pET (for its host, T7 RNA polymerase-expressing BL21 is preferred).

The vector may comprise signal sequences for polypeptide secretion. When the polypeptide is to be produced in the periplasm of *E. coli*, pelB signal sequence (Lei, S. P. et al., J. Bacteriol. (1987) 169, 4379) may be used as a signal sequence for polypeptide secretion. Introduction of the vector into a host cell may be performed, for example, by the calcium chloride method or electroporation.

In cases where a host cell other than *E. coli* is used, vectors useful for producing a desired polypeptide include, but are not limited to, mammal-derived expression vectors [e.g., pcDNA3 from Invitrogen; pEGF-BOS (Nucleic Acids. Res. 1990, 18(17), p. 5322); pEF, pCDM8], insect cell-derived expression vectors (e.g., Bac-to-BAC baculovairus expression system from GIBCO BRL; pBacPAK8), plant-derived expression vectors (e.g., pMH1, pMH2), animal virus-derived expression vectors (e.g., pHSV, pMV, pAdexLcw), retrovirus-derived expression vectors (e.g., pZIpneo), yeast-derived expression vectors (e.g., Pichia Expression Kit fron Invitrogen; pNV11; SP-Q01), and *Bacillus subtilis*-derived expression vectors (e.g., pPL608, pKTH50).

When expression of the polypeptide in animal cells (such as CHO cells, COS cells, NIH3T3 cells, etc.) is intended, the vector preferably has a promoter necessary for expressing the polypeptide in those cells. Examples of such promoter include, but are not limited to, SV40 promoter (Mulligan et al, Nature (1979) 277, 108), MMLV-LTR promoter, EF1α promoter (Mizushima et al., Nucleic Acids Res. (1990) 18, 5322) and CMV promoter. More preferably, the vector also has genes for selecting transformed cells (e.g., drug resistance genes that enable discrimination with drugs such as neomycin or G418). Examples of vectors having such properties include, but are not limited to, pMAM, pDR2, pBK-RSV, pBK-CMV, pOPRSV and pOP13.

Further, when stable expression of a gene of interest and intracellular amplification

of the copy number of the gene are indented, the following method may be used. Briefly, into CHO cells lacking a nucleic acid synthesis pathway, a vector having DHFR gene that complements the lack (e.g., pCHOI) is introduced, followed by amplification with methotrexate (MTX). On the other hand, when tentative expression of a gene of interest is intended, a method may be used in which COS cells carrying a gene expressing SV40T antigen on the chromosome is transformed with a vector having the replication origin of SV40 (e.g., pcD). As the replication origin, a replication origin derived from polyomavirus, adenovirus or bovine papillomavirus (BPV) may also be used. Further, the expression vector may contain selectable markers for amplifying the copy number of the gene in a host cell system. Examples of such selectable markers include, but are not limited to, aminoglycoside phosphotransferase (APH) gene, thymidine kinase (TK) gene, *E. coli* xanthine-guanine phosphoribosyl transferase (Ecogpt) gene and dihydrofolate reductase (dhfr) gene.

The present invention provides a cell which has a transferred DNA encoding ALT and a transferred DNA encoding a taurine transporter, both or either of which may be incorporated into a vector.

When eukaryotes are used, animal cells, plant cells, fungal cells, etc. may be used as the host. Specific examples of animal cells include mammalian cells, such as CHO cells (J. Exp. Med. (1995) 108, 945), COS cells, 3T3 cells, myeloma cells, BHK (baby hamster kidney) cells, HeLa cells and Vero cells; amphibian cells, such as oocytes of Xenopus laevis (Valle, et al., Nature (1981) 291, 358-340); or insect cells, such as sf9, sf21 and Tn5 cells. Amoung CHO cells, dhfr-CHO lacking DHFR gene (Proc. Natl. Acad. Sci. USA (1980) 77, 4216-4420) and CHO K-1 (Proc. Natl. Acad. Sci. USA (1968) 60, 1275) are used with particular advantage. When high expression is intended in an animal cell, CHO cells are especially preferred. Introduction of the DNA which may be incorporated into a vector into the host cell may be performed by such methods as the calcium phosphate method, the DEAE dextran method, a method using a cationic ribosome DOTAP (Boehringer-Mannheim), electroporation, lipofection, etc.

As plant cells for polypeptide production, a *Nicotiana tabacum*-derived cell is known as a polypeptide production system and this may be subjected to callus culture. As fungal cells for polypeptide production, specific examples include yeast belonging to the genus Saccharomyces, e.g., *Saccharomyces cerevisiae*, and filamentous fungi belonging to the genus Aspergillus, e.g., *Aspergillus niger*.

When prokaryotes are used, production systems using bacterial cells are known. Specific examples of such bacterial cells include *E. coli* (such as JM109, DH5α, HB101) and

Bacillus subtilis.

The polypeptide encoded by a gene of interest may be obtained by transforming these cells with the gene of interest and culturing the transformed cells *in vitro*. The culture may be performed by known methods. For example, as a culture broth for animal cells, a medium such as DMEM, MEM, RPMI1640 or IMDM may be used. A serum supplement such as fetal calf serum (FCS) may be used jointly. Alternatively, serum-free culture may be performed. The pH during culture is preferably about 6 to 8. The culture is usually performed at about 30-40°C for about 15-200 hours. If necessary, replacement of the medium, aeration and agitation are carried out.

On the other hand, *in vivo* production systems include those using animals or plants. A gene of interest is transferred into these animals or plants to produce the polypeptide in the animal bodies or plant bodies. Then, the polypeptide is collected. The term "host" as used herein includes such animals or plants.

When animals are used, available production systems include those using mammals or insects. Goat, pig, sheep, mouse and cattle may be used as mammals (Vicki Glaser, SPECTRUM Biotechnology Applications, 1993). When mammals are used, transgenic animals may be used.

First, a gene of interest is fused to a gene encoding a polypeptide produced inherently in milk (such as goat β-casein) to thereby prepare a fusion gene. A DNA fragment containing this fusion gene is injected into a goat embryo, which is then implanted in the uterus of a female goat. The polypeptide of interest can be obtained from the milk produced by transgenic goats born from the goat which accepted the embryo or the offspring of the transgenic goats. In order to increase the yield of milk containing the polypeptide produced by the transgenic goats, hormones may be appropriately administered to the transgenic goats (Ebert, K. M. et al., Bio/Technology (1994) 12, 699-702).

Examples of insects which may be used include silkworm. In this case, silkworm is infected with baculovirus carrying a transferred gene encoding the polypeptide of interest. The polypeptide of interest can be obtained from the body fluid of the silkworm (Susumu, M. et al., Nature (1985) 315, 592-594).

Furthermore, when plants are used, tobacco can typically be used. When tobacco is used, a gene encoding the polypeptide of interest is inserted into a plant expression vector (e.g., pMON 530), which is then transferred into a bacterium such as *Agrobacterium tumefaciens*. A tobacco plant (e.g., Nicotiana tabacum) is infected with the resultant bacterium. The polypeptide of interest can be obtained from leaves of this plant (Julian, K.-C. Ma et al., Eur. J. Immunol. (1994) 24, 131-138).

The polypeptide thus obtained can be isolated from the inside of the host cell or from its outside (e.g., medium), and purified to a substantially pure and homogeneous polypeptide. Isolation and purification of polypeptides can be performed using conventional isolation and purification methods for polypeptides, and are not limited in any way. For example, polypeptides can be isolated and purified by appropriate selection and combination of various tools and techniques, such as chromatography columns, filters, ultrafiltration, salting-out, precipitation with solvent, extraction with solvent, distillation, immunoprecipitation, SDS-polyacrylamide gel electrophoresis, isoelectric focusing, dialysis, recrystallization, etc.

Examples of chromatography include affinity chromatography, ion exchange chromatography, hydrophobic chromatography, gel filtration, reverse-phase chromatography, adsorption chromatography, etc. (Strategies for Protein Purification and Characterization: A Laboratory Course Manual. Ed. Daniel R. Marshak et al., Cold Spring Harbor Laboratory Press, 1996). These chromatographic techniques can be carried out using liquid phase chromatography, for example, HPLC, FPLC, etc. The present invention also includes those polypeptides highly purified using these purification methods.

Before or after the purification, it is also possible to give optional modifications to the polypeptide or remove a partial peptide therefrom by reacting the polypeptide with an appropriate polypeptide modification enzyme. Examples of such enzyme include, but are not limited to, trypsin, chymotrypsin, lysyl endopeptidase, protein kinase and glucosidase.

In the present invention, the concept of "cells into which DNA has been transferred" encompasses not only cells into which exogenous DNA has been incorporated by genetic recombination technology; but also cells in which endogenous DNA has been activated by gene activation technology (see, for example, International Publication WO94/12650) so that expression of a protein corresponding to the endogenous DNA or transcription of the DNA has been initiated or increased.

EXAMPLES

Hereinbelow, the present invention will be described in more detail with reference to the following Examples. It should be noted that these Examples are provided only for illustrating the present invention and not for limiting the scope of the present invention.

[EXAMPLE 1] Cloning of Human Hepatic Cell Alanine Aminotransferase Gene

Using a commercial Human Liver QUICK-Clone cDNA (Clontech Laboratories, Inc.) as a template, alanine aminotransferase (ALT1) gene derived from a human liver was

obtained by a PCR method. The gene thus cloned was sequenced and confirmed to encode ALT1 based on its homology with published human ALT1. The ALT1 gene thus obtained had mutations at five sites in the sequence of 1488 bases (c157a, a215g, c765t, t857c, t995a) and coded for 496 amino acids including four different amino acids (R53S, Q72R, F286S, M332K), but this was used as a PCR clone of the human liver derived ALT1 for cell modulation.

[EXAMPLE 2] Increase in Antibody Yield by Transfer of Human Alanine Aminotransferase

By adding a Kozak sequence to the human ALT1 obtained by cloning in Example 1 (which is hereinafter called ALT1), pPur-ALT1 (Fig. 1) and pHyg-ALT1 (Fig. 2), which were CMV promoter expression plasmids, were constructed. The pPur-ALT1 or pPur expression plasmids that did not contain the ALT1 gene were introduced into anti-glypican-3 antibody-producing CHO cells as parent strains (see International Publication WO 2006/006693) by electroporation, and cell strains that exhibited high proliferation in static culture in the presence of Puromycin (6 μg/ml) (pPur-ALT1: seven strains, pPur: three strains) were selected. After expansion, a total RNA was prepared from the pPur-ALT1 cell strains, and six strains expressing human ALT1 at high levels were selected by a TaqMan method. Further, a comparison was made for the antibody yield between pPur-transferred cells as a control (three strains) and four strains of human ALT1-transferred cells that proliferated at a level equivalent to that observed with the pPur-transferred cells during the shake culture. During fed-batch culture in a 50 ml shaker flask with an initial cell density of 2×10^5 cells/mL, the anti-glypican-3 antibody yield of pPur-ALT1-transferred cells (four strains) on day 17 at the late stage of the shaker culture was significantly higher than that of pPur-transferred cells (three strains) (t-test: $p < 0.01$, Fig. 3). A72, a pPur-ALT1 expressing strain, and P41, a pPur expressing strain, were each found to have produced the largest amount of an antibody in the study using shaker fed-batch culture, and they were subjected to fed-batch culture in 1 L jars (an initial cell density of 10×10^5 cells/mL). As a result, the antibody yield of A72 was 2.9 g/L on day 19 of the culture, which was greater than the antibody yield of P41 (2.2 g/L) (Fig. 4). Since no increase was observed in the antibody yield of P41 on day 14 or subsequent days after the initiation of the culture, the high-yield production of an antibody by A72 was considered to be attributable to the survival ratio maintaining effect (Fig. 5). Further, pHyg/ALT-transferred cells (three strains), which were drug-selected in the presence of Hygromycin (200 μg/mL) by a method similar to the one described above, were subjected to fed-batch culture, together with the parent strain, in 15 ml tubes (an initial cell density of 1 ×

10^5 cells/mL). As a result, the anti-glypican-3 antibody yield of the pHyg-ALT-transferred cells on day 10 at the late stage of the tube culture were 471mg/L, 544mg/L, and 588mg/L, showing that the antibody yield of any one of them was greater than that of the parent strain (400 mg/L) (data not shown).

Then, pPur-ALT1 or pPur was co-transferred into T10 which was a pHyg-TauT-transferred cell used as a parent strain (see Referential Example 2 described later). TauT/ALT1 co-expressing cells that exhibited high proliferation and expressed human ALT1 at high level (six strains) and TauT/pPur co-expressing cells that exhibited high proliferation (eight strains) were selected and subjected to fed-batch culture in 50 mL shaker flasks (an initial cell density of 10×10^5 cells/mL). The anti-glypican-3 antibody yield of TauT/ALT1 co-expressing cells, which were ALT expressing cells, on day 4 of the shaker culture was significantly higher than that of TauT/pPur cells (t-test: $p < 0.01$, Fig. 6).

TA41, which was a TauT/ALT1 co-expressing strain that produced the largest amount of an antibody (881 mg/L/4 days) and expressed ALT1 mRNA at the highest level in the study using the shaker fed-batch culture, was subjected to fed-batch culture in a 1 L jar (an initial cell density of 10×10^5 cells/mL). The antibody yields were as high as 1.3 g/L on day 7 of the culture, 3.0 g/L on day 10 of the culture, 3.5 g/L on day 12 of the culture, 4.6 g/L on day 17 of the culture, and 5.3 g/L on day 21 of the culture (Fig. 7), which were clearly higher than the values for TP08 (656 mg/L/4 days), which was a control strain that produced the largest amount of an antibody among the TauT/pPur co-expressing strains (2.4 g/L on day 10 of the culture).

The anti-glypican-3 antibody yield of TA41, a TauT/ALT1 co-expressing strain, on day 14 of the fed-batch culture in a 50 ml shaker flask was increased by addition of α-ketoglutarate which, like alanine, served as a substrate for ALT (Fig. 22). The anti-glypican-3 antibody yield on day 14 of the culture was 1452 mg/L in the presence of 2.5 mM α-ketoglutarate, and 1239 mg/L in the absence of α-ketoglutarate.

The above results suggest that cells capable of high-yield antibody production at the late stage of culture can be obtained by artificially expressing ALT1.

The present invention is applicable to any antibody-producing cell.

[REFERENTIAL EXAMPLE 1] Cloning of CHO Cell-Derived Hamster Taurine Transporter Gene

Total RNA was extracted from anti-IL-6 receptor antibody-producing cells (A CHO DXB11 cell line into which an anti-IL-6 receptor antibody gene had been transferred) (Japanese Unexamined Patent Publication No. Hei 8-99902), and then cDNA was

synthesized therefrom in a poly(A) dependent manner. Hamster taurine transporter (TauT) gene was obtained by PCR using as a template the cDNA fragmented with three restriction enzymes, SalI, XhoI and EcoRI. As PCR primers, those containing the 5'-end and the 3'-end sequence conserved between rat and mouse TauTs were designed. The nucleotide sequence of the cloned gene was determined. From its homology with other TauT genes of known species, the cloned gene was confirmed to encode hamster TauT (Fig. 8). The amino acid sequence of hamster TauT has high homology with mouse TauT (96% identity), rat TauT (96% identity) and human TauT (93% identity); it was predicted that hamster TauT is a transporter with 12 transmembrane regions (Fig. 9).

[REFERENTIAL EXAMPLE 2] Increase in Viable Cell Density, Inhibition of Lactate Production and Increase in Antibody Yield, as Caused by Transfer of Hamster Taurine Transporter

CMV promoter expression plasmid pHyg/TauT (Fig. 10) was constructed by adding Kozak sequence to the hamster TauT (hereinafter, TauT) gene obtained by cloning in Referential Example 1. Control plasmid pHyg without pHyg/TauT or TauT gene was introduced by electroporation into the parent strain anti-glypican-3 antibody producing CHO cell (see WO 2006/006693). After selection of expression plasmid-transferred cells in the presence of hygromycin (400 μg/ml), all of the stably growing cell strains were expanded (pHyg/TauT: 8 strains; pHyg: 7 strains). TauT mRNA was prepared. Subsequently, 7 strains were confirmed to express TauT more strongly than the parent strain by the TaqMan method; they were selected as pHyg/TauT transferred cells. The mean mRNA expression level of these transferred cells (7 strains) was about 40 times larger than the control (7 strains). Cells of the total 14 strains were subjected to batch culture and fed-batch culture in 50 ml shaker flasks with an initial cell density of 2×10^5 cells/ml. On day 7 of culture (late-stage), viable cell densities, lactate yields and anti-glypican-3 antibody yields in those strains were compared. In batch culture, growth inhibitory substances such as lactate accumulate in culture broth as cells grow and their growth is inhibited. However, the viable cell densities (Fig. 11) and lactate yields (Fig. 12) in pHyg/TauT transferred cells were superior to those in pHyg transferred cells (t test; $p<0.05$). With respect to anti-glypican-3 antibody yield, 4 out of the 7 strains of pHyg/TauT-transferred cell showed antibody yields higher than the highest yield in pHyg-transferred cell (Fig. 13). Further, since superiority of pHyg/TauT transferred cells in anti-glypican-3 antibody yield became more evident (t test; $P<0.01$; Fig. 14) in fed-batch culture, pHyg/TauT transferred T10 strain (which showed the highest growth ability among the above 4 strains) and the parent strain

were subjected to fed-batch culture in 1 L jar. As a result, the viable ratio of T10 was maintained at 80% or more even on day 32 of culture (Fig. 15), with inhibited lactate production. Consequently, its anti-glypican-3 antibody yield achieved 2.9 g/L on day 35 of culture (Fig. 16). It was confirmed by flow cytometric analysis that TauT-transferred T10 cell was expressing TauT molecules on the cell membrane (Fig. 17). These results suggest that by artificially expressing hamster Taut, it is possible to raise the potential of antibody-producing cells and create strains capable of enhanced antibody production.

[REFERENTIAL EXAMPLE 3] Inhibition of Ammonia Production, Taurine Uptake, Increase in Glutamine Consumption and Taurine Non-Dependent Antibody Yield in Hamster TauT Transferred Strains

The parent strain and pHyg/TauT transferred strain were fed-batch cultured in 1 L jar with an initial cell density of 2×10^5 cells/ml. A part of the culture broth containing 450×10^5 cells was taken from the jar at appropriate time points. After the culture supernatant was separated by centrifugation, 1 ml of cooled sterile water containing a protease inhibitor (Complete Mini; Roche Diagnostics; Protease inhibitor cocktail tablets) was added to the cell pellet. Then, the cells were completely disrupted on ice in a sonicator (MISONIX ASTRASON MODEL XL2020) with a set of 5 seconds pulse-on and 5 seconds pulse-off being repeated 12 times. The total volume of the thus treated cells was applied to a centrifugal filter unit to thereby prepare a filtrate with a molecular weight of 5000 or less. This filtrate was used as a sample for determining intracellular amino acids. Each sample was subjected to detection and comparison of absorbance at 570 nm using a ninhydrin reagent L-8500 set (Wako Pure Chemical Industries) and an improved model of Hitachi fully automated amino acid analyzer (L-8500). Thus, various amino acid concentrations in samples were determined. Since the concentrations of amino acids and ammonia in culture broth were directly measured values, concentration comparisons in the order of μM were performed. On the other hand, since intracellular concentrations were obtained after addition of 1 ml of cooled sterile water to the cell pellet and sonication thereof, the measured concentrations of various amino acids and ammonia were converted into values per cell, followed by comparison of the converted values. To determine the ammonia concentration ratios shown in Fig. 18, the detected ammonia value per 450×10^5 cells in the parent strain at the start of 1 L jar fed-batch culture was taken as 1 and compared with detected values at the start of the culture and on days 6, 12 and 18 of the culture in the transferred strain. The taurine values in Fig. 19 and the glutamine values in Fig. 20 were also determined by the above-described amino acid analysis.

As a result, the intracellular ammonia in pHyg/TauT transferred strain was maintained at a low concentration at the late stage of culture; it is believed that this contributes to high antibody yield (Fig. 18).

Intracellular taurine concentration ratios were determined in the same manner as described above for ammonia concentrations (Fig. 19), except that the detected ammonia value per 200 x 10^5 cells in the parent strain on day 4 of 50 ml shaker batch culture was taken as 1.

As a result, it was found that pHyg/TauT transferred strain had taken up taurine in a manner dependent on the amount of taurine added and that its uptake was almost equal to that by the parent strain. However, as shown in Fig. 20, glutamine consumption in pHyg/TauT transferred strain was remarkably high compared to the parent strain and was not dependent on the initial taurine concentration. It has been reported that glutamine improves cell growth, survival ratio and antibody production ability in hybridomas to thereby raise their antibody yields (Enzyme and Microbial Technology 17:47-55, 1995). Therefore, the antibody production enhancement effect of pHyg/TauT transferred strain may be caused by taurine transporter-mediated uptake of amino acids other than taurine (e.g., glutamine). The glutamine concentrations were obtained by converting the values determined by amino acid analysis of the culture broth on day 4 of culture in Fig. 19 into values per 1 x 10^5 cells.

Actually, anti-glypican-3 antibody yield was not dependent on the initial taurine concentration (0-500 mM (62.575 g/L)) at the start of 50 ml shaker fed-batch culture (Fig. 21). No significant difference was observed in the parent strains in the effect of initial taurine concentration on antibody yield.

The results described so far suggest that TauT strongly expressing strains have high antibody production ability even if the medium does not contain taurine at the start of culture and that there is a possibility that such strains also promote uptake of amino acids other than taurine.

The present invention is applicable to any antibody-producing cell.

All publications, patent and patent applications cited herein are incorporated herein by reference in their entirety.

INDUSTRIAL APPLICABILITY

The present invention is applicable to production of polypeptides.

SEQUENCE LISTING FREE TEXT

<SEQ ID NO: 1>

SEQ ID NO: 1 shows the nucleotide sequence of a gene encoding human alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Homo sapiens (human): 2875).

<SEQ ID NO: 2>

SEQ ID NO: 2 shows the amino acid sequence of human alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Homo sapiens (human): 2875).

<SEQ ID NO: 3>

SEQ ID NO: 3 shows the nucleotide sequence of a gene encoding human alanine aminotransferase mutant (ALT2) (KEGG / ENZYME: 2.6.1.2 / Homo sapiens (human): 84706).

<SEQ ID NO: 4>

SEQ ID NO: 4 shows the amino acid sequence of human alanine aminotransferase mutant (ALT2) (KEGG / ENZYME: 2.6.1.2 / Homo sapiens (human): 84706).

<SEQ ID NO: 5>

SEQ ID NO: 5 shows the nucleotide sequence of a gene encoding mouse alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Mus musculus (mouse): 76282).

<SEQ ID NO: 6>

SEQ ID NO: 6 shows the amino acid sequence of mouse alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Mus musculus (mouse): 76282).

<SEQ ID NO: 7>

SEQ ID NO: 7 shows the nucleotide sequence of a gene encoding mouse alanine aminotransferase mutant (ALT2) (KEGG / ENZYME: 2.6.1.2 / Mus musculus (mouse): 108682).

<SEQ ID NO: 8>

SEQ ID NO: 8 shows the amino acid sequence of mouse alanine aminotransferase mutant (ALT2) (KEGG / ENZYME: 2.6.1.2 / Mus musculus (mouse): 108682).

<SEQ ID NO: 9>

SEQ ID NO: 9 shows the nucleotide sequence of a gene encoding rat alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Rattus norvegicus (rat): 81670).

<SEQ ID NO: 10>

SEQ ID NO: 10 shows the amino acid sequence of rat alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Rattus norvegicus (rat): 81670).

<SEQ ID NO: 11>

SEQ ID NO: 11 shows the nucleotide sequence of a gene encoding dog alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Canis familiaris (dog): 609510).

<SEQ ID NO: 12>

SEQ ID NO: 12 shows the amino acid sequence of dog alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Canis familiaris (dog): 609510).

<SEQ ID NO: 13>

SEQ ID NO: 13 shows the nucleotide sequence of a gene encoding African clawed frog alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Xenopus laevis (African clawed frog): 444533).

<SEQ ID NO: 14>

SEQ ID NO: 14 shows the amino acid sequence of African clawed frog alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Xenopus laevis (African clawed frog): 444533).

<SEQ ID NO: 15>

SEQ ID NO: 15 shows the nucleotide sequence of a gene encoding fruit fly alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Drosophila melanogaster (fruit fly): Dmel_CG1640).

<SEQ ID NO: 16>

SEQ ID NO: 16 shows the amino acid sequence of fruit fly alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Drosophila melanogaster (fruit fly): Dmel_CG1640).

<SEQ ID NO: 17>

SEQ ID NO: 17 shows the nucleotide sequence of a gene encoding nematode alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Caenorhabditis elegans (nematode): C32F10.8).

<SEQ ID NO: 18>

SEQ ID NO: 18 shows the amino acid sequence of nematode alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Caenorhabditis elegans (nematode): C32F10.8).

<SEQ ID NO: 19>

SEQ ID NO: 19 shows the nucleotide sequence of a gene encoding one of two kinds of Japanese rice alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Oryza sativa japonica (Japanese rice): 4342210).

<SEQ ID NO: 20>

SEQ ID NO: 20 shows the amino acid sequence of one of two kinds of Japanese rice alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Oryza sativa japonica (Japanese rice): 4342210).

<SEQ ID NO: 21>

SEQ ID NO: 21 shows the nucleotide sequence of a gene encoding one of two kinds of Japanese rice alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Oryza sativa japonica (Japanese rice): 4348524).

<SEQ ID NO: 22>

SEQ ID NO: 22 shows the amino acid sequence of one of two kinds of Japanese rice alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Oryza sativa japonica (Japanese rice): 4348524).

<SEQ ID NO: 23>

SEQ ID NO: 23 shows the nucleotide sequence of a gene encoding Cyanidioschyzon merolae alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Cyanidioschyzon merolae: CMM066C).

<SEQ ID NO: 24>

SEQ ID NO: 24 shows the amino acid sequence of Cyanidioschyzon merolae alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Cyanidioschyzon merolae: CMM066C).

<SEQ ID NO: 25>

SEQ ID NO: 25 shows the nucleotide sequence of a gene encoding Saccharomyces cerevisiae alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Saccharomyces cerevisiae: YLR089C).

<SEQ ID NO: 26>

SEQ ID NO: 26 shows the amino acid sequence of Saccharomyces cerevisiae alanine aminotransferase (ALT1) (KEGG / ENZYME: 2.6.1.2 / Saccharomyces cerevisiae: YLR089C).

<SEQ ID NO: 27>

SEQ ID NO: 27 shows the nucleotide sequence of a gene encoding Saccharomyces cerevisiae alanine aminotransferase mutant (ALT2) (KEGG / ENZYME: 2.6.1.2 / Saccharomyces cerevisiae: YDR111C).

<SEQ ID NO: 28>

SEQ ID NO: 28 shows the amino acid sequence of Saccharomyces cerevisiae alanine aminotransferase mutant (ALT2) (KEGG / ENZYME: 2.6.1.2 / Saccharomyces cerevisiae: YDR111C).

<SEQ ID NO: 29>

SEQ ID NO: 29 shows the nucleotide sequence of a gene encoding Ashbya gossypii alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Ashbya gossypii (Eremothecium gossypii): AGOS_AGR085W).

<SEQ ID NO: 30>

SEQ ID NO: 30 shows the amino acid sequence of Ashbya gossypii alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Ashbya gossypii (Eremothecium gossypii): AGOS_AGR085W).

<SEQ ID NO: 31>

SEQ ID NO: 31 shows the nucleotide sequence of a gene encoding Candida albicans alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Candida albicans: CaO19_346).

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SEQ ID NO: 32 shows the amino acid sequence of Candida albicans alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Candida albicans: CaO19_346).

<SEQ ID NO: 33>

SEQ ID NO: 33 shows the nucleotide sequence of a gene encoding Schizosaccharomyces pombe alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Schizosaccharomyces pombe: SPBC582.08).

<SEQ ID NO: 34>

SEQ ID NO: 34 shows the amino acid sequence of Schizosaccharomyces pombe alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Schizosaccharomyces pombe: SPBC582.08).

<SEQ ID NO: 35>

SEQ ID NO: 35 shows the nucleotide sequence of a gene encoding Aspergillus nidulans alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Aspergillus nidulans: AN1923.2).

<SEQ ID NO: 36>

SEQ ID NO: 36 shows the amino acid sequence of Aspergillus nidulans alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Aspergillus nidulans: AN1923.2).

<SEQ ID NO: 37>

SEQ ID NO: 37 shows the nucleotide sequence of a gene encoding Aspergillus fumigatus alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Aspergillus fumigatus: AFUA_6G07770).

<SEQ ID NO: 38>

SEQ ID NO: 38 shows the amino acid sequence of Aspergillus fumigatus alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Aspergillus fumigatus: AFUA_6G07770).

<SEQ ID NO: 39>

SEQ ID NO: 39 shows the nucleotide sequence of a gene encoding Aspergillus

oryzae alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Aspergillus oryzae: AO090003000164).

<SEQ ID NO: 40>

SEQ ID NO: 40 shows the amino acid sequence of Aspergillus oryzae alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Aspergillus oryzae: AO090003000164).

<SEQ ID NO: 41>

SEQ ID NO: 41 shows the nucleotide sequence of a gene encoding Cryptococcus neoformans alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Cryptococcus neoformans JEC21: CNG01490).

<SEQ ID NO: 42>

SEQ ID NO: 42 shows the amino acid sequence of Cryptococcus neoformans alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Cryptococcus neoformans JEC21: CNG01490).

<SEQ ID NO: 43>

SEQ ID NO: 43 shows the nucleotide sequence of a gene encoding Dictyostelium discoideum alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Dictyostelium discoideum: DDB_0232139).

<SEQ ID NO: 44>

SEQ ID NO: 44 shows the amino acid sequence of Dictyostelium discoideum alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Dictyostelium discoideum: DDB_0232139).

<SEQ ID NO: 45>

SEQ ID NO: 45 shows the nucleotide sequence of a gene encoding Trypanosoma brucei alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Trypanosoma brucei: Tb927.1.3950).

<SEQ ID NO: 46>

SEQ ID NO: 46 shows the amino acid sequence of Trypanosoma brucei alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Trypanosoma brucei: Tb927.1.3950).

<SEQ ID NO: 47>

SEQ ID NO: 47 shows the nucleotide sequence of a gene encoding Leishmania major alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Leishmania major: LmjF12.0630).

<SEQ ID NO: 48>

SEQ ID NO: 48 shows the amino acid sequence of Leishmania major alanine aminotransferase (KEGG / ENZYME: 2.6.1.2 / Leishmania major: LmjF12.0630).

<SEQ ID NO: 49>

SEQ ID NO: 49 shows the nucleotide sequence of a gene encoding one of two kinds of Entamoeba histolytica alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 /Entamoeba histolytica: 233.t00009).

<SEQ ID NO: 50>

SEQ ID NO: 50 shows the amino acid sequence of one of two kinds of Entamoeba histolytica alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 /Entamoeba histolytica: 233.t00009).

<SEQ ID NO: 51>

SEQ ID NO: 51 shows the nucleotide sequence of a gene encoding one of two kinds of Entamoeba histolytica alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 /Entamoeba histolytica: 24.t00016).

<SEQ ID NO: 52>

SEQ ID NO: 52 shows the amino acid sequence of one of two kinds of Entamoeba histolytica alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 /Entamoeba histolytica: 24.t00016).

<SEQ ID NO: 53>

SEQ ID NO: 53 shows the nucleotide sequence of a gene encoding one of four kinds of Trypanosoma cruzi alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Trypanosoma cruzi: 506529.420).

<SEQ ID NO: 54>

SEQ ID NO: 54 shows the amino acid sequence of one of four kinds of Trypanosoma cruzi alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Trypanosoma cruzi: 506529.420).

<SEQ ID NO: 55>

SEQ ID NO: 55 shows the nucleotide sequence of a gene encoding one of four kinds of Trypanosoma cruzi alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Trypanosoma cruzi: 506529.430).

<SEQ ID NO: 56>

SEQ ID NO: 56 shows the amino acid sequence of one of four kinds of Trypanosoma cruzi alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Trypanosoma cruzi: 506529.430).

<SEQ ID NO: 57>

SEQ ID NO: 57 shows the nucleotide sequence of a gene encoding one of four

kinds of Trypanosoma cruzi alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Trypanosoma cruzi: 510889.120).

<SEQ ID NO: 58>

SEQ ID NO: 58 shows the amino acid sequence of one of four kinds of Trypanosoma cruzi alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Trypanosoma cruzi: 510889.120).

<SEQ ID NO: 59>

SEQ ID NO: 59 shows the nucleotide sequence of a gene encoding one of four kinds of Trypanosoma cruzi alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Trypanosoma cruzi: 510889.140).

<SEQ ID NO: 60>

SEQ ID NO: 60 shows the amino acid sequence of one of four kinds of Trypanosoma cruzi alanine aminotransferases (KEGG / ENZYME: 2.6.1.2 / Trypanosoma cruzi: 510889.140).

<SEQ ID NO: 61>

SEQ ID NO: 61 shows the nucleotide sequence of a gene encoding hamster taurine transporter.

<SEQ ID NO: 62>

SEQ ID NO: 62 shows the amino acid sequence of hamster taurine transporter.

<SEQ ID NO: 63>

SEQ ID NO: 63 shows the nucleotide sequence of a gene encoding rat taurine transporter (GenBank NM_017206).

<SEQ ID NO: 64>

SEQ ID NO: 64 shows the amino acid sequence of rat taurine transporter (GenBank NM_017206).

<SEQ ID NO: 65>

SEQ ID NO: 65 shows the nucleotide sequence of a gene encoding mouse taurine transporter (GenBank NM_009320).

<SEQ ID NO: 66>

SEQ ID NO: 66 shows the amino acid sequence of mouse taurine transporter (GenBank NM_009320).

<SEQ ID NO: 67>

SEQ ID NO: 67 shows the nucleotide sequence of a gene encoding human taurine transporter (GenBank NM_003043).

<SEQ ID NO: 68>

SEQ ID NO: 68 shows the amino acid sequence of human taurine transporter (GenBank NM_003043) .

CLAIMS

1. A method of producing a desired polypeptide, comprising culturing a cell which expresses alanine aminotransferase and has a transferred DNA encoding the desired polypeptide and thereby allowing the cell to produce said desired polypeptide, and collecting the produced desired polypeptide, wherein the cell which expresses alanine aminoatrnsferase is a cell into which a DNA encoding the alanine aminotransferase has been transferred.

2. The method of claim 1, wherein the cells that strongly express alanine aminotransferase further express a taurine transporter.

3. The method of claim 2, wherein the cells that express a taurine transporter are cells into which DNA encoding a taurine transporter has been transferred.

4. The method of claim 1 or 3, wherein the cell is Chinese hamster ovary cells.

5. The method of any one claims 1 to 4, wherein the desired polypeptide is an antibody.

6. The method of any one claims 1 to 5, wherein the DNA encoding the alanine aminotransferase is any one of the following (a) to (e):

(a) a DNA encoding a polypeptide having the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60;

(b) a DNA encoding a polypeptide which has an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60 by substitution, deletion, addition and/or insertion of 1 to 30 amino acid residues and yet has alanine aminotransferase activity;

(c) a DNA encoding a polypeptide having 70% or more amino acid sequence homology with the amino acid sequence as shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 or 60 and yet having alanine aminotransferase activity;

(d) a DNA having the nucleotide sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59;

(e) a DNA which hybridizes to a DNA complementary to a DNA having the nucleotide sequence as shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,

37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 or 59 under stringent conditions and yet encodes a polypeptide having alanine aminotransferase activity.

7. A method of preparing a pharmaceutical composition comprising the steps as follows,

i) producing a desired polypeptide by the method of any one of claims 1 to 6,

ii) mixing the polypeptide with pharmaceutically acceptable carriers or additives, and

iii) formulating into a preparation.

8. A CHO cell which has a transferred DNA encoding alanine aminotransferase and a transferred DNA encoding a desired antibody.

9. The cell according to claim 8, which further has a transferred DNA encoding a taurine transporter.

10. A method of producing a desired polypeptide, comprising culturing in an α-ketoglutarate-containing medium a cell which expresses alanine aminotransferase and has a transferred DNA encoding the desired polypeptide and thereby allowing the cell to produce said desired polypeptide.

SEQUENCE LISTING

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<150> JP P2007-205158
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Gln Phe Ser Arg Glu Lys Glu Ser Val Leu Gly Asn Leu Ala Lys Lys
405 410 415

Ala Lys Leu Thr Glu Asp Leu Phe Asn Gln Val Pro Gly Ile His Cys
420 425 430

Asn Pro Leu Gln Gly Ala Met Tyr Ala Phe Pro Arg Ile Phe Ile Pro
435 440 445

Ala Lys Ala Val Glu Ala Ala Gln Ala His Gln Met Ala Pro Asp Met

450 455 460

Phe Tyr Cys Met Lys Leu Leu Glu Glu Thr Gly Ile Cys Val Val Pro
465 470 475 480

Gly Ser Gly Phe Gly Gln Arg Glu Gly Thr Tyr His Phe Arg Met Thr
485 490 495

Ile Leu Pro Pro Val Glu Lys Leu Lys Thr Val Leu Gln Lys Val Lys
500 505 510

Asp Phe His Ile Asn Phe Leu Glu Lys Tyr Ala
515 520

<210> 5
<211> 1491
<212> DNA
<213> Mus musculus

<400> 5
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ctaactctgg ataccatgaa cccatgtgtg cggagggtgg agtatgcagt ccgaggcccc 120

atcgtgcaac gtgccttgga gctggagcag gagctgcgcc agggtgtgaa gaagcctttt 180

actgaggtta tccgtgccaa tattggggat gcacaagcca tggggcagag acccatcacc 240

ttcttccgcc aggtcctggc cctctgtgtc taccccaatc ttctgagcag tccggacttc 300

ccagaggatg ccaagagaag ggcagaacgc atcttgcagg catgcggggg ccacagcctg 360

ggtgcctata gcattagctc tggaatccag ccgattcggg aggatgtggc gcaatatatt 420

gagaggagag acggaggcat ccctgcagac ccgaacaaca tatttctgtc cacaggggcc 480

agcgatgcca tcgtgaccat gctcaagctg ctggtagccg gcgagggccg tgcgcgaacc 540

ggtgtactca ttcccattcc tcagtaccca ctgtactcag ctgcgctggc tgagctggac 600

gccgtgcaag tggactacta cctggacgaa gagcgcgcct gggctcttga catcgctgag 660

ctgcggcgcg ctctgtgcca ggcacgtgac cgctgctgcc ctcgagtact atgcgtcatc 720

aaccccggca accccacggg gcaggtgcag acccgtgaat gcatcgaggc cgtaatccgc 780

tttgctttcg aagagggact cttcctgatg gctgatgagg tataccaaga caatgtatat 840

gccgagggct ctcagttcca ttcattcaag aaggtgctca cggagatggg gccaccatat 900

gccacgcagc aggagctcgc gtctttccac tcagtctcta agggctacat gggcgagtgc 960

gggtttcgtg gtggctatgt ggaagtggta aacatggatg ccgaggtgca gaaacagatg 1020

gcgaaactga tgagcgtgcg gttgtgtcca ccagtgccgg gccaggcttt gatgggcatg 1080

gtggtcagtc cgccaacccc ctcggagccg tccttcaagc agtttcaagc agagaggcag 1140

gaggtgctgg ctgaactggc agccaaggct aaactcacgg agcaggtctt caacgaggcc 1200

cccgggatcc gctgcaaccc ggtgcagggc gctatgtatt ccttccctca aattcagctg 1260

cctttgaaag cagtgcagcg tgcgcaggac ctgggcctgg cccctgacat gttcttctgt 1320

ctgtgcctcc tggaagagac tggcatctgc gttgtgcctg ggagtggctt tgggcagcag 1380

gagggcacct atcatttccg gatgaccatt ctgcccccca tggagaaact gcgggtgctg 1440

ctggagaaac tgaggcactt ccatgctaaa ttcactcatg agtactcctg a 1491

<210> 6
<211> 496
<212> PRT
<213> Mus musculus

<400> 6

Met Ala Ser Gln Arg Asn Asp Arg Ile Gln Ala Ser Arg Asn Gly Leu
1 5 10 15

Lys Gly Lys Val Leu Thr Leu Asp Thr Met Asn Pro Cys Val Arg Arg
20 25 30

Val Glu Tyr Ala Val Arg Gly Pro Ile Val Gln Arg Ala Leu Glu Leu
35 40 45

Glu Gln Glu Leu Arg Gln Gly Val Lys Lys Pro Phe Thr Glu Val Ile

50 55 60

Arg Ala Asn Ile Gly Asp Ala Gln Ala Met Gly Gln Arg Pro Ile Thr
65 70 75 80

Phe Phe Arg Gln Val Leu Ala Leu Cys Val Tyr Pro Asn Leu Leu Ser
85 90 95

Ser Pro Asp Phe Pro Glu Asp Ala Lys Arg Arg Ala Glu Arg Ile Leu
100 105 110

Gln Ala Cys Gly Gly His Ser Leu Gly Ala Tyr Ser Ile Ser Ser Gly
115 120 125

Ile Gln Pro Ile Arg Glu Asp Val Ala Gln Tyr Ile Glu Arg Arg Asp
130 135 140

Gly Gly Ile Pro Ala Asp Pro Asn Asn Ile Phe Leu Ser Thr Gly Ala
145 150 155 160

Ser Asp Ala Ile Val Thr Met Leu Lys Leu Leu Val Ala Gly Glu Gly
165 170 175

Arg Ala Arg Thr Gly Val Leu Ile Pro Ile Pro Gln Tyr Pro Leu Tyr
180 185 190

Ser Ala Ala Leu Ala Glu Leu Asp Ala Val Gln Val Asp Tyr Tyr Leu
195 200 205

Asp Glu Glu Arg Ala Trp Ala Leu Asp Ile Ala Glu Leu Arg Arg Ala
210 215 220

Leu Cys Gln Ala Arg Asp Arg Cys Cys Pro Arg Val Leu Cys Val Ile
225 230 235 240

Asn Pro Gly Asn Pro Thr Gly Gln Val Gln Thr Arg Glu Cys Ile Glu

245 250 255

Ala Val Ile Arg Phe Ala Phe Glu Glu Gly Leu Phe Leu Met Ala Asp
260 265 270

Glu Val Tyr Gln Asp Asn Val Tyr Ala Glu Gly Ser Gln Phe His Ser
275 280 285

Phe Lys Lys Val Leu Thr Glu Met Gly Pro Pro Tyr Ala Thr Gln Gln
290 295 300

Glu Leu Ala Ser Phe His Ser Val Ser Lys Gly Tyr Met Gly Glu Cys
305 310 315 320

Gly Phe Arg Gly Gly Tyr Val Glu Val Val Asn Met Asp Ala Glu Val
325 330 335

Gln Lys Gln Met Ala Lys Leu Met Ser Val Arg Leu Cys Pro Pro Val
340 345 350

Pro Gly Gln Ala Leu Met Gly Met Val Val Ser Pro Pro Thr Pro Ser
355 360 365

Glu Pro Ser Phe Lys Gln Phe Gln Ala Glu Arg Gln Glu Val Leu Ala
370 375 380

Glu Leu Ala Ala Lys Ala Lys Leu Thr Glu Gln Val Phe Asn Glu Ala
385 390 395 400

Pro Gly Ile Arg Cys Asn Pro Val Gln Gly Ala Met Tyr Ser Phe Pro
405 410 415

Gln Ile Gln Leu Pro Leu Lys Ala Val Gln Arg Ala Gln Asp Leu Gly
420 425 430

Leu Ala Pro Asp Met Phe Phe Cys Leu Cys Leu Leu Glu Glu Thr Gly

435 440 445

Ile Cys Val Val Pro Gly Ser Gly Phe Gly Gln Gln Glu Gly Thr Tyr
450 455 460

His Phe Arg Met Thr Ile Leu Pro Pro Met Glu Lys Leu Arg Val Leu
465 470 475 480

Leu Glu Lys Leu Arg His Phe His Ala Lys Phe Thr His Glu Tyr Ser
485 490 495

<210> 7
<211> 1569
<212> DNA
<213> Mus musculus

<400> 7
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ggccgtagtc acagcagcgc tgcagccgaa gcctcggcgg cgctcaaggt gcgaccggag 120

cgcagccctc gagaccgcat cctcaccctg gagtccatga acccgcaggt gaaggcggtg 180

gagtacgctg tgcggggacc catcgtgctc aaagccggcg agatcgagat ggagctgcag 240

cggggtatca aaaaaccatt cactgaggta atccgagcca acattgggga tgcccatgct 300

atgggccagc agccaatcac cttcctccgt caggtgatgg cactctgcac ctacccaaac 360

ctactaaaca gccccagctt cccagaagac gctaagaaac gagcgcggcg gatcctgcag 420

gcttgtggtg gaaacagctt gggatcttac agtgctagcc aaggcgttaa ctgtatccgt 480

gaagatgtgg cagcctttat caccaggaga gatggtgtgc ctgcagaccc agacaacatt 540

tacctgacta ctggagctag cgacggtatt tctacaatcc tgaagctcct ggtctccggt 600

ggtggcaagt cacggaccgg cgtgatgatt cccatccccc agtatccctt gtactccgcg 660

gtcatctctg agctcgacgc ggtgcaggtc aactactatc tggatgaaga gaactgctgg 720

gctttgaatg tggacgagct ccggcgggca ttgcggcaag ccaaagacca ctgtgaccct 780

aaagttctct gcattatcaa ccccggaaac cccacaggcc aggtacaaag cagaaagtgc 840

atagaagatg tgattcactt tgcctgggaa gagaagcttt ttctcctggc tgatgaggtg 900

taccaggaca acgtgtactc tccagactgc agattccact cgtttaagaa agtgctttac 960

cagatggggc acgagtactc cagcaacgtg gagctcgcct ccttccactc cacctccaag 1020

ggctacatgg gcgagtgtgg ctacagaggg ggctacatgg aggtgatcaa tttgcacccc 1080

gagatcaaag gccagctggt gaagctactc tcggttcgcc tctgtccgcc agtgtcagga 1140

caggccgcca tggacattgt tgtgaatcca ccggaaccag gagaggagtc ctttgagcaa 1200

ttcagcaggg aaaaagaatt cgtccttggt aatctggcca aaaaagcaaa gctgacagaa 1260

gatctgttta accaagtccc agggatccag tgcaaccccc tgcaaggagc tatgtatgcg 1320

ttccctcgga ttctcatccc tgccaaggcc gtggaggcag ctcagtccca taaaatggct 1380

ccagacatgt tctactgcat gaagctcctg gaggagactg gcatctgtgt cgtgcctggc 1440

agtggctttg ggcagcgaga aggcacttac cacttcagaa tgaccattct ccctccggtg 1500

gataaactga agaccgtgct ccacaaggtg aaagactttc acctgaagtt cctggagcag 1560

tactcatga 1569

<210> 8
<211> 522
<212> PRT
<213> Mus musculus

<400> 8

Met Gln Arg Ala Ala Val Leu Val Arg Arg Gly Ser Cys Pro Arg Ala
1 5 10 15

Ser Gly Pro Trp Gly Arg Ser His Ser Ser Ala Ala Ala Glu Ala Ser
20 25 30

Ala Ala Leu Lys Val Arg Pro Glu Arg Ser Pro Arg Asp Arg Ile Leu
35 40 45

Thr Leu Glu Ser Met Asn Pro Gln Val Lys Ala Val Glu Tyr Ala Val

50 55 60

Arg Gly Pro Ile Val Leu Lys Ala Gly Glu Ile Glu Met Glu Leu Gln
65 70 75 80

Arg Gly Ile Lys Lys Pro Phe Thr Glu Val Ile Arg Ala Asn Ile Gly
85 90 95

Asp Ala His Ala Met Gly Gln Gln Pro Ile Thr Phe Leu Arg Gln Val
100 105 110

Met Ala Leu Cys Thr Tyr Pro Asn Leu Leu Asn Ser Pro Ser Phe Pro
115 120 125

Glu Asp Ala Lys Lys Arg Ala Arg Arg Ile Leu Gln Ala Cys Gly Gly
130 135 140

Asn Ser Leu Gly Ser Tyr Ser Ala Ser Gln Gly Val Asn Cys Ile Arg
145 150 155 160

Glu Asp Val Ala Ala Phe Ile Thr Arg Arg Asp Gly Val Pro Ala Asp
165 170 175

Pro Asp Asn Ile Tyr Leu Thr Thr Gly Ala Ser Asp Gly Ile Ser Thr
180 185 190

Ile Leu Lys Leu Leu Val Ser Gly Gly Gly Lys Ser Arg Thr Gly Val
195 200 205

Met Ile Pro Ile Pro Gln Tyr Pro Leu Tyr Ser Ala Val Ile Ser Glu
210 215 220

Leu Asp Ala Val Gln Val Asn Tyr Tyr Leu Asp Glu Glu Asn Cys Trp
225 230 235 240

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

245 250 255

His Cys Asp Pro Lys Val Leu Cys Ile Ile Asn Pro Gly Asn Pro Thr
260 265 270

Gly Gln Val Gln Ser Arg Lys Cys Ile Glu Asp Val Ile His Phe Ala
275 280 285

Trp Glu Glu Lys Leu Phe Leu Leu Ala Asp Glu Val Tyr Gln Asp Asn
290 295 300

Val Tyr Ser Pro Asp Cys Arg Phe His Ser Phe Lys Lys Val Leu Tyr
305 310 315 320

Gln Met Gly His Glu Tyr Ser Ser Asn Val Glu Leu Ala Ser Phe His
325 330 335

Ser Thr Ser Lys Gly Tyr Met Gly Glu Cys Gly Tyr Arg Gly Gly Tyr
340 345 350

Met Glu Val Ile Asn Leu His Pro Glu Ile Lys Gly Gln Leu Val Lys
355 360 365

Leu Leu Ser Val Arg Leu Cys Pro Pro Val Ser Gly Gln Ala Ala Met
370 375 380

Asp Ile Val Val Asn Pro Pro Glu Pro Gly Glu Glu Ser Phe Glu Gln
385 390 395 400

Phe Ser Arg Glu Lys Glu Phe Val Leu Gly Asn Leu Ala Lys Lys Ala
405 410 415

Lys Leu Thr Glu Asp Leu Phe Asn Gln Val Pro Gly Ile Gln Cys Asn
420 425 430

Pro Leu Gln Gly Ala Met Tyr Ala Phe Pro Arg Ile Leu Ile Pro Ala

435 440 445

Lys Ala Val Glu Ala Ala Gln Ser His Lys Met Ala Pro Asp Met Phe
450 455 460

Tyr Cys Met Lys Leu Leu Glu Glu Thr Gly Ile Cys Val Val Pro Gly
465 470 475 480

Ser Gly Phe Gly Gln Arg Glu Gly Thr Tyr His Phe Arg Met Thr Ile
485 490 495

Leu Pro Pro Val Asp Lys Leu Lys Thr Val Leu His Lys Val Lys Asp
500 505 510

Phe His Leu Lys Phe Leu Glu Gln Tyr Ser
515 520

<210> 9
<211> 1491
<212> DNA
<213> Rattus norvegicus

<400> 9
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ctaactctgg acactatgaa cccatgtgtg cggagggtgg agtatgcagt tcgaggaccc 120

attgtgcagc gtgccttgga gctggagcag gagctgcgtc agggtgtgaa gaagccgttt 180

actgaggtca tccgtgccaa cattggggat gcacaagcca tggggcagag acccatcacc 240

ttcttccgcc aggtcctggc cctctgtgtc taccccaatc ttctgagcag tcctgacttc 300

ccagaggatg ccaagagaag ggcagaacgc atcttgcagg cctgcggggg ccacagcctg 360

ggtgcctata gcattagctc tggaatccag ccgatccggg aggatgtggc gcaatacatt 420

gagagaagag acggaggcat ccccgcagac ccgaacaaca tatttctatc cacaggggcc 480

agcgatgcca tcgtgacaat gctcaagctg ctggtatctg gcgagggccg tgcacgaaca 540

ggtgtactca ttcccattcc tcagtaccca ctgtactcag ccgcgctggc tgaactggac 600

gccgtgcaag tggactacta cctggacgaa gagcgcgcct gggctctgga catcgcagag 660

ctgcggcgcg ctctgtgcca ggcacgtgac cgttgctgcc ctcgagtact gtgcgtcatc 720

aaccccggca accccactgg gcaggtgcag acccgtgagt gcatcgaggc cgtaatccgc 780

tttgctttca aagaaggact cttcttgatg gctgatgagg tataccagga caacgtgtat 840

gccgagggct ctcagttcca ttcattcaag aaggtgctca tggagatggg gccaccgtat 900

tccacgcagc aggagcttgc ttctttccac tcagtctcta agggctacat gggcgagtgc 960

gggtttcgtg gtggctatgt ggaggtggta aacatggatg ctgaggtgca gaaacagatg 1020

gggaagctga tgagtgtgcg gctgtgtcca ccagtgccag gccaggcctt gatggacatg 1080

gtggtcagtc cgccaacacc ctccgagccg tccttcaagc agtttcaagc agagagacag 1140

gaggtgctgg ctgaactggc agccaaggct aagctcacgg agcaggtctt caatgaggct 1200

cccgggatcc gctgcaaccc agtgcagggc gccatgtatt ccttccctca agtgcagctg 1260

cccttgaaag cggtgcagcg tgctcaggaa ctgggcctgg cccctgacat gttcttctgc 1320

ctgtgcctcc tggaagagac tggcatctgc gttgtgcccg ggagtggctt tgggcagcag 1380

gagggcacct atcatttccg gatgaccatt ctgccccca tggagaaact gcggctgctg 1440

ctggaaaaac tcagtcactt ccatgccaag ttcacccatg agtactcctg a 1491

<210> 10
<211> 496
<212> PRT
<213> Rattus norvegicus

<400> 10

Met Ala Ser Arg Val Asn Asp Gln Ser Gln Ala Ser Arg Asn Gly Leu
1 5 10 15

Lys Gly Lys Val Leu Thr Leu Asp Thr Met Asn Pro Cys Val Arg Arg
20 25 30

Val Glu Tyr Ala Val Arg Gly Pro Ile Val Gln Arg Ala Leu Glu Leu

35 40 45

Glu Gln Glu Leu Arg Gln Gly Val Lys Lys Pro Phe Thr Glu Val Ile
50 55 60

Arg Ala Asn Ile Gly Asp Ala Gln Ala Met Gly Gln Arg Pro Ile Thr
65 70 75 80

Phe Phe Arg Gln Val Leu Ala Leu Cys Val Tyr Pro Asn Leu Leu Ser
85 90 95

Ser Pro Asp Phe Pro Glu Asp Ala Lys Arg Arg Ala Glu Arg Ile Leu
100 105 110

Gln Ala Cys Gly Gly His Ser Leu Gly Ala Tyr Ser Ile Ser Ser Gly
115 120 125

Ile Gln Pro Ile Arg Glu Asp Val Ala Gln Tyr Ile Glu Arg Arg Asp
130 135 140

Gly Gly Ile Pro Ala Asp Pro Asn Asn Ile Phe Leu Ser Thr Gly Ala
145 150 155 160

Ser Asp Ala Ile Val Thr Met Leu Lys Leu Leu Val Ser Gly Glu Gly
165 170 175

Arg Ala Arg Thr Gly Val Leu Ile Pro Ile Pro Gln Tyr Pro Leu Tyr
180 185 190

Ser Ala Ala Leu Ala Glu Leu Asp Ala Val Gln Val Asp Tyr Tyr Leu
195 200 205

Asp Glu Glu Arg Ala Trp Ala Leu Asp Ile Ala Glu Leu Arg Arg Ala
210 215 220

Leu Cys Gln Ala Arg Asp Arg Cys Cys Pro Arg Val Leu Cys Val Ile

225 230 235 240

Asn Pro Gly Asn Pro Thr Gly Gln Val Gln Thr Arg Glu Cys Ile Glu
245 250 255

Ala Val Ile Arg Phe Ala Phe Lys Glu Gly Leu Phe Leu Met Ala Asp
260 265 270

Glu Val Tyr Gln Asp Asn Val Tyr Ala Glu Gly Ser Gln Phe His Ser
275 280 285

Phe Lys Lys Val Leu Met Glu Met Gly Pro Pro Tyr Ser Thr Gln Gln
290 295 300

Glu Leu Ala Ser Phe His Ser Val Ser Lys Gly Tyr Met Gly Glu Cys
305 310 315 320

Gly Phe Arg Gly Gly Tyr Val Glu Val Val Asn Met Asp Ala Glu Val
325 330 335

Gln Lys Gln Met Gly Lys Leu Met Ser Val Arg Leu Cys Pro Pro Val
340 345 350

Pro Gly Gln Ala Leu Met Asp Met Val Val Ser Pro Pro Thr Pro Ser
355 360 365

Glu Pro Ser Phe Lys Gln Phe Gln Ala Glu Arg Gln Glu Val Leu Ala
370 375 380

Glu Leu Ala Ala Lys Ala Lys Leu Thr Glu Gln Val Phe Asn Glu Ala
385 390 395 400

Pro Gly Ile Arg Cys Asn Pro Val Gln Gly Ala Met Tyr Ser Phe Pro
405 410 415

Gln Val Gln Leu Pro Leu Lys Ala Val Gln Arg Ala Gln Glu Leu Gly

420 425 430

Leu Ala Pro Asp Met Phe Phe Cys Leu Cys Leu Leu Glu Glu Thr Gly
435 440 445

Ile Cys Val Val Pro Gly Ser Gly Phe Gly Gln Gln Glu Gly Thr Tyr
450 455 460

His Phe Arg Met Thr Ile Leu Pro Pro Met Glu Lys Leu Arg Leu Leu
465 470 475 480

Leu Glu Lys Leu Ser His Phe His Ala Lys Phe Thr His Glu Tyr Ser
485 490 495

<210> 11
<211> 1125
<212> DNA
<213> Canis familiaris

<400> 11
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ggcgctacgc ctgatgccgg gatcgagggc ctgaccacct gttgcctcct ctttgctcag 120

ggtatcaaga aaccgttcac cgaggtcatc cgcgccaaca tcggggacgc ccaggccatg 180

ggccagcagc ctataacctt cctccgacag gtgatggcac tgtgcaccta ccccaacctg 240

ctggacagcc ccagcttccc agaagatgct aagaaacgag cccggaggat cctacaggct 300

tgtggcggga acagcctggg gtcctacagt gccagccagg gcgtcaactg catccgcgag 360

gacgtggccg cctacgtcac caggagggac ggcggggtgc ccgcggaccc cttcaacatt 420

tacctgacca ctggagccag cgacggcatt tctacgatcc tgaagatcct ggtgtccggg 480

ggtggcaagt cgcggacggg cgtgctgatc cccatcccac agtacccccc ctactcggcc 540

gtcatctccg agctcgacgc catccaggtg aactactact tggacgagga gaactgctgg 600

gccctcgacg tgaacgagct ccggcgggcc gtgcaggagg ctaaggacca ctgtaacccc 660

aaggtgctgt gcatcatcaa ccccgggaac cccacaggtc aggtgcaaag caggaagtgc 720

atagaggacg tcatccactt tgcctgggaa gagaagctct ttctcctggc agatgaggtg 780

taccaggaca acgtgtactc tccggactgc agattccact ccttcaagaa ggtgctctac 840

gagatggggc ccgagtactc gagcaacgtg gagcttgcgt ccttccactc tacctccaag 900

ggctacatgg gcgagtacgt tggccttggc ttcctcccgc ggccccacca ctcggccctg 960

cccgctggcg gcctgctgcg cggggaacac ggggcccatc tcaggggccc tgtgcatgag 1020

ctcagccctg gtgcagggac gcccgtgcgg cgaggtcctg ctggggcccc gggctccccg 1080

cgcttcctgc cgggcccacg ctgctgccct gggactgaac cctga 1125

<210> 12
<211> 374
<212> PRT
<213> Canis familiaris

<400> 12

Met Leu Ala Leu His Gly Ala Val Val Lys Val Lys Arg Gly Arg Leu
1 5 10 15

Arg Pro Gly Leu Gly Ala Thr Pro Asp Ala Gly Ile Glu Gly Leu Thr
20 25 30

Thr Cys Cys Leu Leu Phe Ala Gln Gly Ile Lys Lys Pro Phe Thr Glu
35 40 45

Val Ile Arg Ala Asn Ile Gly Asp Ala Gln Ala Met Gly Gln Gln Pro
50 55 60

Ile Thr Phe Leu Arg Gln Val Met Ala Leu Cys Thr Tyr Pro Asn Leu
65 70 75 80

Leu Asp Ser Pro Ser Phe Pro Glu Asp Ala Lys Lys Arg Ala Arg Arg
85 90 95

Ile Leu Gln Ala Cys Gly Gly Asn Ser Leu Gly Ser Tyr Ser Ala Ser

100 105 110

Gln Gly Val Asn Cys Ile Arg Glu Asp Val Ala Ala Tyr Val Thr Arg
115 120 125

Arg Asp Gly Gly Val Pro Ala Asp Pro Phe Asn Ile Tyr Leu Thr Thr
130 135 140

Gly Ala Ser Asp Gly Ile Ser Thr Ile Leu Lys Ile Leu Val Ser Gly
145 150 155 160

Gly Gly Lys Ser Arg Thr Gly Val Leu Ile Pro Ile Pro Gln Tyr Pro
165 170 175

Leu Tyr Ser Ala Val Ile Ser Glu Leu Asp Ala Ile Gln Val Asn Tyr
180 185 190

Tyr Leu Asp Glu Glu Asn Cys Trp Ala Leu Asp Val Asn Glu Leu Arg
195 200 205

Arg Ala Val Gln Glu Ala Lys Asp His Cys Asn Pro Lys Val Leu Cys
210 215 220

Ile Ile Asn Pro Gly Asn Pro Thr Gly Gln Val Gln Ser Arg Lys Cys
225 230 235 240

Ile Glu Asp Val Ile His Phe Ala Trp Glu Glu Lys Leu Phe Leu Leu
245 250 255

Ala Asp Glu Val Tyr Gln Asp Asn Val Tyr Ser Pro Asp Cys Arg Phe
260 265 270

His Ser Phe Lys Lys Val Leu Tyr Glu Met Gly Pro Glu Tyr Ser Ser
275 280 285

Asn Val Glu Leu Ala Ser Phe His Ser Thr Ser Lys Gly Tyr Met Gly

290 295 300

Glu Tyr Val Gly Leu Gly Phe Leu Pro Arg Pro His His Ser Ala Leu
305 310 315 320

Pro Ala Gly Gly Leu Leu Arg Gly Glu His Gly Ala His Leu Arg Gly
325 330 335

Pro Val His Glu Leu Ser Pro Gly Ala Gly Thr Pro Val Arg Arg Gly
340 345 350

Pro Ala Gly Ala Pro Gly Ser Pro Arg Phe Leu Pro Gly Pro Arg Cys
355 360 365

Cys Pro Gly Thr Glu Pro
370

<210> 13
<211> 1623
<212> DNA
<213> Xenopus laevis

<400> 13
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aggagcagat tgccccccca gctcacttct gccctcctgt gccccctcag gtcgctgtcg 120

ggaacgccgc tggctgaacc ggacgggaaa gttactcgca agatgtctga gaacgggaca 180

tgcaaccgga tcctgactct ggactccatg aatccctgta tccagaaagt ggaatacgca 240

gtgaggggcc ccatcgtcat cagggctgtg gagctggaga aagaactgca gcaggggta 300

aagaagccat tcacagaagt gatcaaagcc aatattggag atgcccatgc aatgggtcag 360

aaacccgtta ctttcctgcg ccaggtgagt gccatctgtc tgtaccccga gctcatgaat 420

gacaacaagt tcccggagga cgtgaagcag aaggcagcga ggatcctgca ggcgtgtggc 480

gggcacagca ttggggccta cagcgccagc caagggattg aagtgatccg acaagatgtg 540

gccaagtaca ttgagagaag ggatgggggt atcctgtccg accccaacaa catctacctc 600

tccacggggg ccagtgactc tattgtgaca atgctgaagt tgctggtgtc tgggcaaggg 660

aaatcccgaa ctggggtgat gatcccgatc cctcaatacc cgctgtattc tgcggccctg 720

gcagagttgg atgccgtgca ggttaattat tatctggatg aggagaactg ctgggccctg 780

gacatcaacg agctgcggag agcactagcg gaggcccgaa aacattgtga ccccaaagta 840

ctgtgcatta ttaacccagg aaaccctaca gggcaggtgc agagccgcaa gtgcattgag 900

gacgtgatcc gttttgctgc tgaagagaat cttttcctga tggcggatga ggtctaccaa 960

gataatgtct atgccaaggg ctgtgccttt cactccttca aaaaggttct ctttgagatg 1020

ggacccaagt attcagaaac gctggaactg gcttctttcc actccacatc caagggatac 1080

atgggagagt gcgggttcag agggggttac atggaagtga tcaatatgga tcctgctgtc 1140

aagcaacaac taaccaagtt ggtgtctgtg cgtctgtgcc ccccagtgcc ggggcaagta 1200

ttacttgatg tgattgtgaa cccaccaaag cctggggagc cctcctacaa acagttcatt 1260

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aggatccaca tcccagagaa ggccattaaa cttgcacagg ctgagggaca ggccccagac 1440

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tttggacaac gtgagggcac tcaccatttc aggatgacca tcctccctcc caccgataag 1560

ctgaagagcc tgttagagcg gctgaaggat ttccaccaga aatttatgga tgagtattcc 1620

tag 1623

<210> 14
<211> 540
<212> PRT
<213> Xenopus laevis

<400> 14

Met Ser Ile Leu Arg Gly Ser Leu Arg Gly Val Leu Ala Pro Asn Ala
1 5 10 15

Ser Val Val Phe Arg Ser Arg Leu Pro Pro Gln Leu Thr Ser Ala Leu
20 25 30

Leu Cys Pro Leu Arg Ser Leu Ser Gly Thr Pro Leu Ala Glu Pro Asp
35 40 45

Gly Lys Val Thr Arg Lys Met Ser Glu Asn Gly Thr Cys Asn Arg Ile
50 55 60

Leu Thr Leu Asp Ser Met Asn Pro Cys Ile Gln Lys Val Glu Tyr Ala
65 70 75 80

Val Arg Gly Pro Ile Val Ile Arg Ala Val Glu Leu Glu Lys Glu Leu
85 90 95

Gln Gln Gly Val Lys Lys Pro Phe Thr Glu Val Ile Lys Ala Asn Ile
100 105 110

Gly Asp Ala His Ala Met Gly Gln Lys Pro Val Thr Phe Leu Arg Gln
115 120 125

Val Ser Ala Ile Cys Leu Tyr Pro Glu Leu Met Asn Asp Asn Lys Phe
130 135 140

Pro Glu Asp Val Lys Gln Lys Ala Ala Arg Ile Leu Gln Ala Cys Gly
145 150 155 160

Gly His Ser Ile Gly Ala Tyr Ser Ala Ser Gln Gly Ile Glu Val Ile
165 170 175

Arg Gln Asp Val Ala Lys Tyr Ile Glu Arg Arg Asp Gly Gly Ile Leu
180 185 190

Ser Asp Pro Asn Asn Ile Tyr Leu Ser Thr Gly Ala Ser Asp Ser Ile
195 200 205

Val Thr Met Leu Lys Leu Leu Val Ser Gly Gln Gly Lys Ser Arg Thr
210 215 220

Gly Val Met Ile Pro Ile Pro Gln Tyr Pro Leu Tyr Ser Ala Ala Leu
225 230 235 240

Ala Glu Leu Asp Ala Val Gln Val Asn Tyr Tyr Leu Asp Glu Glu Asn
245 250 255

Cys Trp Ala Leu Asp Ile Asn Glu Leu Arg Arg Ala Leu Ala Glu Ala
260 265 270

Arg Lys His Cys Asp Pro Lys Val Leu Cys Ile Ile Asn Pro Gly Asn
275 280 285

Pro Thr Gly Gln Val Gln Ser Arg Lys Cys Ile Glu Asp Val Ile Arg
290 295 300

Phe Ala Ala Glu Glu Asn Leu Phe Leu Met Ala Asp Glu Val Tyr Gln
305 310 315 320

Asp Asn Val Tyr Ala Lys Gly Cys Ala Phe His Ser Phe Lys Lys Val
325 330 335

Leu Phe Glu Met Gly Pro Lys Tyr Ser Glu Thr Leu Glu Leu Ala Ser
340 345 350

Phe His Ser Thr Ser Lys Gly Tyr Met Gly Glu Cys Gly Phe Arg Gly
355 360 365

Gly Tyr Met Glu Val Ile Asn Met Asp Pro Ala Val Lys Gln Gln Leu
370 375 380

Thr Lys Leu Val Ser Val Arg Leu Cys Pro Pro Val Pro Gly Gln Val
385 390 395 400

Leu Leu Asp Val Ile Val Asn Pro Pro Lys Pro Gly Glu Pro Ser Tyr
405 410 415

Lys Gln Phe Ile Ser Glu Lys Gln Ala Val Leu Asn Asn Leu Ala Glu
420 425 430

Lys Ala Arg Leu Thr Glu Glu Ile Leu Asn Gln Ala Pro Gly Ile Arg
435 440 445

Cys Asn Pro Val Gln Gly Ala Met Tyr Ser Phe Pro Arg Ile His Ile
450 455 460

Pro Glu Lys Ala Ile Lys Leu Ala Gln Ala Glu Gly Gln Ala Pro Asp
465 470 475 480

Met Phe Phe Cys Met Lys Leu Leu Glu Glu Thr Gly Ile Cys Val Val
485 490 495

Pro Gly Ser Gly Phe Gly Gln Arg Glu Gly Thr His His Phe Arg Met
500 505 510

Thr Ile Leu Pro Pro Thr Asp Lys Leu Lys Ser Leu Leu Glu Arg Leu
515 520 525

Lys Asp Phe His Gln Lys Phe Met Asp Glu Tyr Ser
530 535 540

<210> 15
<211> 1707
<212> DNA
<213> Drosophila melanogaster

<400> 15
atgagtcgaa tgctaattaa acctgctgcc gccacagttt cggccgcatt gcagcagcac 60

cagcgccagc agcaacagta cgttattcgc cgctggaaat cgttcctgca caacaacagc 120

aacaatgcca atcgacgtgc ggcgaaatca acggcaacag caacggtgac ggcagcagcg 180

acgtcgcagc gccatggaac aagcggcgat ttcattcaac cgttagacgt ccgccgttcc 240

ttttcaacca gccacaaaat gccgtcgtcg tcgaaagcgc tcacactgga taacataaat 300

cccaacttta ttgccatgga atatgccgtt cgcggtcctc tggtgattcg tgctggggaa 360

atcgagaagg aactggaaaa gggtgtcaag aagccattcg accaggtgat ccgtgccaac 420

atcggtgatt gccatgcgat gggccagcag cccttgacct tcctgcgaca gctgttggcg 480

ctgaccttcg agacacgtct gctggattca cccgattatc ccgaggacgt caagaagcgc 540

gcctgtgcca ttttgaacgg ctgccagggt caatcggtgg gctcgtacac cgactccgcc 600

ggtctggagg tggtgcgtcg ccaggttgct cagtacatcg agaaaaggga tggcggcatc 660

gcctccaatt ggcaggacat ctatctaacc ggcggtgcct ctcccggcat caagagcatt 720

ctctccatga tcaacgccga ggtgggatgc aaggcgcctg gtgtcatggt gcccattccg 780

cagtacccac tgtactcggc caccatctcc gaatacggca tgaccaaggt ggattactat 840

ctggaggagg agaccggttg gagcctggac aggaaggagc tgcaacggtc ctacgatgag 900

gcgaagaagg tctgcaatcc gcgtgccctg gtcgtgatca atccgggcaa tcccaccgga 960

caggtactga cccgcgagaa catcgaggag atcattaagt tcgcacacga taacaaggtg 1020

ctggtgctgg ccgatgaggt gtaccaggac aatgtctacg acaagaactc caagttctgg 1080

tcgttcaaga aggtggccta cgaaatgggc gacccctatc gtaatctgga aatggtcagt 1140

ttcctgtcca cctcgaaggg ctatctgggc gagtgcggca ttcgcggcgg ttacatggag 1200

gttctcaatc ttgatcccaa ggtcaaggcc atgctgacca agtcgataac ggcggcgctt 1260

tgcagcacca ccgctggcca ggtggccgtg agtgccctgg tcaatccacc gcagcccgga 1320

gagccatcat acgatctgta caagaaggag cgcgatggca ttctggccgc tctaaaagaa 1380

cgggccgagc tcgtccacaa ggcactgaac agcttcgaag gctacaaggt taaccccgta 1440

cagggcgcca tgtacgtctt tccacagatc gagatcccgc ccaaggcgat cgaggcggcc 1500

aaggccaagg gcatggcccc cgatgttttc tacgcatttg agctgctcga gacgagcggc 1560

atttgcattg ttcctggcag tggatttggt cagaagcccg gcacgtggca tttccgaagc 1620

acgatcctcc cgcaaacgga caagctgaag ctgatgatgg agaagttccg tgtgttccac 1680

gccgagttca tgaagaagta caagtag 1707

<210> 16
<211> 568
<212> PRT
<213> Drosophila melanogaster

<400> 16

Met Ser Arg Met Leu Ile Lys Pro Ala Ala Ala Thr Val Ser Ala Ala
1 5 10 15

Leu Gln Gln His Gln Arg Gln Gln Gln Gln Tyr Val Ile Arg Arg Trp
20 25 30

Lys Ser Phe Leu His Asn Asn Ser Asn Asn Ala Asn Arg Arg Ala Ala
35 40 45

Lys Ser Thr Ala Thr Ala Thr Val Thr Ala Ala Ala Thr Ser Gln Arg
50 55 60

His Gly Thr Ser Gly Asp Phe Ile Gln Pro Leu Asp Val Arg Arg Ser
65 70 75 80

Phe Ser Thr Ser His Lys Met Pro Ser Ser Ser Lys Ala Leu Thr Leu
85 90 95

Asp Asn Ile Asn Pro Asn Phe Ile Ala Met Glu Tyr Ala Val Arg Gly
100 105 110

Pro Leu Val Ile Arg Ala Gly Glu Ile Glu Lys Glu Leu Glu Lys Gly
115 120 125

Val Lys Lys Pro Phe Asp Gln Val Ile Arg Ala Asn Ile Gly Asp Cys
130 135 140

His Ala Met Gly Gln Gln Pro Leu Thr Phe Leu Arg Gln Leu Leu Ala
145 150 155 160

Leu Thr Phe Glu Thr Arg Leu Leu Asp Ser Pro Asp Tyr Pro Glu Asp
165 170 175

Val Lys Lys Arg Ala Cys Ala Ile Leu Asn Gly Cys Gln Gly Gln Ser
180 185 190

Val Gly Ser Tyr Thr Asp Ser Ala Gly Leu Glu Val Val Arg Arg Gln
195 200 205

Val Ala Gln Tyr Ile Glu Lys Arg Asp Gly Gly Ile Ala Ser Asn Trp
210 215 220

Gln Asp Ile Tyr Leu Thr Gly Gly Ala Ser Pro Gly Ile Lys Ser Ile
225 230 235 240

Leu Ser Met Ile Asn Ala Glu Val Gly Cys Lys Ala Pro Gly Val Met
245 250 255

Val Pro Ile Pro Gln Tyr Pro Leu Tyr Ser Ala Thr Ile Ser Glu Tyr
260 265 270

Gly Met Thr Lys Val Asp Tyr Tyr Leu Glu Glu Glu Thr Gly Trp Ser
275 280 285

Leu Asp Arg Lys Glu Leu Gln Arg Ser Tyr Asp Glu Ala Lys Lys Val
290 295 300

Cys Asn Pro Arg Ala Leu Val Val Ile Asn Pro Gly Asn Pro Thr Gly
305 310 315 320

Gln Val Leu Thr Arg Glu Asn Ile Glu Glu Ile Ile Lys Phe Ala His
325 330 335

Asp Asn Lys Val Leu Val Leu Ala Asp Glu Val Tyr Gln Asp Asn Val
340 345 350

Tyr Asp Lys Asn Ser Lys Phe Trp Ser Phe Lys Lys Val Ala Tyr Glu
355 360 365

Met Gly Asp Pro Tyr Arg Asn Leu Glu Met Val Ser Phe Leu Ser Thr
370 375 380

Ser Lys Gly Tyr Leu Gly Glu Cys Gly Ile Arg Gly Gly Tyr Met Glu
385 390 395 400

Val Leu Asn Leu Asp Pro Lys Val Lys Ala Met Leu Thr Lys Ser Ile
405 410 415

Thr Ala Ala Leu Cys Ser Thr Thr Ala Gly Gln Val Ala Val Ser Ala
420 425 430

Leu Val Asn Pro Pro Gln Pro Gly Glu Pro Ser Tyr Asp Leu Tyr Lys
435 440 445

Lys Glu Arg Asp Gly Ile Leu Ala Ala Leu Lys Glu Arg Ala Glu Leu
450 455 460

Val His Lys Ala Leu Asn Ser Phe Glu Gly Tyr Lys Val Asn Pro Val
465 470 475 480

Gln Gly Ala Met Tyr Val Phe Pro Gln Ile Glu Ile Pro Pro Lys Ala
485 490 495

Ile Glu Ala Ala Lys Ala Lys Gly Met Ala Pro Asp Val Phe Tyr Ala
500 505 510

Phe Glu Leu Leu Glu Thr Ser Gly Ile Cys Ile Val Pro Gly Ser Gly
515 520 525

Phe Gly Gln Lys Pro Gly Thr Trp His Phe Arg Ser Thr Ile Leu Pro
530 535 540

Gln Thr Asp Lys Leu Lys Leu Met Met Glu Lys Phe Arg Val Phe His
545 550 555 560

Ala Glu Phe Met Lys Lys Tyr Lys
565

<210> 17
<211> 1515
<212> DNA
<213> Caenorhabditis elegans

<400> 17
atgcgaaccg tacaagcaat ttccggactc gtcacaagtc gctttttcgg cacatccact 60

agaatcatgg ctagcggaaa gactttgaac acctccaaca tcaatccaaa tgttatcaag 120

atggagtatg ctgttcgtgg accaatcgtg atccgtgccg tggagcttga aaaagagctt 180

gcgaccggtg ctcagaagcc attcccaaat gtcatcaagg ctaatattgg agatgctcat 240

gctatgggtc aaaagccgat tactttcatt cgccagctcc tcgcgtgtat tgtcaaccca 300

gagatcatga aaacggacaa atcaattcca tctgatgtta tcgaacatgc aaatgcattc 360

cttggaagtt gtggaggaaa atccgctgga gcatacagtc agagtacggg agtggaaatt 420

gtacgaaaac acgtggcaga gtatattaag agacgtgatg gaggaattcc atgcaattca 480

gaagatgtct gcttgtctgg aggagcttct gaatcaatcc gaaatgttct caaacttttt 540

atcaatcata acaacgcaaa gaaagtcgga gtcatgattc caattccaca atatccactc 600

tattctgcca ctatcgaaga attcggactt ggacaagttg gatactattt gagtgaatcg 660

tctaattggt ccatggatga agctgaactt gaaagatctt tcaatgatca ctgcaaagaa 720

tacgatattc gagttttgtg tatcatcaat ccaggaaatc ctaccggaca agcactttct 780

cgtgaaaata ttgagactat catcaagttt gcacaaaaga agaacctgtt ccttatggct 840

gatgaggttt atcaagacaa cgtctacgct caaggatcgc aattccattc attcaagaag 900

gttcttgtgg agatgggaga gccatacaat aaaatggaat tggcttcttt ccattcggta 960

tccaaaggat acatgggaga atgcggaatg cgtggaggat atgttgaatt cttgaatctc 1020

gacccagaag tgtatgtcct tttcaaaaaa atgatctctg ccaaattgtg ctccacagta 1080

ctcggacaag ccgtcattga tgccgttgtg aatccaccaa aggaaggaga tgcatcgtat 1140

gctctgtgga aacaagaaaa ggatgcagta cttgcttctc ttaaggaacg tgctacactc 1200

gtcgagaagg catacagtag cattgatgga atcagctgta atccagttca aggagccatg 1260

tacgctttcc cgcaaatcac gattccacag agagctgttg aaaaagctca gtctttgaac 1320

caacaacctg atttcttcta tgctatgcaa cttcttgaga ccaccggaat ctgtatcgtg 1380

ccaggaagtg gatttggaca aaaagacgga acttatcatt tcagaacgac aattcttcca 1440

cagccagaac tcttcaaaga catgctctcc cggttcactg atttccacca aaaattcctt 1500

gccgaataca agtag 1515

<210> 18
<211> 504
<212> PRT
<213> Caenorhabditis elegans

<400> 18

Met Arg Thr Val Gln Ala Ile Ser Gly Leu Val Thr Ser Arg Phe Phe
1 5 10 15

Gly Thr Ser Thr Arg Ile Met Ala Ser Gly Lys Thr Leu Asn Thr Ser
20 25 30

Asn Ile Asn Pro Asn Val Ile Lys Met Glu Tyr Ala Val Arg Gly Pro
35 40 45

Ile Val Ile Arg Ala Val Glu Leu Glu Lys Glu Leu Ala Thr Gly Ala
50 55 60

Gln Lys Pro Phe Pro Asn Val Ile Lys Ala Asn Ile Gly Asp Ala His

65 70 75 80

Ala Met Gly Gln Lys Pro Ile Thr Phe Ile Arg Gln Leu Leu Ala Cys
85 90 95

Ile Val Asn Pro Glu Ile Met Lys Thr Asp Lys Ser Ile Pro Ser Asp
100 105 110

Val Ile Glu His Ala Asn Ala Phe Leu Gly Ser Cys Gly Gly Lys Ser
115 120 125

Ala Gly Ala Tyr Ser Gln Ser Thr Gly Val Glu Ile Val Arg Lys His
130 135 140

Val Ala Glu Tyr Ile Lys Arg Arg Asp Gly Gly Ile Pro Cys Asn Ser
145 150 155 160

Glu Asp Val Cys Leu Ser Gly Gly Ala Ser Glu Ser Ile Arg Asn Val
165 170 175

Leu Lys Leu Phe Ile Asn His Asn Asn Ala Lys Lys Val Gly Val Met
180 185 190

Ile Pro Ile Pro Gln Tyr Pro Leu Tyr Ser Ala Thr Ile Glu Glu Phe
195 200 205

Gly Leu Gly Gln Val Gly Tyr Tyr Leu Ser Glu Ser Ser Asn Trp Ser
210 215 220

Met Asp Glu Ala Glu Leu Glu Arg Ser Phe Asn Asp His Cys Lys Glu
225 230 235 240

Tyr Asp Ile Arg Val Leu Cys Ile Ile Asn Pro Gly Asn Pro Thr Gly
245 250 255

Gln Ala Leu Ser Arg Glu Asn Ile Glu Thr Ile Ile Lys Phe Ala Gln

260 265 270

Lys Lys Asn Leu Phe Leu Met Ala Asp Glu Val Tyr Gln Asp Asn Val
275 280 285

Tyr Ala Gln Gly Ser Gln Phe His Ser Phe Lys Lys Val Leu Val Glu
290 295 300

Met Gly Glu Pro Tyr Asn Lys Met Glu Leu Ala Ser Phe His Ser Val
305 310 315 320

Ser Lys Gly Tyr Met Gly Glu Cys Gly Met Arg Gly Gly Tyr Val Glu
325 330 335

Phe Leu Asn Leu Asp Pro Glu Val Tyr Val Leu Phe Lys Lys Met Ile
340 345 350

Ser Ala Lys Leu Cys Ser Thr Val Leu Gly Gln Ala Val Ile Asp Ala
355 360 365

Val Val Asn Pro Pro Lys Glu Gly Asp Ala Ser Tyr Ala Leu Trp Lys
370 375 380

Gln Glu Lys Asp Ala Val Leu Ala Ser Leu Lys Glu Arg Ala Thr Leu
385 390 395 400

Val Glu Lys Ala Tyr Ser Ser Ile Asp Gly Ile Ser Cys Asn Pro Val
405 410 415

Gln Gly Ala Met Tyr Ala Phe Pro Gln Ile Thr Ile Pro Gln Arg Ala
420 425 430

Val Glu Lys Ala Gln Ser Leu Asn Gln Gln Pro Asp Phe Phe Tyr Ala
435 440 445

Met Gln Leu Leu Glu Thr Thr Gly Ile Cys Ile Val Pro Gly Ser Gly

450 455 460

Phe Gly Gln Lys Asp Gly Thr Tyr His Phe Arg Thr Thr Ile Leu Pro
465 470 475 480

Gln Pro Glu Leu Phe Lys Asp Met Leu Ser Arg Phe Thr Asp Phe His
485 490 495

Gln Lys Phe Leu Ala Glu Tyr Lys
500

<210> 19
<211> 1458
<212> DNA
<213> Oryza sativa japonica

<400> 19
atgttcggcg gcggcggcgg cggcgggagg aagccgctgg actacgagga gctgaacgag 60

aacgtgaaga aggtgcagta cgcggtgcgg ggggagctgt acctgcgcgc ctccgagctc 120

cagaaggagg gcaagaagat catcttcacc aacgtcggca acccacacgc gctcggccag 180

aagccgctca ccttcccccg ccaggttgtg gcgctgtgcc aggcccccct cctgctcgat 240

gatcccaacg tcggccttat cttccccgcc gacgccatcg cgcgggccaa gcactacctc 300

gccatggcac ccggtggact aggtgcttac agtgattccc gaggtatccc tggtattagg 360

aaggaagtcg ccgagttcat cgagaggcgt gatggttatc caagtgatcc agaacttatt 420

tacctcacag atggtgccag caaaggtgtg atgcaaatgc tgaataccat tatcagaaat 480

gagagagatg ggattctggt tcctgttcca caatacccgc tttattctgc tgccatttcc 540

ctctttggtg gttctctcgt gccatactac ttagaagaag aggctaactg gggacttgac 600

ttcgtcaatc tccgacagac tgtggcgtca gcgcggtcaa agggaatcac tgttcgagca 660

atggtgatta tcaacccagg aaaccctact ggccaatgcc ttagtgaagg aaacataaag 720

gaacttctca aattctgctt ccatgagaac ttagttctgc ttgcagatga agtctatcaa 780

cagaacattt atcaagatga gcgcccattt ataagtgcta gaaaggttct gtttgacatg 840

ggtcctccta tgagcaggga agttcagctg gtttctttcc atactgtgtc aaaaggatat 900

tggggggagt gtggacaacg tggagggtat tttgaaatga caaatcttcc tcccaagaca 960

gtagacgaga tctacaaggt tgcatcaatc gcactcagtc caaatgttcc tgggcagatc 1020

tttatgggtt taatggttaa ccctcctaag cctggagata tctcttatct gaagttttct 1080

gctgaaagca agtctatcct cgagtctttg aggaggagag cacgcctgat gacagatggt 1140

ttcaatagtt gccgaaatgt tgtctgcaat ttcacagaag gagctatgta ctctttcccc 1200

caaatacgct taccaccaaa agctatagat gcagccaaaa gggctggcaa agcggccgat 1260

gttttctact gcctcaagct tcttgaagca actggaatat ccactgttcc agggtcaggt 1320

ttcggacaaa aagaaggggt gttccacctg aggacgacca tcctgccagc tgaggaggac 1380

atgcctgcca tcatgaccag cttcaagaag ttcaacgaca ctttcatgga tcagtacgat 1440

ggctactcca ggatgtga 1458

<210> 20
<211> 485
<212> PRT
<213> Oryza sativa japonica

<400> 20

Met Phe Gly Gly Gly Gly Gly Gly Gly Arg Lys Pro Leu Asp Tyr Glu
1 5 10 15

Glu Leu Asn Glu Asn Val Lys Lys Val Gln Tyr Ala Val Arg Gly Glu
20 25 30

Leu Tyr Leu Arg Ala Ser Glu Leu Gln Lys Glu Gly Lys Lys Ile Ile
35 40 45

Phe Thr Asn Val Gly Asn Pro His Ala Leu Gly Gln Lys Pro Leu Thr
50 55 60

Phe Pro Arg Gln Val Val Ala Leu Cys Gln Ala Pro Phe Leu Leu Asp

65 70 75 80

Asp Pro Asn Val Gly Leu Ile Phe Pro Ala Asp Ala Ile Ala Arg Ala
85 90 95

Lys His Tyr Leu Ala Met Ala Pro Gly Gly Leu Gly Ala Tyr Ser Asp
100 105 110

Ser Arg Gly Ile Pro Gly Ile Arg Lys Glu Val Ala Glu Phe Ile Glu
115 120 125

Arg Arg Asp Gly Tyr Pro Ser Asp Pro Glu Leu Ile Tyr Leu Thr Asp
130 135 140

Gly Ala Ser Lys Gly Val Met Gln Met Leu Asn Thr Ile Ile Arg Asn
145 150 155 160

Glu Arg Asp Gly Ile Leu Val Pro Val Pro Gln Tyr Pro Leu Tyr Ser
165 170 175

Ala Ala Ile Ser Leu Phe Gly Gly Ser Leu Val Pro Tyr Tyr Leu Glu
180 185 190

Glu Glu Ala Asn Trp Gly Leu Asp Phe Val Asn Leu Arg Gln Thr Val
195 200 205

Ala Ser Ala Arg Ser Lys Gly Ile Thr Val Arg Ala Met Val Ile Ile
210 215 220

Asn Pro Gly Asn Pro Thr Gly Gln Cys Leu Ser Glu Gly Asn Ile Lys
225 230 235 240

Glu Leu Leu Lys Phe Cys Phe His Glu Asn Leu Val Leu Leu Ala Asp
245 250 255

Glu Val Tyr Gln Gln Asn Ile Tyr Gln Asp Glu Arg Pro Phe Ile Ser

260 265 270

Ala Arg Lys Val Leu Phe Asp Met Gly Pro Pro Met Ser Arg Glu Val
275 280 285

Gln Leu Val Ser Phe His Thr Val Ser Lys Gly Tyr Trp Gly Glu Cys
290 295 300

Gly Gln Arg Gly Gly Tyr Phe Glu Met Thr Asn Leu Pro Pro Lys Thr
305 310 315 320

Val Asp Glu Ile Tyr Lys Val Ala Ser Ile Ala Leu Ser Pro Asn Val
325 330 335

Pro Gly Gln Ile Phe Met Gly Leu Met Val Asn Pro Pro Lys Pro Gly
340 345 350

Asp Ile Ser Tyr Leu Lys Phe Ser Ala Glu Ser Lys Ser Ile Leu Glu
355 360 365

Ser Leu Arg Arg Arg Ala Arg Leu Met Thr Asp Gly Phe Asn Ser Cys
370 375 380

Arg Asn Val Val Cys Asn Phe Thr Glu Gly Ala Met Tyr Ser Phe Pro
385 390 395 400

Gln Ile Arg Leu Pro Pro Lys Ala Ile Asp Ala Ala Lys Arg Ala Gly
405 410 415

Lys Ala Ala Asp Val Phe Tyr Cys Leu Lys Leu Leu Glu Ala Thr Gly
420 425 430

Ile Ser Thr Val Pro Gly Ser Gly Phe Gly Gln Lys Glu Gly Val Phe
435 440 445

His Leu Arg Thr Thr Ile Leu Pro Ala Glu Glu Asp Met Pro Ala Ile

450 455 460

Met Thr Ser Phe Lys Lys Phe Asn Asp Thr Phe Met Asp Gln Tyr Asp
465 470 475 480

Gly Tyr Ser Arg Met
485

<210> 21
<211> 1452
<212> DNA
<213> Oryza sativa japonica

<400> 21
atggctgctc ccagcgtcgc cgtcgacaac ctcaacccca aggttttgaa ttgtgagtat 60

gcagtgcgtg gagagattgt gatccatgct cagcgcctgc agcaacagct acagactcaa 120

ccagggtctc ttccttttga tgagatccta tactgcaaca ttgggaatcc ccagtctctt 180

ggtcagaagc cagttacatt cttcagggag gttattgctc tttgtgatca tccatgcttg 240

ttggaaaagg aggaaaccaa atcattgttc agtgctgatg ccatttctcg agcaacaaca 300

attcttgcct cgattcctgg aagagcaact ggagcataca gccacagcca gggcatcaaa 360

gggctgcgtg atgcaattgc tgctggaatt gcatcacgtg acggataccc tgcaaatgca 420

gacgacattt tccttactga cggagcaagc cctggagttc acatgatgat gcagttactg 480

ataaggaacg agaaagatgg cattctctgc ccaattcctc aatatccttt gtactcagcc 540

tccattgctc ttcatggtgg agctcttgtc ccgtattatc ttaatgaatc aacaggctgg 600

ggtttggaga tctctgacct taagaagcaa ctcgaagatt ctcggttgaa aggcattgat 660

gttagggctt tggtagttat caatccagga aatccaactg ggcaggttct tgctgaggaa 720

aaccaacggg acatagtgaa gttctgcaaa aatgagggac ttgttcttct ggctgatgag 780

gtgtaccaag agaacatcta tgttgacaac aagaaattta actctttcaa gaagatagcg 840

agatccatgg gatacaacga ggatgatctc cctttagtat catttcaatc tgtttctaag 900

ggatattatg gtgaatgtgg caaaagagga ggctacatgg agattactgg cttcagtgct 960

ccagttagag agcagatcta caaagtggcg tcagtgaact tatgttccaa tatcactggc 1020

cagatccttg ccagcctcgt catgaatcca ccaaaggctg gagatgcatc atatgcttca 1080

tacaaggcag agaaagatgg aatcctccaa tcattagctc gccgtgcaaa ggcattggag 1140

aatgctttca acagtcttga gggaattaca tgcaacaaaa ctgaaggagc aatgtacctc 1200

ttccctcagc ttagtctgcc acaaaaggca attgacgctg ctaaagctgc taacaaagca 1260

cctgatgctt tctatgccct tcgtctcctc gaggcaaccg gaattgttgt tgtcctgga 1320

tctggatttg gccaagttcc tggcacatgg cacatcagat gcacaatcct gccacaggag 1380

gagaagatcc ccgcgatcat ctcccgcttc aaggcattcc atgagggctt catggcagcg 1440

taccgcgact ga 1452

<210> 22
<211> 483
<212> PRT
<213> Oryza sativa japonica

<400> 22

Met Ala Ala Pro Ser Val Ala Val Asp Asn Leu Asn Pro Lys Val Leu
1 5 10 15

Asn Cys Glu Tyr Ala Val Arg Gly Glu Ile Val Ile His Ala Gln Arg
20 25 30

Leu Gln Gln Gln Leu Gln Thr Gln Pro Gly Ser Leu Pro Phe Asp Glu
35 40 45

Ile Leu Tyr Cys Asn Ile Gly Asn Pro Gln Ser Leu Gly Gln Lys Pro
50 55 60

Val Thr Phe Phe Arg Glu Val Ile Ala Leu Cys Asp His Pro Cys Leu
65 70 75 80

Leu Glu Lys Glu Glu Thr Lys Ser Leu Phe Ser Ala Asp Ala Ile Ser

85 90 95

Arg Ala Thr Thr Ile Leu Ala Ser Ile Pro Gly Arg Ala Thr Gly Ala
100 105 110

Tyr Ser His Ser Gln Gly Ile Lys Gly Leu Arg Asp Ala Ile Ala Ala
115 120 125

Gly Ile Ala Ser Arg Asp Gly Tyr Pro Ala Asn Ala Asp Asp Ile Phe
130 135 140

Leu Thr Asp Gly Ala Ser Pro Gly Val His Met Met Met Gln Leu Leu
145 150 155 160

Ile Arg Asn Glu Lys Asp Gly Ile Leu Cys Pro Ile Pro Gln Tyr Pro
165 170 175

Leu Tyr Ser Ala Ser Ile Ala Leu His Gly Gly Ala Leu Val Pro Tyr
180 185 190

Tyr Leu Asn Glu Ser Thr Gly Trp Gly Leu Glu Ile Ser Asp Leu Lys
195 200 205

Lys Gln Leu Glu Asp Ser Arg Leu Lys Gly Ile Asp Val Arg Ala Leu
210 215 220

Val Val Ile Asn Pro Gly Asn Pro Thr Gly Gln Val Leu Ala Glu Glu
225 230 235 240

Asn Gln Arg Asp Ile Val Lys Phe Cys Lys Asn Glu Gly Leu Val Leu
245 250 255

Leu Ala Asp Glu Val Tyr Gln Glu Asn Ile Tyr Val Asp Asn Lys Lys
260 265 270

Phe Asn Ser Phe Lys Lys Ile Ala Arg Ser Met Gly Tyr Asn Glu Asp

275 280 285

Asp Leu Pro Leu Val Ser Phe Gln Ser Val Ser Lys Gly Tyr Tyr Gly
290 295 300

Glu Cys Gly Lys Arg Gly Gly Tyr Met Glu Ile Thr Gly Phe Ser Ala
305 310 315 320

Pro Val Arg Glu Gln Ile Tyr Lys Val Ala Ser Val Asn Leu Cys Ser
325 330 335

Asn Ile Thr Gly Gln Ile Leu Ala Ser Leu Val Met Asn Pro Pro Lys
340 345 350

Ala Gly Asp Ala Ser Tyr Ala Ser Tyr Lys Ala Glu Lys Asp Gly Ile
355 360 365

Leu Gln Ser Leu Ala Arg Arg Ala Lys Ala Leu Glu Asn Ala Phe Asn
370 375 380

Ser Leu Glu Gly Ile Thr Cys Asn Lys Thr Glu Gly Ala Met Tyr Leu
385 390 395 400

Phe Pro Gln Leu Ser Leu Pro Gln Lys Ala Ile Asp Ala Ala Lys Ala
405 410 415

Ala Asn Lys Ala Pro Asp Ala Phe Tyr Ala Leu Arg Leu Leu Glu Ala
420 425 430

Thr Gly Ile Val Val Val Pro Gly Ser Gly Phe Gly Gln Val Pro Gly
435 440 445

Thr Trp His Ile Arg Cys Thr Ile Leu Pro Gln Glu Glu Lys Ile Pro
450 455 460

Ala Ile Ile Ser Arg Phe Lys Ala Phe His Glu Gly Phe Met Ala Ala

465 470 475 480

Tyr Arg Asp

<210> 23
<211> 1722
<212> DNA
<213> Cyanidioschyzon merolae

<400> 23
atgcaacacg tgttggcggg tcgggtaggg cgtagaacgt ttgggctgct caatttcagt 60

tatctccgta tagggcgaag gaataggagc cacggtgtaa gcgcagggat gccgcacgaa 120

gccgacggga cgcgccggcg aaaagcgctc gacttgcgaa ccataaacca gcgcgtggta 180

gcggcgcagt acgctgtgcg tggtgaattg cccactcgcg ctgcgcgact gcaacagact 240

ctagaaaaag gaggaccaga agctgccgca ctgccgttta aggaaataat ttactgcaac 300

atcggaaatc cacaggcact tgggaacccg ccattcactt accaccggcg ggtcatggca 360

ctgtgcgact gtccggactt ggcagcggca ctcccggaga aggagcgtga aaaactgttc 420

cccgccgacg tgcgcgaagc gacggaacga atcctacgct ccgctggact cggcggtacg 480

ggagcgtact cggactccca gggagtgccg atcattcgac aagatgtggc agagttcatg 540

aacaagcggg acggcattca cgaggactcc gaatttgcag ctcgagtgaa ggatgtgttt 600

ttgacaaatg gttcatcgag cgcgatcctc atgctcatgg cgctgttgag cggttccgac 660

gcagcgctca gcgcggacgg taccaacggc gtatcgcatg gacgcgaaac acgttccatg 720

cgaccgggtg tgctgattcc agtgccacag tatccgattt actcggcgct ttgcacagtc 780

ctagggatcg aagcgctaca ctaccatctc gttcaggagc agaattggtc tattcaagtc 840

acggagctaa cggaacaggt tcgacaggca cgctcccgtg gcatcgaagc gcgcgccctg 900

gtcgtcatct caccggggaa tcctaccgga caattgcttc atccggcgaa catgcgagaa 960

ctgatggatt ttgcgtatcg agagggactc ctactcctgg ctgatgaggt ctatgcagac 1020

aacgtgtact tggatggtcg gaaattcgag tcgtttcgaa gagtgctgca ttcgagtatg 1080

ccggaggagg tccaggagtc gctggaactc gtgtcgctct actccgccag caaagggctt 1140

gtcggagagt gtggtcgccg cggcggctac atgctgttat caccgggcgt tacaaacgag 1200

gcacgtgaac aactcctgaa actcgctagt atcatgctct gcccaaacct cggcggacag 1260

gtcatgatcg actgtgtggt gcgcccgccg gagccgggcc aaccatcata tgagctctac 1320

cagaaagaga aacttgagcg ttatgaaagt ttgcggcgac gtgcgcatcg cgttgtagag 1380

gcatttaaga gtatgcgcgg tgtgcaatgc aaccctagtg agggcgccat gtacgccttt 1440

ccgagcatca ctgtgggcac gaaagcactc caggcagcgc aaaagtccaa tatgccgctg 1500

gatacgtttt actgtgtcag ccttttggaa cgaactggta tctgtgtggt gccgggcgca 1560

gggttcggca tgcattccaa tgaaccaaca tccagtgtcc cgaacggttc gtgtcggttt 1620

tacctgcgga cgactatttt gcctccggag gaaaagctcg aacccgtcat cgcgctgctt 1680

cgggctcatc acgaggagtt tcttcaaaag tatcccccgg ac 1722

<210> 24
<211> 574
<212> PRT
<213> Cyanidioschyzon merolae

<400> 24

Met Gln His Val Leu Ala Gly Arg Val Gly Arg Arg Thr Phe Gly Leu
1 5 10 15

Leu Asn Phe Ser Tyr Leu Arg Ile Gly Arg Arg Asn Arg Ser His Gly
20 25 30

Val Ser Ala Gly Met Pro His Glu Ala Asp Gly Thr Arg Arg Arg Lys
35 40 45

Ala Leu Asp Leu Arg Thr Ile Asn Gln Arg Val Val Ala Ala Gln Tyr
50 55 60

Ala Val Arg Gly Glu Leu Pro Thr Arg Ala Ala Arg Leu Gln Gln Thr

65 70 75 80

Leu Glu Lys Gly Gly Pro Glu Ala Ala Ala Leu Pro Phe Lys Glu Ile
85 90 95

Ile Tyr Cys Asn Ile Gly Asn Pro Gln Ala Leu Gly Asn Pro Pro Phe
100 105 110

Thr Tyr His Arg Arg Val Met Ala Leu Cys Asp Cys Pro Asp Leu Ala
115 120 125

Ala Ala Leu Pro Glu Lys Glu Arg Glu Lys Leu Phe Pro Ala Asp Val
130 135 140

Arg Glu Ala Thr Glu Arg Ile Leu Arg Ser Ala Gly Leu Gly Gly Thr
145 150 155 160

Gly Ala Tyr Ser Asp Ser Gln Gly Val Pro Ile Ile Arg Gln Asp Val
165 170 175

Ala Glu Phe Met Asn Lys Arg Asp Gly Ile His Glu Asp Ser Glu Phe
180 185 190

Ala Ala Arg Val Lys Asp Val Phe Leu Thr Asn Gly Ser Ser Ser Ala
195 200 205

Ile Leu Met Leu Met Ala Leu Leu Ser Gly Ser Asp Ala Ala Leu Ser
210 215 220

Ala Asp Gly Thr Asn Gly Val Ser His Gly Arg Glu Thr Arg Ser Met
225 230 235 240

Arg Pro Gly Val Leu Ile Pro Val Pro Gln Tyr Pro Ile Tyr Ser Ala
245 250 255

Leu Cys Thr Val Leu Gly Ile Glu Ala Leu His Tyr His Leu Val Gln

260 265 270

Glu Gln Asn Trp Ser Ile Gln Val Thr Glu Leu Thr Glu Gln Val Arg
275 280 285

Gln Ala Arg Ser Arg Gly Ile Glu Ala Arg Ala Leu Val Val Ile Ser
290 295 300

Pro Gly Asn Pro Thr Gly Gln Leu Leu His Pro Ala Asn Met Arg Glu
305 310 315 320

Leu Met Asp Phe Ala Tyr Arg Glu Gly Leu Leu Leu Leu Ala Asp Glu
325 330 335

Val Tyr Ala Asp Asn Val Tyr Leu Asp Gly Arg Lys Phe Glu Ser Phe
340 345 350

Arg Arg Val Leu His Ser Ser Met Pro Glu Glu Val Gln Glu Ser Leu
355 360 365

Glu Leu Val Ser Leu Tyr Ser Ala Ser Lys Gly Leu Val Gly Glu Cys
370 375 380

Gly Arg Arg Gly Gly Tyr Met Leu Leu Ser Pro Gly Val Thr Asn Glu
385 390 395 400

Ala Arg Glu Gln Leu Leu Lys Leu Ala Ser Ile Met Leu Cys Pro Asn
405 410 415

Leu Gly Gly Gln Val Met Ile Asp Cys Val Val Arg Pro Pro Glu Pro
420 425 430

Gly Gln Pro Ser Tyr Glu Leu Tyr Gln Lys Glu Lys Leu Glu Arg Tyr
435 440 445

Glu Ser Leu Arg Arg Arg Ala His Arg Val Val Glu Ala Phe Lys Ser

450 455 460

Met Arg Gly Val Gln Cys Asn Pro Ser Glu Gly Ala Met Tyr Ala Phe
465 470 475 480

Pro Ser Ile Thr Val Gly Thr Lys Ala Leu Gln Ala Ala Gln Lys Ser
485 490 495

Asn Met Pro Leu Asp Thr Phe Tyr Cys Val Ser Leu Leu Glu Arg Thr
500 505 510

Gly Ile Cys Val Val Pro Gly Ala Gly Phe Gly Met His Ser Asn Glu
515 520 525

Pro Thr Ser Ser Val Pro Asn Gly Ser Cys Arg Phe Tyr Leu Arg Thr
530 535 540

Thr Ile Leu Pro Pro Glu Glu Lys Leu Glu Pro Val Ile Ala Leu Leu
545 550 555 560

Arg Ala His His Glu Glu Phe Leu Gln Lys Tyr Pro Pro Asp
565 570

<210> 25
<211> 1779
<212> DNA
<213> Saccharomyces cerevisiae

<400> 25
atgttatcac tgtctgccaa aaatcacttc acagtgagta attctataac tcacgttatt 60

aagtcatatc atataaggac tctcacttca agcgcagaaa aaatgccaca tatcactact 120

ccttttttcta cctcagccag tagtacaaag ttaaaagctt tcaggaaagt tagacccgtc 180

ctacagagac atagctcttc ctggattgtt gctcaaaatc atagacgttc attatctggt 240

caatcttcgc taaacgacct gcgtcatttg aatcgctttc cacaccacac gttgaaaact 300

tcgaataacg agttttatcc cgccgaacaa ttgactttgg aagacgtaaa tgaaaatgtc 360

ttgaaggcta agtacgccgt tagaggtgcc atcccaatga gagctgaaga attgaaagct 420

caactggaga aggatcctca atctctgcca tttgacagga ttatcaacgc caatattggt 480

aatcctcagc aactacaaca gaaacctctg acttactaca gacaggtctt gtctctctta 540

caatacccag aactattaaa ccaaaacgaa cagcagctag ttgattcgaa attgtttaaa 600

ctagatgcca ttaaacgtgc aaagagttta atggaagata tcggtggttc tgttggtgct 660

tactcttctt ctcaaggtgt agaaggtata aggaaaagtg tcgctgaatt tataacgaag 720

agggacgaag gcgagatatc atacccagag gatattttcc taactgctgg tgcatccgca 780

gctgtcaatt acttgttatc aattttctgt agagggccag aaacgggtgt cttgattcca 840

attcctcaat atccattata taccgctact ctagctttga acaattctca agctttacca 900

tactatttag atgagaattc aggttggtca actaatccag aagaaattga aactgtcgtc 960

aaagaggcta tacagaacga aatcaaacct acagttctag tggttatcaa tccaggtaat 1020

cctacaggag ctgtcctatc acctgagtct atagctcaga tttttgaagt cgcagccaag 1080

tacggtacag tagtgatagc tgacgaagtt tatcaagaaa atatcttccc gggcaccaag 1140

ttccattcta tgaagaaaat tttgagacat ttacagaggg aacatccagg taaattcgat 1200

aatgttcagc tagcttcttt gcattcgact tctaagggtg tttctggtga atgtggtcaa 1260

aggggtggct acatggaact cactggattc agccatgaga tgagacaagt tatcttgaaa 1320

ctagcctcga tttcattgtg tcccgttgtc acaggtcaag ctttggttga tttgatggtt 1380

cgtccaccag tggaagggga ggaatcattc gagtcggacc aagcagaacg taactccatc 1440

catgaaaagt taattacaag agcaatgaca ctgtatgaga catttaactc tttagaaggc 1500

attgaatgtc aaaagcctca aggtgccatg tatttattcc ctaagataga cttacctttc 1560

aaggcagttc aagaagctcg ccacttagag ttaactccgg atgaatttta ttgtaagaag 1620

ttgttagaat ctactggcat ttgcactgtt cccggttctg ggtttggtca agaacctggt 1680

acttaccatt taagaacaac atttttggca cctggtctgg aatggattaa gaaatgggaa 1740

agtttccata aagaattttt tgaccaatac cgtgactga 1779

<210> 26
<211> 592
<212> PRT
<213> Saccharomyces cerevisiae

<400> 26

Met Leu Ser Leu Ser Ala Lys Asn His Phe Thr Val Ser Asn Ser Ile
1 5 10 15

Thr His Val Ile Lys Ser Tyr His Ile Arg Thr Leu Thr Ser Ser Ala
20 25 30

Glu Lys Met Pro His Ile Thr Thr Pro Phe Ser Thr Ser Ala Ser Ser
35 40 45

Thr Lys Leu Lys Ala Phe Arg Lys Val Arg Pro Val Leu Gln Arg His
50 55 60

Ser Ser Ser Trp Ile Val Ala Gln Asn His Arg Arg Ser Leu Ser Gly
65 70 75 80

Gln Ser Ser Leu Asn Asp Leu Arg His Leu Asn Arg Phe Pro His His
85 90 95

Thr Leu Lys Thr Ser Asn Asn Glu Phe Tyr Pro Ala Glu Gln Leu Thr
100 105 110

Leu Glu Asp Val Asn Glu Asn Val Leu Lys Ala Lys Tyr Ala Val Arg
115 120 125

Gly Ala Ile Pro Met Arg Ala Glu Glu Leu Lys Ala Gln Leu Glu Lys
130 135 140

Asp Pro Gln Ser Leu Pro Phe Asp Arg Ile Ile Asn Ala Asn Ile Gly
145 150 155 160

Asn Pro Gln Gln Leu Gln Gln Lys Pro Leu Thr Tyr Tyr Arg Gln Val
165 170 175

Leu Ser Leu Leu Gln Tyr Pro Glu Leu Leu Asn Gln Asn Glu Gln Gln
180 185 190

Leu Val Asp Ser Lys Leu Phe Lys Leu Asp Ala Ile Lys Arg Ala Lys
195 200 205

Ser Leu Met Glu Asp Ile Gly Gly Ser Val Gly Ala Tyr Ser Ser Ser
210 215 220

Gln Gly Val Glu Gly Ile Arg Lys Ser Val Ala Glu Phe Ile Thr Lys
225 230 235 240

Arg Asp Glu Gly Glu Ile Ser Tyr Pro Glu Asp Ile Phe Leu Thr Ala
245 250 255

Gly Ala Ser Ala Ala Val Asn Tyr Leu Leu Ser Ile Phe Cys Arg Gly
260 265 270

Pro Glu Thr Gly Val Leu Ile Pro Ile Pro Gln Tyr Pro Leu Tyr Thr
275 280 285

Ala Thr Leu Ala Leu Asn Asn Ser Gln Ala Leu Pro Tyr Tyr Leu Asp
290 295 300

Glu Asn Ser Gly Trp Ser Thr Asn Pro Glu Glu Ile Glu Thr Val Val
305 310 315 320

Lys Glu Ala Ile Gln Asn Glu Ile Lys Pro Thr Val Leu Val Val Ile
325 330 335

Asn Pro Gly Asn Pro Thr Gly Ala Val Leu Ser Pro Glu Ser Ile Ala
340 345 350

Gln Ile Phe Glu Val Ala Ala Lys Tyr Gly Thr Val Val Ile Ala Asp
355 360 365

Glu Val Tyr Gln Glu Asn Ile Phe Pro Gly Thr Lys Phe His Ser Met
370 375 380

Lys Lys Ile Leu Arg His Leu Gln Arg Glu His Pro Gly Lys Phe Asp
385 390 395 400

Asn Val Gln Leu Ala Ser Leu His Ser Thr Ser Lys Gly Val Ser Gly
405 410 415

Glu Cys Gly Gln Arg Gly Gly Tyr Met Glu Leu Thr Gly Phe Ser His
420 425 430

Glu Met Arg Gln Val Ile Leu Lys Leu Ala Ser Ile Ser Leu Cys Pro
435 440 445

Val Val Thr Gly Gln Ala Leu Val Asp Leu Met Val Arg Pro Pro Val
450 455 460

Glu Gly Glu Glu Ser Phe Glu Ser Asp Gln Ala Glu Arg Asn Ser Ile
465 470 475 480

His Glu Lys Leu Ile Thr Arg Ala Met Thr Leu Tyr Glu Thr Phe Asn
485 490 495

Ser Leu Glu Gly Ile Glu Cys Gln Lys Pro Gln Gly Ala Met Tyr Leu
500 505 510

Phe Pro Lys Ile Asp Leu Pro Phe Lys Ala Val Gln Glu Ala Arg His
515 520 525

Leu Glu Leu Thr Pro Asp Glu Phe Tyr Cys Lys Lys Leu Leu Glu Ser
530 535 540

Thr Gly Ile Cys Thr Val Pro Gly Ser Gly Phe Gly Gln Glu Pro Gly
545 550 555 560

Thr Tyr His Leu Arg Thr Thr Phe Leu Ala Pro Gly Leu Glu Trp Ile
565 570 575

Lys Lys Trp Glu Ser Phe His Lys Glu Phe Phe Asp Gln Tyr Arg Asp
580 585 590

<210> 27
<211> 1524
<212> DNA
<213> Saccharomyces cerevisiae

<400> 27
atgacaatga cacaccaaca ggatttgaaa ggtgtgttca ccgcaaagga tttggatttt 60

aagcccgctg gcaagattac taaaaaagat ttgaatacag gtgtcactaa ggcagaatat 120

gctgtaagag gagctattcc aaccagagct gacgagctaa aagaggaatt gaaaaaaaac 180

ccagaagttt tgcctttcga tgatattatc aatgcgaaca ttggtaatcc gcagcaactg 240

gatcagaagc ctttgacctt taccaggcaa gtactggcca tcctggagta cccggaaatt 300

ttacgagtag gccataatga actggcttct ttgaacttgt tttccaggga cgccttggaa 360

agagctgagc gcctcttgaa tgatattggc ggttctatag gggcatattc gcattctcaa 420

ggtgtgccag gaataaggca aacagttgct gacttcatta ctagaagaga cggcggtgag 480

cccgctacac cggaagatat ttatttaacc actggcgctt cgtccgcggc aacttctttg 540

ttatctttat tgtgtaaaga ttctcaaaca ggcctgctga ttccaattcc gcagtatccg 600

ctttatactg catccgcatc tcttttcaat gcacaagtgc tgccatacta cttagatgag 660

gagtcaaatt ggtctacaaa cagcgacgaa attgaaaaag tagtgcaaga tgctttgaaa 720

aaacagatca gaccatctgt gctgatagtt attaatccag gtaacccaac cggtgcagtt 780

ctttctgaag aaaccattgc caggatctgt ttgatcgctg cgaaatacgg cattacaatc 840

atttctgatg aggtctatca agaaaacatt ttcaacgatg ttaaatttca ttcgatgaag 900

aaagtcctaa gaaaattgca gcatctttat ccaggaaaat tcgataacgt tcagctcgcc 960

tctttacact ccatttctaa aggattcatg gatgagtgcg gccaaagagg cggttacatg 1020

gaaattattg ggttttctca agaaataaga gatgctcttt tcaaactcat gtctatatcc 1080

atatgttctg ttgtcacagg acaagctgtg gttgatttaa tggtcaaacc accccagcct 1140

ggagacgagt cctatgaaca agatcatgac gaaaggctga aaatttttca tgaaatgcgt 1200

acgagagcaa acttattgta cgagacgttt aaggaactag agggtatcga atgccaaaaa 1260

cctcagggtg caatgtatct tttccctagg cttgttttac ctaagaaagc tctttgtgaa 1320

agcgaacgcc ttggcatcga acctgatgag ttctattgca catctttgct agaatctaca 1380

ggtatttgta ctgtcccagg gtctgggttc ggacaaagac ccgggactta tcatgtgcga 1440

acaacgtttt tggctccagg gactaaatgg attcaagact ggaaagaatt tcatcaagat 1500

ttcttcagca agtatcgtaa ttga 1524

<210> 28
<211> 507
<212> PRT
<213> Saccharomyces cerevisiae

<400> 28

Met Thr Met Thr His Gln Gln Asp Leu Lys Gly Val Phe Thr Ala Lys
1 5 10 15

Asp Leu Asp Phe Lys Pro Ala Gly Lys Ile Thr Lys Lys Asp Leu Asn
20 25 30

Thr Gly Val Thr Lys Ala Glu Tyr Ala Val Arg Gly Ala Ile Pro Thr
35 40 45

Arg Ala Asp Glu Leu Lys Glu Glu Leu Lys Lys Asn Pro Glu Val Leu
50 55 60

Pro Phe Asp Asp Ile Ile Asn Ala Asn Ile Gly Asn Pro Gln Gln Leu

65 70 75 80

Asp Gln Lys Pro Leu Thr Phe Thr Arg Gln Val Leu Ala Ile Leu Glu
85 90 95

Tyr Pro Glu Ile Leu Arg Val Gly His Asn Glu Leu Ala Ser Leu Asn
100 105 110

Leu Phe Ser Arg Asp Ala Leu Glu Arg Ala Glu Arg Leu Leu Asn Asp
115 120 125

Ile Gly Gly Ser Ile Gly Ala Tyr Ser His Ser Gln Gly Val Pro Gly
130 135 140

Ile Arg Gln Thr Val Ala Asp Phe Ile Thr Arg Arg Asp Gly Gly Glu
145 150 155 160

Pro Ala Thr Pro Glu Asp Ile Tyr Leu Thr Thr Gly Ala Ser Ser Ala
165 170 175

Ala Thr Ser Leu Leu Ser Leu Leu Cys Lys Asp Ser Gln Thr Gly Leu
180 185 190

Leu Ile Pro Ile Pro Gln Tyr Pro Leu Tyr Thr Ala Ser Ala Ser Leu
195 200 205

Phe Asn Ala Gln Val Leu Pro Tyr Tyr Leu Asp Glu Glu Ser Asn Trp
210 215 220

Ser Thr Asn Ser Asp Glu Ile Glu Lys Val Val Gln Asp Ala Leu Lys
225 230 235 240

Lys Gln Ile Arg Pro Ser Val Leu Ile Val Ile Asn Pro Gly Asn Pro
245 250 255

Thr Gly Ala Val Leu Ser Glu Glu Thr Ile Ala Arg Ile Cys Leu Ile

260 265 270

Ala Ala Lys Tyr Gly Ile Thr Ile Ile Ser Asp Glu Val Tyr Gln Glu
275 280 285

Asn Ile Phe Asn Asp Val Lys Phe His Ser Met Lys Lys Val Leu Arg
290 295 300

Lys Leu Gln His Leu Tyr Pro Gly Lys Phe Asp Asn Val Gln Leu Ala
305 310 315 320

Ser Leu His Ser Ile Ser Lys Gly Phe Met Asp Glu Cys Gly Gln Arg
325 330 335

Gly Gly Tyr Met Glu Ile Ile Gly Phe Ser Gln Glu Ile Arg Asp Ala
340 345 350

Leu Phe Lys Leu Met Ser Ile Ser Ile Cys Ser Val Val Thr Gly Gln
355 360 365

Ala Val Val Asp Leu Met Val Lys Pro Pro Gln Pro Gly Asp Glu Ser
370 375 380

Tyr Glu Gln Asp His Asp Glu Arg Leu Lys Ile Phe His Glu Met Arg
385 390 395 400

Thr Arg Ala Asn Leu Leu Tyr Glu Thr Phe Lys Glu Leu Glu Gly Ile
405 410 415

Glu Cys Gln Lys Pro Gln Gly Ala Met Tyr Leu Phe Pro Arg Leu Val
420 425 430

Leu Pro Lys Lys Ala Leu Cys Glu Ser Glu Arg Leu Gly Ile Glu Pro
435 440 445

Asp Glu Phe Tyr Cys Thr Ser Leu Leu Glu Ser Thr Gly Ile Cys Thr

450 455 460

Val Pro Gly Ser Gly Phe Gly Gln Arg Pro Gly Thr Tyr His Val Arg
465 470 475 480

Thr Thr Phe Leu Ala Pro Gly Thr Lys Trp Ile Gln Asp Trp Lys Glu
485 490 495

Phe His Gln Asp Phe Phe Ser Lys Tyr Arg Asn
500 505

<210> 29
<211> 1566
<212> DNA
<213> Ashbya gossypii

<400> 29
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cgtgtgcttc gcactcgtag attgagctca gtaaaggacg ggtcgcggtt tgtgcctgcg 120

gaaccgatga cactagcgga cgtgaacgaa aacgtggtca aggcgaagta cgcggtgcgg 180

gggaagattc caacgcgtgc agaggagctg gagcggcggc tggaggagca cccgggctcg 240

ctgccgttca gcaaaatcat ccaagcgaac atcggcaatc cgcagcagct gggccagaag 300

ccgctgacat tctaccggca agtgatctcg ctgatgcaga atccacagtt gctggagatg 360

cccgcagaat ggctgcagca ggcgttcaag gcggatgtgg tggtgcgtgc gcggaggatg 420

ctgcaggacg ccggaggctc cgtgggagcg tactcggcgt cgcagggtgt gaaaggctac 480

cggcgcacgg ttgcgcagtt tattgagcgg cgcgatggga tcccagcgaa tccagacaac 540

gtgtacctga ccgcgggtgc gtcctctgct gtgtcttgtc tgctgtcgac attctgcaag 600

ggaccggaga caggcgtgtt gatcccaatc cctcagtacc cgctgtacac tgctacgatc 660

acacagaata acgcggttgc gctgccgtac tacctaaatg aggctgatgg gtggtctacg 720

aatccagatg agatggaacg tgtcatcctc gattctaaga agaggaacat cgcgcccaaa 780

tgtctggttg tgattaaccc tgggaatccc actggttccg tactgtctgt aaaggatatg 840

gaggctattc taacacttgc tgcgaagtat gggattgtcg ttattgcgga cgaggtatac 900

caggataatg tgtttggcga tgccaagttc cactctatgc gtaaggtgct gaaaaacctt 960

caactcagag agccaacgct ctacaagaat gtccagttag cctctcttca ctcgatctcg 1020

aaggggctct ccggcgaatg tggccagcgt ggtggctaca tggaattgat cggtttccgt 1080

gaggagctca ggaaggtttt cgttaagttg gcttctatat ctctttgtcc agtggttacc 1140

ggacaagctc tagtcgacct tatggttggg cctcccagcc aaggggatcc atcctatgag 1200

caatataccc aggaaacaag gagtatctat cacgaattgg aggaacggtc gcaactgctg 1260

tggaaaacgt tctgttcctt ggagggtata gaatgcaata tgccacaagg tgctctatat 1320

ctattcccta agttgcatct tccacagaaa gctattgaag cggcgcaaaa gctgggtata 1380

ccagcggatg agctctactg tagcgaatta cttgatgaaa caggcatctg cactgtccct 1440

ggaactggtt tcggccaaat cccgggcaca tatcacgtta gaactacgtt tttgccacct 1500

ggtactaagt ggatcgaaag ttggaaggac ttccacaaga aattttatga caagtatagg 1560

gactaa 1566

<210> 30
<211> 521
<212> PRT
<213> Ashbya gossypii

<400> 30

Met Ala Ile Gly Met Leu Arg Arg Asn Ser Ser Gly Thr Ala Val Ser
1 5 10 15

Val Leu Gln Gly Arg Val Leu Arg Thr Arg Arg Leu Ser Ser Val Lys
20 25 30

Asp Gly Ser Arg Phe Val Pro Ala Glu Pro Met Thr Leu Ala Asp Val
35 40 45

Asn Glu Asn Val Val Lys Ala Lys Tyr Ala Val Arg Gly Lys Ile Pro

60

50 55 60

Thr Arg Ala Glu Glu Leu Glu Arg Arg Leu Glu Glu His Pro Gly Ser
65 70 75 80

Leu Pro Phe Ser Lys Ile Ile Gln Ala Asn Ile Gly Asn Pro Gln Gln
85 90 95

Leu Gly Gln Lys Pro Leu Thr Phe Tyr Arg Gln Val Ile Ser Leu Met
100 105 110

Gln Asn Pro Gln Leu Leu Glu Met Pro Ala Glu Trp Leu Gln Gln Ala
115 120 125

Phe Lys Ala Asp Val Val Val Arg Ala Arg Arg Met Leu Gln Asp Ala
130 135 140

Gly Gly Ser Val Gly Ala Tyr Ser Ala Ser Gln Gly Val Lys Gly Tyr
145 150 155 160

Arg Arg Thr Val Ala Gln Phe Ile Glu Arg Arg Asp Gly Ile Pro Ala
165 170 175

Asn Pro Asp Asn Val Tyr Leu Thr Ala Gly Ala Ser Ser Ala Val Ser
180 185 190

Cys Leu Leu Ser Thr Phe Cys Lys Gly Pro Glu Thr Gly Val Leu Ile
195 200 205

Pro Ile Pro Gln Tyr Pro Leu Tyr Thr Ala Thr Ile Thr Gln Asn Asn
210 215 220

Ala Val Ala Leu Pro Tyr Tyr Leu Asn Glu Ala Asp Gly Trp Ser Thr
225 230 235 240

Asn Pro Asp Glu Met Glu Arg Val Ile Leu Asp Ser Lys Lys Arg Asn

245 250 255

Ile Ala Pro Lys Cys Leu Val Val Ile Asn Pro Gly Asn Pro Thr Gly
260 265 270

Ser Val Leu Ser Val Lys Asp Met Glu Ala Ile Leu Thr Leu Ala Ala
275 280 285

Lys Tyr Gly Ile Val Val Ile Ala Asp Glu Val Tyr Gln Asp Asn Val
290 295 300

Phe Gly Asp Ala Lys Phe His Ser Met Arg Lys Val Leu Lys Asn Leu
305 310 315 320

Gln Leu Arg Glu Pro Thr Leu Tyr Lys Asn Val Gln Leu Ala Ser Leu
325 330 335

His Ser Ile Ser Lys Gly Leu Ser Gly Glu Cys Gly Gln Arg Gly Gly
340 345 350

Tyr Met Glu Leu Ile Gly Phe Arg Glu Glu Leu Arg Lys Val Phe Val
355 360 365

Lys Leu Ala Ser Ile Ser Leu Cys Pro Val Val Thr Gly Gln Ala Leu
370 375 380

Val Asp Leu Met Val Gly Pro Pro Ser Gln Gly Asp Pro Ser Tyr Glu
385 390 395 400

Gln Tyr Thr Gln Glu Thr Arg Ser Ile Tyr His Glu Leu Glu Glu Arg
405 410 415

Ser Gln Leu Leu Trp Lys Thr Phe Cys Ser Leu Glu Gly Ile Glu Cys
420 425 430

Asn Met Pro Gln Gly Ala Leu Tyr Leu Phe Pro Lys Leu His Leu Pro

435 440 445

Gln Lys Ala Ile Glu Ala Ala Gln Lys Leu Gly Ile Pro Ala Asp Glu
450 455 460

Leu Tyr Cys Ser Glu Leu Leu Asp Glu Thr Gly Ile Cys Thr Val Pro
465 470 475 480

Gly Thr Gly Phe Gly Gln Ile Pro Gly Thr Tyr His Val Arg Thr Thr
485 490 495

Phe Leu Pro Pro Gly Thr Lys Trp Ile Glu Ser Trp Lys Asp Phe His
500 505 510

Lys Lys Phe Tyr Asp Lys Tyr Arg Asp
515 520

<210> 31
<211> 1563
<212> DNA
<213> Candida albicans

<400> 31
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aacccacaaa cggtcgaggc aaaatacgct gtacgtggga aaatcccaat tattgccgat 180

gaattgaatg aattgattca aaagcaacca cagctgcatg gattaccatt tagcaaaatc 240

attaatgcca acattggtaa cccacagcaa ttggaacaac gtccattgac atggtatcgt 300

caagtattgt ctcttttaca atacccggat ttattgaaaa atggagaccc tgaaaccgtt 360

aaatcacttt atcctgaaga tgtgattgag cgagcacaat caattttgaa acacattgga 420

tcaatagggg catactctca ttctcagggt gccagttatt tccgacaatc tattgctgaa 480

tttataacta accgtgatgg tggttatgta tcccacgcca acaacatttt tttaacttcc 540

ggggcatcaa ctgcagtgtc gtatttatta caaattttgt ctgtcaatga aaactccggg 600

ttcttaattc cgatcccaca gtatcctttg tatactgcca ctattgcctt gaataatgcc 660

aagccaattg gttattatct cgatgagtcg aaccattggt caaccaatcc tcaagagatt 720

agagaattga tcgaaaccaa tcaactgcaa ggtattaaca tcaaggcatt ggtggtgatt 780

aacccgggga acccaacggg ggcaatttta tcatcacaag atataattga attgatagat 840

attgctgctg aatatggaat tgtattaatt gccgatgagg tttatcaaga aaatattttc 900

aaagggaaat ttgtttcatt caagaagatt ttgtcggaat taattgagca agaccctcaa 960

acttataaac atgttcaatt agcatcatta cactcgacat cgaaaggtgt tagtggagaa 1020

tgtggacaac gtggtggata tatggaatta gttgggttca aaccggaagt taaagatgtg 1080

gttttcaaat tggcatcgat taatttatgt tctgttgtct ctggtcaagc attaatggag 1140

ttaatgatta atcctcctca agaaggtgat cctagttacc ccttgtacaa aagcgaaacc 1200

gaatcaatcc ataacgattt ggaatcaaga gcagaatcac tctatcaagc ttttttacaa 1260

atggaagata tcaaatgtaa taaaccaatg ggggccatgt atattttccc cactttagat 1320

tttgatccag cccgatacca taagttatat tcgagagcta agaattccaa tttacaaatt 1380

gatgatattt attgtatcga gttattagaa ggtacaggta tttgttgtgt tcctggtaat 1440

ggatttggtc agaaaccaga tacttatcat ttaagaacaa catttttacc accaggtaaa 1500

gaatggattg ataaatggat aaatttccat aaatcattta ttaaaaaata taaagatgaa 1560

tag 1563

<210> 32
<211> 520
<212> PRT
<213> Candida albicans

<400> 32

Met Leu Arg Val Asn Ser Arg Leu Leu Thr Thr Arg Lys Ser Gln Phe
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Met Phe Thr Ser Asn Ser Leu Arg Phe Leu Ala Thr Phe Lys Pro Ala

20 25 30

Asp Pro Leu Thr Thr His Asp Ile Asn Pro Gln Thr Val Glu Ala Lys
35 40 45

Tyr Ala Val Arg Gly Lys Ile Pro Ile Ile Ala Asp Glu Leu Asn Glu
50 55 60

Leu Ile Gln Lys Gln Pro Gln Ser His Gly Leu Pro Phe Ser Lys Ile
65 70 75 80

Ile Asn Ala Asn Ile Gly Asn Pro Gln Gln Leu Glu Gln Arg Pro Leu
85 90 95

Thr Trp Tyr Arg Gln Val Leu Ser Leu Leu Gln Tyr Pro Asp Leu Leu
100 105 110

Lys Asn Gly Asp Pro Glu Thr Val Lys Ser Leu Tyr Pro Glu Asp Val
115 120 125

Ile Glu Arg Ala Gln Ser Ile Leu Lys His Ile Gly Ser Ile Gly Ala
130 135 140

Tyr Ser His Ser Gln Gly Ala Ser Tyr Phe Arg Gln Ser Ile Ala Glu
145 150 155 160

Phe Ile Thr Asn Arg Asp Gly Gly Tyr Val Ser His Ala Asn Asn Ile
165 170 175

Phe Leu Thr Ser Gly Ala Ser Thr Ala Val Ser Tyr Leu Leu Gln Ile
180 185 190

Leu Ser Val Asn Glu Asn Ser Gly Phe Leu Ile Pro Ile Pro Gln Tyr
195 200 205

Pro Leu Tyr Thr Ala Thr Ile Ala Leu Asn Asn Ala Lys Pro Ile Gly

210 215 220

Tyr Tyr Leu Asp Glu Ser Asn His Trp Ser Thr Asn Pro Gln Glu Ile
225 230 235 240

Arg Glu Leu Ile Glu Thr Asn Gln Ser Gln Gly Ile Asn Ile Lys Ala
245 250 255

Leu Val Val Ile Asn Pro Gly Asn Pro Thr Gly Ala Ile Leu Ser Ser
260 265 270

Gln Asp Ile Ile Glu Leu Ile Asp Ile Ala Ala Glu Tyr Gly Ile Val
275 280 285

Leu Ile Ala Asp Glu Val Tyr Gln Glu Asn Ile Phe Lys Gly Lys Phe
290 295 300

Val Ser Phe Lys Lys Ile Leu Ser Glu Leu Ile Glu Gln Asp Pro Gln
305 310 315 320

Thr Tyr Lys His Val Gln Leu Ala Ser Leu His Ser Thr Ser Lys Gly
325 330 335

Val Ser Gly Glu Cys Gly Gln Arg Gly Gly Tyr Met Glu Leu Val Gly
340 345 350

Phe Lys Pro Glu Val Lys Asp Val Val Phe Lys Leu Ala Ser Ile Asn
355 360 365

Leu Cys Ser Val Val Ser Gly Gln Ala Leu Met Glu Leu Met Ile Asn
370 375 380

Pro Pro Gln Glu Gly Asp Pro Ser Tyr Pro Leu Tyr Lys Ser Glu Thr
385 390 395 400

Glu Ser Ile His Asn Asp Leu Glu Ser Arg Ala Glu Ser Leu Tyr Gln

405 410 415

Ala Phe Leu Gln Met Glu Asp Ile Lys Cys Asn Lys Pro Met Gly Ala
420 425 430

Met Tyr Ile Phe Pro Thr Leu Asp Phe Asp Pro Ala Arg Tyr His Lys
435 440 445

Leu Tyr Ser Arg Ala Lys Asn Ser Asn Leu Gln Ile Asp Asp Ile Tyr
450 455 460

Cys Ile Glu Leu Leu Glu Gly Thr Gly Ile Cys Cys Val Pro Gly Asn
465 470 475 480

Gly Phe Gly Gln Lys Pro Asp Thr Tyr His Leu Arg Thr Thr Phe Leu
485 490 495

Pro Pro Gly Lys Glu Trp Ile Asp Lys Trp Ile Asn Phe His Lys Ser
500 505 510

Phe Ile Lys Lys Tyr Lys Asp Glu
515 520

<210> 33
<211> 1518
<212> DNA
<213> Schizosaccharomyces pombe

<400> 33
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aattacgccg tccgtggagc tttagccatt cttgcggacg agatccaaga tgatttactt 180

gaaaatcctt cttcatatcc tttcagtgag atcgtctatg caaacatcgg taatcctcag 240

cagatgggac agtctcctat tacattcgtt cgacaggttt tatctctttg ccagtaccct 300

accttgttag accatgctga ggaaaagtgg tttcaaaatt tgttccctac ggatgtcgta 360

caacgatcca aaatgctctt aaaggaatct ggaagtttgg gtgcctatag tgcttctcaa 420

ggtattccgc ttgtaaggcg acatgttgcg gatttcatta gagcgagaga tggatttgat 480

tgcgagccat ctgacatata tttgactagt ggtgcctcac acgctgcccg gcttataatg 540

actttgataa tcgctaggcc aacagatggt gtaatggttc ccgctcctca atatcctttg 600

tacggtgccc aaattgatct catgagtgga tctatggtat cttacagcct ctccgaggaa 660

aataattggg acattgattt tgaccaattt aaaaaatcat ttgatgaagc atctaaaaaa 720

ggtatcaacg ttcgtttatg cgtggttatt aatcccggta atcctactgg agcttgcatt 780

tctgaaaata gcatggaaaa agttttgcgc tttgctaagg caaagggcat agtattgctt 840

gccgacgaag tctatcaaaa caatatttac caaaacaagt ttcattcttt taggagaaaa 900

cttggtgaat taagagaaaa ggaacccgac aatcattggg accaagtttc gcttatttcc 960

gtaaattctg ttagcaaagg tcaatttggt gaatgtggtc aaagaggtgg atatttggac 1020

gttgttaata ttccagagcc cgctaaggat caaatcctca aactagctac cattgacatt 1080

tgtccaccag ttgctggtca attattagta gacatgctag taaatcctcc taaacctggt 1140

gatcccagtt atgatttgtt catcaaagaa gttgatgaga ttcatgaagc actgcgttta 1200

caatgccgtc agctctacga gggaacaaag cgcatgaaga gagtttcatg tttagaaccc 1260

cacggggcca tgtatttgca tcccagcgtc tcacttcccg aaaagttaat cactacagcc 1320

aaagctcaga aaattcaacc tgacgaattc tatgcgatag aattgcttaa gcgttcaggt 1380

atatgtgttg ttcctggaag tggatttggg caaccagaag gtgattatca tattcgaatc 1440

acgtttttgg ctaaaggaac tgaatacatt gaacgatttg tcaaagctca taatgaaata 1500

atggacctct atgaataa 1518

<210> 34
<211> 505
<212> PRT
<213> Schizosaccharomyces pombe

<400> 34

Met Phe Thr Asp Tyr Pro Asn Asp Ile Asn Cys Glu Ser Pro Arg Met
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Ser Asp Leu Asp Gly Phe Cys Gln Asn Ala Phe Ser Asp Leu Asn Ser
20 25 30

Leu Asn Gln Gln Val Phe Lys Ala Asn Tyr Ala Val Arg Gly Ala Leu
35 40 45

Ala Ile Leu Ala Asp Glu Ile Gln Asp Asp Leu Leu Glu Asn Pro Ser
50 55 60

Ser Tyr Pro Phe Ser Glu Ile Val Tyr Ala Asn Ile Gly Asn Pro Gln
65 70 75 80

Gln Met Gly Gln Ser Pro Ile Thr Phe Val Arg Gln Val Leu Ser Leu
85 90 95

Cys Gln Tyr Pro Thr Leu Leu Asp His Ala Glu Glu Lys Trp Phe Gln
100 105 110

Asn Leu Phe Pro Thr Asp Val Val Gln Arg Ser Lys Met Leu Leu Lys
115 120 125

Glu Ser Gly Ser Leu Gly Ala Tyr Ser Ala Ser Gln Gly Ile Pro Leu
130 135 140

Val Arg Arg His Val Ala Asp Phe Ile Arg Ala Arg Asp Gly Phe Asp
145 150 155 160

Cys Glu Pro Ser Asp Ile Tyr Leu Thr Ser Gly Ala Ser His Ala Ala
165 170 175

Arg Leu Ile Met Thr Leu Ile Ile Ala Arg Pro Thr Asp Gly Val Met
180 185 190

Val Pro Ala Pro Gln Tyr Pro Leu Tyr Gly Ala Gln Ile Asp Leu Met
195 200 205

Ser Gly Ser Met Val Ser Tyr Ser Leu Ser Glu Glu Asn Asn Trp Asp
210 215 220

Ile Asp Phe Asp Gln Phe Lys Lys Ser Phe Asp Glu Ala Ser Lys Lys
225 230 235 240

Gly Ile Asn Val Arg Leu Cys Val Val Ile Asn Pro Gly Asn Pro Thr
245 250 255

Gly Ala Cys Ile Ser Glu Asn Ser Met Glu Lys Val Leu Arg Phe Ala
260 265 270

Lys Ala Lys Gly Ile Val Leu Leu Ala Asp Glu Val Tyr Gln Asn Asn
275 280 285

Ile Tyr Gln Asn Lys Phe His Ser Phe Arg Arg Lys Leu Gly Glu Leu
290 295 300

Arg Glu Lys Glu Pro Asp Asn His Trp Asp Gln Val Ser Leu Ile Ser
305 310 315 320

Val Asn Ser Val Ser Lys Gly Gln Phe Gly Glu Cys Gly Gln Arg Gly
325 330 335

Gly Tyr Leu Asp Val Val Asn Ile Pro Glu Pro Ala Lys Asp Gln Ile
340 345 350

Leu Lys Leu Ala Thr Ile Asp Ile Cys Pro Pro Val Ala Gly Gln Leu
355 360 365

Leu Val Asp Met Leu Val Asn Pro Pro Lys Pro Gly Asp Pro Ser Tyr
370 375 380

Asp Leu Phe Ile Lys Glu Val Asp Glu Ile His Glu Ala Leu Arg Leu
385 390 395 400

Gln Cys Arg Gln Leu Tyr Glu Gly Thr Lys Arg Met Lys Arg Val Ser
405 410 415

Cys Leu Glu Pro His Gly Ala Met Tyr Leu His Pro Ser Val Ser Leu
420 425 430

Pro Glu Lys Leu Ile Thr Thr Ala Lys Ala Gln Lys Ile Gln Pro Asp
435 440 445

Glu Phe Tyr Ala Ile Glu Leu Leu Lys Arg Ser Gly Ile Cys Val Val
450 455 460

Pro Gly Ser Gly Phe Gly Gln Pro Glu Gly Asp Tyr His Ile Arg Ile
465 470 475 480

Thr Phe Leu Ala Lys Gly Thr Glu Tyr Ile Glu Arg Phe Val Lys Ala
485 490 495

His Asn Glu Ile Met Asp Leu Tyr Glu
500 505

<210> 35
<211> 1500
<212> DNA
<213> Aspergillus nidulans

<400> 35
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cgttgcctga ccctagacaa catcaattcg aacgtcaagg ctgccaagta tgctgttcgt 120

ggagaactcg ccgttaaggc ggaggaatac cgtgtgaggc tggctcaggg agacaagaca 180

ctgccgtttg acagcgttat tttcgccaac atcggcaatc ctcagcagct cgaccaaaag 240

cccatcactt tcttccgtca agtcctcagt cttatggaaa accctctact gttaagcaac 300

aaagatgccc ttcgtacgtc tttcggctat caggatgatg ttatcgagcg ggccgagaag 360

cttctggccg aagtccagag tgttggtgca tacagtcaca gccaaggtgc tcccctgatt 420

cgcgagagtg tggccaagtt cattgaagaa cgtgatggct tccccgccga ccctcagtcg 480

ctttaccttа ctggtggtgc ctcttccggt gtaaacacca ttctgaacgt catttgtaat 540

gggccaaatg ctggtgtcct agttccgatt ccccagtatc ctctgtacac agccacttta 600

tccctcttga atgctcagtg tgttccttac cacttagaag agcagaaggc ttggggtacc 660

gacatcggta caatcaagaa gtcattggaa caggccaagg ctgcaggcac tgacgttcgc 720

gccattgttg ttatcaaccc tggcaacccg acgggcgctt ctttgagtcc agctgatatc 780

aagagcgtcc ttgacatcgc cgcggaagag aagctcgtcg taattgcgga cgaggtatac 840

cagacaaatg tgtttatcgg agaattcaca tcgttcaaaa agaggctccg ggagctgcag 900

caagaagtac ctggtaaata cgacaatgtc gagcttgttt cccttcacag tacttccaag 960

ggtatggttg gtgaatgtgg ccatcgcgga ggttacttcg aactggttgg atttgatccc 1020

ttggttgctg cccaggtcta caagttcatc agcatcatgc tctgccctcc tgtcatcggg 1080

caatgtttgg ttgaactgat ggtgaaccct ccaaaggagg gcgagcccag ccatgagttg 1140

tatcagaagg agtacaacgg catccgggaa ggactgcgcc agcgcgcctt tgccctctat 1200

gaagcttttc aacggatgga gggtgtcgag tgccaagagc ctcagggtgc catgtacctt 1260

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acggactggg tggagcgtat cgtgaagttc cattccgagt tcatggccaa atacaaatag 1500

<210> 36
<211> 499
<212> PRT
<213> Aspergillus nidulans

<400> 36

Met Thr Thr Arg Thr Thr Val Pro Asn Ala Ser Gln Arg Ala Leu Ser
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Thr Ala Ala Val Arg Cys Leu Thr Leu Asp Asn Ile Asn Ser Asn Val
20 25 30

Lys Ala Ala Lys Tyr Ala Val Arg Gly Glu Leu Ala Val Lys Ala Glu
35 40 45

Glu Tyr Arg Val Arg Leu Ala Gln Gly Asp Lys Thr Leu Pro Phe Asp
50 55 60

Ser Val Ile Phe Ala Asn Ile Gly Asn Pro Gln Gln Leu Asp Gln Lys
65 70 75 80

Pro Ile Thr Phe Phe Arg Gln Val Leu Ser Leu Met Glu Asn Pro Leu
85 90 95

Leu Leu Ser Asn Lys Asp Ala Leu Arg Thr Ser Phe Gly Tyr Gln Asp
100 105 110

Asp Val Ile Glu Arg Ala Glu Lys Leu Leu Ala Glu Val Gln Ser Val
115 120 125

Gly Ala Tyr Ser His Ser Gln Gly Ala Pro Leu Ile Arg Glu Ser Val
130 135 140

Ala Lys Phe Ile Glu Glu Arg Asp Gly Phe Pro Ala Asp Pro Gln Ser
145 150 155 160

Leu Tyr Leu Thr Gly Gly Ala Ser Ser Gly Val Asn Thr Ile Leu Asn
165 170 175

Val Ile Cys Asn Gly Pro Asn Ala Gly Val Leu Val Pro Ile Pro Gln
180 185 190

Tyr Pro Leu Tyr Thr Ala Thr Leu Ser Leu Leu Asn Ala Gln Cys Val
195 200 205

Pro Tyr His Leu Glu Glu Gln Lys Ala Trp Gly Thr Asp Ile Gly Thr
210 215 220

Ile Lys Lys Ser Leu Glu Gln Ala Lys Ala Ala Gly Thr Asp Val Arg
225 230 235 240

Ala Ile Val Val Ile Asn Pro Gly Asn Pro Thr Gly Ala Ser Leu Ser
245 250 255

Pro Ala Asp Ile Lys Ser Val Leu Asp Ile Ala Ala Glu Glu Lys Leu
260 265 270

Val Val Ile Ala Asp Glu Val Tyr Gln Thr Asn Val Phe Ile Gly Glu
275 280 285

Phe Thr Ser Phe Lys Lys Arg Leu Arg Glu Leu Gln Gln Glu Val Pro
290 295 300

Gly Lys Tyr Asp Asn Val Glu Leu Val Ser Leu His Ser Thr Ser Lys
305 310 315 320

Gly Met Val Gly Glu Cys Gly His Arg Gly Gly Tyr Phe Glu Leu Val
325 330 335

Gly Phe Asp Pro Leu Val Ala Ala Gln Val Tyr Lys Phe Ile Ser Ile
340 345 350

Met Leu Cys Pro Pro Val Ile Gly Gln Cys Leu Val Glu Leu Met Val
355 360 365

Asn Pro Pro Lys Glu Gly Glu Pro Ser His Glu Leu Tyr Gln Lys Glu
370 375 380

Tyr Asn Gly Ile Arg Glu Gly Leu Arg Gln Arg Ala Phe Ala Leu Tyr
385 390 395 400

Glu Ala Phe Gln Arg Met Glu Gly Val Glu Cys Gln Glu Pro Gln Gly
405 410 415

Ala Met Tyr Leu Phe Pro Thr Ile Ser Leu Pro Pro Lys Ala Ile Glu
420 425 430

Ala Ala Ala Ala Glu Asn Arg Ala Ala Asp Glu Phe Tyr Cys Leu Arg
435 440 445

Leu Leu Asp Ala Thr Gly Val Cys Val Val Pro Gly Ser Gly Phe Gly
450 455 460

Gln Lys Glu Asn Thr Leu His Phe Arg Thr Thr Phe Leu Ala Pro Gly
465 470 475 480

Thr Asp Trp Val Glu Arg Ile Val Lys Phe His Ser Glu Phe Met Ala
485 490 495

Lys Tyr Lys

<210> 37
<211> 1506
<212> DNA
<213> Aspergillus fumigatus

<400> 37
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ggccctcgtc gtctccgtgc cgataatatc aatcccaacg tcaaggcggc caagtatgct 120

gtccgtggtg agcttgccgt caaggcggag gaataccgtg tgagattggc caagggagac 180

aagtctttgc cctttgacag tgtcatttte gccaatattg gcaaccccca gcagctggat 240

caaaaaccca tcaccttctt ccgtcaagta ctcagtcttc tcgagaacac cgcattgctt 300

gaaaaaccgg aggtcctgcg gtcgtctttc ggctacaacc aggacgtcat tgaccgggct 360

aagaagcttc ttgcggacat tcagagcgtc ggtgcctaca gtcacagcca gggagcacca 420

gtaattcggg agagcgtggc caaattcatc gaggagcgtg atggcttccc cgccaacccg 480

caagacctgt acctctgcgc tggtgcgtcg tccggtgtta gcacgctgct gaatgtcatc 540

tgcaacggtc ccaccgccgg tgtccttgtg ccgattcccc aatatcctct gtacaccgcc 600

accctgtccc ttctcaatgc acagtgcgtc ccataccatt tagaggagga caaggcctgg 660

ggtaccgacg tggaggccat ccggcaatct ctggtgcgcg ccaaggccga gggcactgag 720

gttcgtgcta tcgtcgtcat caaccccggt aacccgacgg gtgcctcgct cagccccgag 780

gacatcaaga gcgtgcttga catcgccgcc gaggagaagc tggtcgtcat cgccgacgag 840

gtgtaccaga ccaacgtctt cgtgggcgag ttcacatcct tcaagaagag actgcgccaa 900

ctccagcagg aggtgcctgg caagtacgac aatgtcgaac ttgcttctct gcacagtgtg 960

tccaagggta tggtgggcga atgcggtcac cgaggcggtt actttgaact cgtcggattc 1020

gaccccttgg tcgcggccga gatttacaag tttgttagca ttatgctgtg cccgccggtg 1080

atcggtcagt gcctggtcga acttatggtg aacccaccca agaagggcga gcccagttac 1140

gagttgtatc agaaggagta caacagcatt agcgatggcc tacacaagcg tgccctcgcc 1200

ctgtacgaag ccttcaagca gatggagggc gttgaatgcc aggagcctca gggcgccatg 1260

tacctcttcc ccagcatcac cctgcccccc aaggccgtcg aagccgccgc tgccgaaggt 1320

cggaacgccg acgaattcta ctgtctgcgc ctcctcgacg caacgggtgt ttgcgtggtc 1380

cccggttccg gctttggaca gaaggagaac acgctccact tccgcacaac cttccttgcc 1440

cccggcactg actgggtcga gcggatcgtc aagttccacg ccgagttcat ggccaagtat 1500

aaatag 1506

<210> 38
<211> 501
<212> PRT
<213> Aspergillus fumigatus

<400> 38

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Asn Val Lys Ala Ala Lys Tyr Ala Val Arg Gly Glu Leu Ala Val Lys
        35                  40                  45

Ala Glu Glu Tyr Arg Val Arg Leu Ala Lys Gly Asp Lys Ser Leu Pro
    50                  55                  60

Phe Asp Ser Val Ile Phe Ala Asn Ile Gly Asn Pro Gln Gln Leu Asp
65                  70                  75                  80

Gln Lys Pro Ile Thr Phe Phe Arg Gln Val Leu Ser Leu Leu Glu Asn
                85                  90                  95

Thr Ala Leu Leu Glu Lys Pro Glu Val Leu Arg Ser Ser Phe Gly Tyr
            100                 105                 110

Asn Gln Asp Val Ile Asp Arg Ala Lys Lys Leu Leu Ala Asp Ile Gln
        115                 120                 125

Ser Val Gly Ala Tyr Ser His Ser Gln Gly Ala Pro Val Ile Arg Glu
    130                 135                 140

Ser Val Ala Lys Phe Ile Glu Glu Arg Asp Gly Phe Pro Ala Asn Pro
145                 150                 155                 160

Gln Asp Leu Tyr Leu Cys Ala Gly Ala Ser Ser Gly Val Ser Thr Leu
                165                 170                 175

Leu Asn Val Ile Cys Asn Gly Pro Thr Ala Gly Val Leu Val Pro Ile
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180 185 190

Pro Gln Tyr Pro Leu Tyr Thr Ala Thr Leu Ser Leu Leu Asn Ala Gln
195 200 205

Cys Val Pro Tyr His Leu Glu Glu Asp Lys Ala Trp Gly Thr Asp Val
210 215 220

Glu Ala Ile Arg Gln Ser Leu Val Arg Ala Lys Ala Glu Gly Thr Glu
225 230 235 240

Val Arg Ala Ile Val Val Ile Asn Pro Gly Asn Pro Thr Gly Ala Ser
245 250 255

Leu Ser Pro Glu Asp Ile Lys Ser Val Leu Asp Ile Ala Ala Glu Glu
260 265 270

Lys Leu Val Val Ile Ala Asp Glu Val Tyr Gln Thr Asn Val Phe Val
275 280 285

Gly Glu Phe Thr Ser Phe Lys Lys Arg Leu Arg Gln Leu Gln Gln Glu
290 295 300

Val Pro Gly Lys Tyr Asp Asn Val Glu Leu Ala Ser Leu His Ser Val
305 310 315 320

Ser Lys Gly Met Val Gly Glu Cys Gly His Arg Gly Gly Tyr Phe Glu
325 330 335

Leu Val Gly Phe Asp Pro Leu Val Ala Ala Glu Ile Tyr Lys Phe Val
340 345 350

Ser Ile Met Leu Cys Pro Pro Val Ile Gly Gln Cys Leu Val Glu Leu
355 360 365

Met Val Asn Pro Pro Lys Lys Gly Glu Pro Ser Tyr Glu Leu Tyr Gln

370 375 380

Lys Glu Tyr Asn Ser Ile Ser Asp Gly Leu His Lys Arg Ala Leu Ala
385 390 395 400

Leu Tyr Glu Ala Phe Lys Gln Met Glu Gly Val Glu Cys Gln Glu Pro
405 410 415

Gln Gly Ala Met Tyr Leu Phe Pro Ser Ile Thr Leu Pro Pro Lys Ala
420 425 430

Val Glu Ala Ala Ala Ala Glu Gly Arg Asn Ala Asp Glu Phe Tyr Cys
435 440 445

Leu Arg Leu Leu Asp Ala Thr Gly Val Cys Val Val Pro Gly Ser Gly
450 455 460

Phe Gly Gln Lys Glu Asn Thr Leu His Phe Arg Thr Thr Phe Leu Ala
465 470 475 480

Pro Gly Thr Asp Trp Val Glu Arg Ile Val Lys Phe His Ala Glu Phe
485 490 495

Met Ala Lys Tyr Lys
500

<210> 39
<211> 1497
<212> DNA
<213> Aspergillus oryzae

<400> 39
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tgcctgaacc ctgataacat caaccccccac gtcacggagg ccaagtatgc cgtccgtggt 120

gagcttgctg tcaaggccga ggagtaccgc gtgaaactgg ccaatggaga caaatcgtta 180

cctttcgaca gtgtcatctt tgccaacatc ggcaatcccc aacagctcga ccagaaaccc 240

atcaccttct tccgccaagt actcagtctc ctcgagaacc ctcaactgtt gaacaacacg 300

gaagcacttc gtacatcctt tttttatgaa caagatgtcg ttgaccgggc caagaagctc 360

ctcgcggatg tccagagcgt tggtgcttac agtcacagcc agggagcgcc tgtgatccgc 420

caaagtatcg ccaaattcat tgaggagcgt gatggattcc cggccaaccc tcaggatttg 480

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ccccaggccg gtgtcctcgt ccctattccg caataccctc tttacactgc cacccttttct 600

ctcctgaatg cgcaatgtgt accctacctc ctcgaagagc aaaaggcttg gggtaccgat 660

gtgactgcca tccgtaactc gttggcgcag gcccggtcta ccggcactga cgttcgttcg 720

attgtggtca tcaaccccgg taaccctact ggtgcctctt tgagcgccga ggatatcaag 780

aatgttcttg accttgctgc ggaggagaag cttgttgtta ttgcggacga ggtttaccag 840

acgaacgttt tcgagggcga gttcatttcg ttcaagaaga ggcttcgtca gctgcaacag 900

gagacaccag gcaagtatga ttatgtggag ttggtctctc ttcacagtgt gtctaaaggt 960

atggtgggcg agtgtggcca ccgtggtggc tactttgagc tggttggatt cgaccctgag 1020

gttcaggccc agatctacaa gcttgtgagc atcggacttt gcccaccagt cattggacag 1080

tgtttgcttg agcttatggt gaacccaccc aaggagggcg aaggcagcta tgagctgtac 1140

cagaaggagt acaatggaat cagcgaggga ctgcacaagc gcgcctttgc cttatacgag 1200

gccttccaac agatggaggg cgttgagtgt cagaaacctc agggtgccat gtatctcttc 1260

cccaccatca ctctcccacc caaggccatt gaggctgcca aggctgagaa ccgtgccgcc 1320

gatgagttct actgcttgcg tctcctcgac gctaccggtg tctgtgttgt ccctggctcc 1380

ggcttcggcc agaaggagaa cactctgcac ttccgcacaa ctttcctggc ccctggcact 1440

gattgggttg aacggatcgt caagttccac tccgaattta tggccaagta caaataa 1497

<210> 40
<211> 498
<212> PRT
<213> Aspergillus oryzae

<400> 40

Met Ala Thr Gln Thr Thr Val Ser Tyr Thr Thr Thr Arg Thr Leu Ser
1 5 10 15

Thr Pro Ala Arg Cys Leu Asn Pro Asp Asn Ile Asn Pro His Val Thr
20 25 30

Glu Ala Lys Tyr Ala Val Arg Gly Glu Leu Ala Val Lys Ala Glu Glu
35 40 45

Tyr Arg Val Lys Leu Ala Asn Gly Asp Lys Ser Leu Pro Phe Asp Ser
50 55 60

Val Ile Phe Ala Asn Ile Gly Asn Pro Gln Gln Leu Asp Gln Lys Pro
65 70 75 80

Ile Thr Phe Phe Arg Gln Val Leu Ser Leu Leu Glu Asn Pro Gln Leu
85 90 95

Leu Asn Asn Thr Glu Ala Leu Arg Thr Ser Phe Phe Tyr Glu Gln Asp
100 105 110

Val Val Asp Arg Ala Lys Lys Leu Leu Ala Asp Val Gln Ser Val Gly
115 120 125

Ala Tyr Ser His Ser Gln Gly Ala Pro Val Ile Arg Gln Ser Ile Ala
130 135 140

Lys Phe Ile Glu Glu Arg Asp Gly Phe Pro Ala Asn Pro Gln Asp Leu
145 150 155 160

Phe Cys Cys Ala Gly Ala Ser Ser Gly Val Ser Thr Ile Leu Asn Ile
165 170 175

Ile Cys Asn Gly Pro Gln Ala Gly Val Leu Val Pro Ile Pro Gln Tyr

180 185 190

Pro Leu Tyr Thr Ala Thr Leu Ser Leu Leu Asn Ala Gln Cys Val Pro
195 200 205

Tyr Leu Leu Glu Glu Gln Lys Ala Trp Gly Thr Asp Val Thr Ala Ile
210 215 220

Arg Asn Ser Leu Ala Gln Ala Arg Ser Thr Gly Thr Asp Val Arg Ser
225 230 235 240

Ile Val Val Ile Asn Pro Gly Asn Pro Thr Gly Ala Ser Leu Ser Ala
245 250 255

Glu Asp Ile Lys Asn Val Leu Asp Leu Ala Ala Glu Glu Lys Leu Val
260 265 270

Val Ile Ala Asp Glu Val Tyr Gln Thr Asn Val Phe Glu Gly Glu Phe
275 280 285

Ile Ser Phe Lys Lys Arg Leu Arg Gln Leu Gln Gln Glu Thr Pro Gly
290 295 300

Lys Tyr Asp Tyr Val Glu Leu Val Ser Leu His Ser Val Ser Lys Gly
305 310 315 320

Met Val Gly Glu Cys Gly His Arg Gly Gly Tyr Phe Glu Leu Val Gly
325 330 335

Phe Asp Pro Glu Val Gln Ala Gln Ile Tyr Lys Leu Val Ser Ile Gly
340 345 350

Leu Cys Pro Pro Val Ile Gly Gln Cys Leu Leu Glu Leu Met Val Asn
355 360 365

Pro Pro Lys Glu Gly Glu Gly Ser Tyr Glu Leu Tyr Gln Lys Glu Tyr

370 375 380

Asn Gly Ile Ser Glu Gly Leu His Lys Arg Ala Phe Ala Leu Tyr Glu
385 390 395 400

Ala Phe Gln Gln Met Glu Gly Val Glu Cys Gln Lys Pro Gln Gly Ala
405 410 415

Met Tyr Leu Phe Pro Thr Ile Thr Leu Pro Pro Lys Ala Ile Glu Ala
420 425 430

Ala Lys Ala Glu Asn Arg Ala Ala Asp Glu Phe Tyr Cys Leu Arg Leu
435 440 445

Leu Asp Ala Thr Gly Val Cys Val Val Pro Gly Ser Gly Phe Gly Gln
450 455 460

Lys Glu Asn Thr Leu His Phe Arg Thr Thr Phe Leu Ala Pro Gly Thr
465 470 475 480

Asp Trp Val Glu Arg Ile Val Lys Phe His Ser Glu Phe Met Ala Lys
485 490 495

Tyr Lys

<210> 41
<211> 1542
<212> DNA
<213> Cryptococcus neoformans

<400> 41
atgcccagac ttagcaacgt ctattgtccc aaatcactct tacaacgtca gaccatccaa 60

atcaggtcat tcagtcagac tatgtcacct ttcaaacccg cgcttactct tgataccatc 120

aaccccgcgg ttcaggctgt tcactatgct gtccgaggcg agctcgcgat caaggcggac 180

aaatatgtcc aagtccttgc cgatataact cacaagcctt tgccgtttga aaagatcgtc 240

actgccaaca tcggtaatcc ccaacaacaa ggtcttgatc aagttcctct cacttattgg 300

cgacaaatta tttccttatt ggagtatccc gatctgatgc agaaacatga gcagttggcc 360

aagcagattt accctggaga tgtgattgag cgagccaggg cgttacataa cgaaattgga 420

agtacgggtg cgtacactca ttccaagggt gtgttgggta tcagaaagag agtcgccaag 480

tttattgaag aacgcgacgg ttacccggcg gaccctcaaa atatcttcct caccgccggt 540

gcttctgccg gtgttgcttc gatccttggt gtcgccctcc gcagaggtga tggctgcatg 600

atccccatcc cccaatatcc cctctatacc gccaccctcg cttacctcga gtctgagcct 660

ctgccatact acctttctga agcggacgac tggtcgatga accacgattc tttgctcaag 720

agcgtggagg aaggcaagaa gaagggtatc cccatcaagg cgcttgtaat cattaacccc 780

ggaaacccta ccggcgcatg tttgagccaa gaggcgatgg aggcggttgt gcatctctgt 840

tatgaggaag gtatcgtcct cctcgcagac gaggtttacc agatgaacgt ctttgacccc 900

gaacagcgac cgttcatttc tttcaaaaag gttttgatgg atatgcccaa ggagatcagg 960

gaaagtgtgg aactggtatc tttccattcg atctcaaaag gtgttagtgg agaatgtgga 1020

aggagaggtg gatactttga atgtgtcaac attgataagg atgtgatgga ccaggtttac 1080

aagatggcga gtgtcacttt atgtcctccc gtctcaggcc agatcggtgt cgacctcatg 1140

gtctccctc cgaaacccgg agacgaatct tacccttat ggaaagaaga aaccgatctg 1200

atccaaaaca atctcaagtc ccgatcatat ctcatggctg agcatttcaa caaaatggaa 1260

ggtgtttctt gcaacaatgc ggaaggagcc atgtacttgt tcccgaggat taatatccct 1320

cccaaagctg tagaggcggc gaagaagttg ggtaaggaac cggatgtgat gtatgctttg 1380

gatcttcttg atgcgaccgg tatctgtgcg gtggcaggca gcggttttgg ccaagaaccg 1440

gggacgttcc atttgcgagt gactgccctg tgtcccgata ctgctgaatt tatcggtcga 1500

ttccaaaagt tcaacaagga atttatggaa aagtatgcct aa 1542

<210> 42
<211> 480

<212> PRT
<213> Cryptococcus neoformans

<400> 42

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Met Pro Arg Leu Ser Asn Val Tyr Cys Pro Lys Ser Leu Leu Gln Arg
1               5                  10                  15

Gln Thr Ile Gln Ile Arg Ser Phe Ser Gln Thr Met Ser Pro Phe Lys
            20                  25                  30

Pro Ala Leu Thr Leu Asp Thr Ile Asn Pro Ala Val Gln Ala Val His
        35                  40                  45

Tyr Ala Val Arg Gly Glu Leu Ala Ile Lys Ala Asp Lys Tyr Val Gln
    50                  55                  60

Val Leu Ala Asp Ile Thr His Lys Pro Leu Pro Phe Glu Lys Ile Val
65                  70                  75                  80

Thr Ala Asn Ile Gly Asn Pro Gln Gln Gln Gly Leu Asp Gln Val Pro
                85                  90                  95

Leu Thr Tyr Trp Arg Gln Ile Ile Ser Leu Leu Glu Tyr Pro Asp Leu
            100                 105                 110

Met Gln Lys His Glu Gln Leu Ala Lys Gln Ile Tyr Pro Gly Asp Val
        115                 120                 125

Ile Glu Arg Ala Arg Ala Leu His Asn Glu Ile Gly Ser Thr Gly Ala
    130                 135                 140

Tyr Thr His Ser Lys Gly Val Leu Gly Ile Arg Lys Arg Val Ala Lys
145                 150                 155                 160

Phe Ile Glu Glu Arg Asp Gly Tyr Pro Ala Asp Pro Gln Asn Ile Phe
                165                 170                 175
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Leu Thr Ala Gly Ala Ser Ala Gly Val Ala Ser Ile Leu Gly Val Ala
180 185 190

Leu Arg Arg Gly Asp Gly Cys Met Ile Pro Ile Pro Gln Tyr Pro Leu
195 200 205

Tyr Thr Ala Thr Leu Ala Tyr Leu Glu Ser Glu Pro Leu Pro Tyr Tyr
210 215 220

Leu Ser Glu Ala Asp Asp Trp Ser Met Asn His Asp Ser Leu Leu Lys
225 230 235 240

Ser Val Glu Glu Gly Lys Lys Lys Gly Ile Pro Ile Lys Ala Leu Val
245 250 255

Ile Ile Asn Pro Gly Asn Pro Thr Gly Ala Cys Leu Ser Gln Glu Ala
260 265 270

Met Glu Ala Val Val His Leu Cys Tyr Glu Glu Gly Ile Val Leu Leu
275 280 285

Ala Asp Glu Val Tyr Gln Met Asn Val Phe Asp Pro Glu Gln Arg Pro
290 295 300

Phe Ile Ser Phe Lys Lys Val Leu Met Asp Met Pro Lys Glu Ile Arg
305 310 315 320

Glu Ser Val Glu Leu Val Ser Phe His Ser Ile Ser Lys Gly Val Ser
325 330 335

Gly Glu Cys Gly Arg Arg Gly Gly Tyr Phe Glu Cys Val Asn Ile Asp
340 345 350

Lys Asp Val Met Asp Gln Val Tyr Lys Met Ala Ser Val Thr Leu Cys
355 360 365

Pro Pro Val Ser Gly Gln Ile Gly Val Asp Leu Met Val Ser Pro Pro
370 375 380

Lys Pro Gly Asp Glu Ser Tyr Pro Leu Trp Lys Glu Glu Thr Asp Leu
385 390 395 400

Ile Gln Asn Asn Leu Lys Ser Arg Ser Tyr Leu Met Ala Glu His Phe
405 410 415

Asn Lys Met Glu Gly Val Ser Cys Asn Asn Ala Glu Gly Ala Met Tyr
420 425 430

Leu Phe Pro Arg Ile Asn Ile Pro Pro Lys Ala Val Glu Ala Ala Lys
435 440 445

Lys Leu Gly Lys Glu Pro Asp Val Met Tyr Ala Leu Asp Leu Leu Asp
450 455 460

Ala Thr Gly Ile Cys Ala Val Ala Gly Ser Gly Phe Gly Gln Glu Pro
465 470 475 480

<210> 43
<211> 1605
<212> DNA
<213> Dictyostelium discoideum

<400> 43
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tcttcaacaa ttattcaacc actttcaaat actactacaa caacaataat taataataat 120

aatataacta attttgaaaa aatgacacat aaaaaatcta tgacaattga taatatttgc 180

caaaatgtaa gaaatgcaca atatgcagta cgtggtgaat tagttattcg tgcagaagca 240

atttcacatc aattacaaaa acaaaaaaca gaaggcacaa aaacattacc atttgaagag 300

attgtctatt gtaatattgg taatccacaa caattgaaac aaaaaccatt aacttatttc 360

cgtcaagttg tatcattagt tgaatgtcca gatttattag ataatccata cgttgaaaag 420

atatatccag ccgatgttat ctcacgtgct aaagagatat taggatcaat taataataca 480

acaggtgcct attccaatag tcaaggtatt ggtttagttt taagatcagt tgcagatttc 540

atagagagac gtgatggaca taaatctgat ccatccgaaa ttttccttac agatggtgca 600

tcagttggtg tacaacgtat tttgaaactt ttaattaaag atcgttcaga cggtatctta 660

attccaattc cacaatatcc actctacagt gccaccattg aattatataa tggcagtcaa 720

ttagggtacc tattaaatga agagaaaggt tggtcactcg agatctccca attggagcat 780

tcctacaatg atgcagtttc aaagggtatt aatccacgtg cactcgttat catcaatcca 840

ggtaatccaa ctggtcaatg tttagataga gcaaatatgg aagagattgt caagttttgt 900

ttagaaaaga atgtagtatt attggctgat gaagtctatc aagagaatgt ttatgtcaaa 960

gagagtaaac cattcatctc attcaaaaag gttgtcaaag atatgggtgg tgattatgca 1020

gatttagaga tggtttcatt ccattcagtt agtaaaggtt tcgttggtga atgtggtaaa 1080

cgtggtggtt atatggaatt aaatggtgtc actcaagatg ttaaagctga aatttataaa 1140

ctcgcatcaa ttggtttatg tccaaatgtt attggtcaat tggttgttga tttaatggtt 1200

cgtccaccag ttgctggtga acaatcacat gatctctacc ttaaagaaag agataatatc 1260

tatgaatctt taaaaaaacg tgcaaatctc ttaacaaatg ctttaaataa tcttgaaggt 1320

gtaacttgta atccatcaga aggtgcaatg tatgctttcc cacaaattcg tcttccagct 1380

aaagctgtag aatatgcaaa ttcaattggt aaagcaccag atgcttacta ttgtattcaa 1440

ttactcgaag ccactggtat ctgtgttgta ccaggtagtg gtttcggtca aaaagatggt 1500

acttggcatt ttagaactac cttcttacct tctgaagaag caattgaagg tgtttgtaag 1560

agaatcgctg atttccatca atcatttatg aataaatata aataa 1605

<210> 44
<211> 534
<212> PRT
<213> Dictyostelium discoideum

<400> 44

Met Phe Lys Arg Ser Leu Lys Val Leu Leu Ser Asn Pro Pro Ile Asn
1 5 10 15

Arg Val Lys Pro Ser Ser Thr Ile Ile Gln Pro Leu Ser Asn Thr Thr
20 25 30

Thr Thr Thr Ile Ile Asn Asn Asn Asn Ile Thr Asn Phe Glu Lys Met
35 40 45

Thr His Lys Lys Ser Met Thr Ile Asp Asn Ile Cys Gln Asn Val Arg
50 55 60

Asn Ala Gln Tyr Ala Val Arg Gly Glu Leu Val Ile Arg Ala Glu Ala
65 70 75 80

Ile Ser His Gln Leu Gln Lys Gln Lys Thr Glu Gly Thr Lys Thr Leu
85 90 95

Pro Phe Glu Glu Ile Val Tyr Cys Asn Ile Gly Asn Pro Gln Gln Leu
100 105 110

Lys Gln Lys Pro Leu Thr Tyr Phe Arg Gln Val Val Ser Leu Val Glu
115 120 125

Cys Pro Asp Leu Leu Asp Asn Pro Tyr Val Glu Lys Ile Tyr Pro Ala
130 135 140

Asp Val Ile Ser Arg Ala Lys Glu Ile Leu Gly Ser Ile Asn Asn Thr
145 150 155 160

Thr Gly Ala Tyr Ser Asn Ser Gln Gly Ile Gly Leu Val Leu Arg Ser
165 170 175

Val Ala Asp Phe Ile Glu Arg Arg Asp Gly His Lys Ser Asp Pro Ser
180 185 190

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Glu Ile Phe Leu Thr Asp Gly Ala Ser Val Gly Val Gln Arg Ile Leu
        195                 200                 205

Lys Leu Leu Ile Lys Asp Arg Ser Asp Gly Ile Leu Ile Pro Ile Pro
    210                 215                 220

Gln Tyr Pro Leu Tyr Ser Ala Thr Ile Glu Leu Tyr Asn Gly Ser Gln
225                 230                 235                 240

Leu Gly Tyr Leu Leu Asn Glu Glu Lys Gly Trp Ser Leu Glu Ile Ser
                245                 250                 255

Gln Leu Glu His Ser Tyr Asn Asp Ala Val Ser Lys Gly Ile Asn Pro
            260                 265                 270

Arg Ala Leu Val Ile Ile Asn Pro Gly Asn Pro Thr Gly Gln Cys Leu
        275                 280                 285

Asp Arg Ala Asn Met Glu Glu Ile Val Lys Phe Cys Leu Glu Lys Asn
    290                 295                 300

Val Val Leu Leu Ala Asp Glu Val Tyr Gln Glu Asn Val Tyr Val Lys
305                 310                 315                 320

Glu Ser Lys Pro Phe Ile Ser Phe Lys Lys Val Val Lys Asp Met Gly
                325                 330                 335

Gly Asp Tyr Ala Asp Leu Glu Met Val Ser Phe His Ser Val Ser Lys
            340                 345                 350

Gly Phe Val Gly Glu Cys Gly Lys Arg Gly Gly Tyr Met Glu Leu Asn
        355                 360                 365

Gly Val Thr Gln Asp Val Lys Ala Glu Ile Tyr Lys Leu Ala Ser Ile
    370                 375                 380
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Gly Leu Cys Pro Asn Val Ile Gly Gln Leu Val Val Asp Leu Met Val
385 390 395 400

Arg Pro Pro Val Ala Gly Glu Gln Ser His Asp Leu Tyr Leu Lys Glu
405 410 415

Arg Asp Asn Ile Tyr Glu Ser Leu Lys Lys Arg Ala Asn Leu Leu Thr
420 425 430

Asn Ala Leu Asn Asn Leu Glu Gly Val Thr Cys Asn Pro Ser Glu Gly
435 440 445

Ala Met Tyr Ala Phe Pro Gln Ile Arg Leu Pro Ala Lys Ala Val Glu
450 455 460

Tyr Ala Asn Ser Ile Gly Lys Ala Pro Asp Ala Tyr Tyr Cys Ile Gln
465 470 475 480

Leu Leu Glu Ala Thr Gly Ile Cys Val Val Pro Gly Ser Gly Phe Gly
485 490 495

Gln Lys Asp Gly Thr Trp His Phe Arg Thr Thr Phe Leu Pro Ser Glu
500 505 510

Glu Ala Ile Glu Gly Val Cys Lys Arg Ile Ala Asp Phe His Gln Ser
515 520 525

Phe Met Asn Lys Tyr Lys
530

<210> 45
<211> 1710
<212> DNA
<213> Trypanosoma brucei

<400> 45
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ctaaacatta gtaagaagaa caaagccaag tcgagcgtac aacacattgg cgggttagcg 120

cgaaaacaga atcctgaacc cacaaaatca atttttgtgt cgagatacgg agcacgatca 180

ctgaagacct cgacaatgaa aggtaaccag gaatttttc agaagggtgg ggcccacgtt 240

tccaagggcg ttcacatcaa cccacgcgta aagaaggctc agtatgccgt gcgcgggctt 300

gtgccgatgc gagccgacga aatcagggag gaaatccgtt caggcacggg gaagtcgaag 360

ttctccttca acgaactggt ttactgcaac attggcaacc cccaagccct ggagcagaag 420

ccgcttacct ttcaccgcca agtgatgtcg cttatcgatg ctccatttct gcttgaggat 480

aacgccgtcg tctctcgata tccctctgat gctgtttccc gtgcgcgtct ctacttgggc 540

cacatcggcc aacgtactgg cgcctacacg gactccgcag gctatgcctt tgtacgtgac 600

atcgtcgcgc agtatgtgaa tgagcgtgac gcctatgtaa aaccgcttca ggaggcatcg 660

tcgattgtgc ttacagacgg cgcaagcact ggtgtgcgca taatcttaca gacgcttgtg 720

ggcgatgaga aggacgctgt gatgattccc atcccgcagt atccgctgta cacggcacag 780

attgcattgt tgggaggtac ccccgcgatg tattaccttc gtgagagcga aggctgggcg 840

ctgaacgttg gagagctcga ggcagtatac aaagactgtg tggcgaacgg aaacgcgacg 900

ccccgcgtgc tcgtcgtgat taaccctggt aaccctacag gtggcgtgtt ggagcgcact 960

gtgatggagg aggttgccaa gttctgttgc gatcacggtg ttgtgctcat ggccgatgag 1020

gtttaccagg aaaatatcta caccgcgacc aagcggtttg agagttttcg gaagattgtg 1080

ctcgaacttc caccaccata caacaccgac accgtgcttg tttccttgca ctccgtgtcg 1140

aagggtatta tcggtgagtg tggtcgccgt ggtgggtact tcacactcac aaacgctccg 1200

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cactacacgg cagagtacag tggcattttt gaaagcctta agcgccgtgc tgacctgctt 1380

gcaaaggaac tgaacaacat ccgtggtttc aagtcccaat ctgttgaggg cgccatgtac 1440

gctttcccca ctattgagct ccctcccaag tacgtgaagc acaacgatga gatgaactca 1500

aaggagggcc gacagcttgc gccggacgcg cgttgggcac tggagcttct cgagagcacc 1560

ggtattgttg tggtgccggg ttctggcttt gggcagcagc ctgggacact gcacttccgc 1620

acgacgatcc tcccacccga agcgcatatg gagcgtgtgg tgaaggctct gcgccagttc 1680

caggagggca tttgggccaa gtatgcataa 1710

<210> 46
<211> 569
<212> PRT
<213> Trypanosoma brucei

<400> 46

Met Asp Ile Tyr Leu Phe Ser Val Trp Phe Ile Gln Asn Glu Glu Lys
1 5 10 15

Cys Leu Asp Phe Leu Asn Ile Ser Lys Lys Asn Lys Ala Lys Ser Ser
20 25 30

Val Gln His Ile Gly Gly Leu Ala Arg Lys Gln Asn Pro Glu Pro Thr
35 40 45

Lys Ser Ile Phe Val Ser Arg Tyr Gly Ala Arg Ser Leu Lys Thr Ser
50 55 60

Thr Met Lys Gly Asn Gln Glu Phe Phe Gln Lys Gly Gly Ala His Val
65 70 75 80

Ser Lys Gly Val His Ile Asn Pro Arg Val Lys Lys Ala Gln Tyr Ala
85 90 95

Val Arg Gly Leu Val Pro Met Arg Ala Asp Glu Ile Arg Glu Glu Ile
100 105 110

Arg Ser Gly Thr Gly Lys Ser Lys Phe Ser Phe Asn Glu Leu Val Tyr
115 120 125

```
Cys Asn Ile Gly Asn Pro Gln Ala Leu Glu Gln Lys Pro Leu Thr Phe
    130                 135                 140

His Arg Gln Val Met Ser Leu Ile Asp Ala Pro Phe Leu Leu Glu Asp
145                 150                 155                 160

Asn Ala Val Val Ser Arg Tyr Pro Ser Asp Ala Val Ser Arg Ala Arg
                165                 170                 175

Leu Tyr Leu Gly His Ile Gly Gln Arg Thr Gly Ala Tyr Thr Asp Ser
            180                 185                 190

Ala Gly Tyr Ala Phe Val Arg Asp Ile Val Ala Gln Tyr Val Asn Glu
        195                 200                 205

Arg Asp Ala Tyr Val Lys Pro Leu Gln Glu Ala Ser Ser Ile Val Leu
    210                 215                 220

Thr Asp Gly Ala Ser Thr Gly Val Arg Ile Ile Leu Gln Thr Leu Val
225                 230                 235                 240

Gly Asp Glu Lys Asp Ala Val Met Ile Pro Ile Pro Gln Tyr Pro Leu
                245                 250                 255

Tyr Thr Ala Gln Ile Ala Leu Leu Gly Gly Thr Pro Ala Met Tyr Tyr
            260                 265                 270

Leu Arg Glu Ser Glu Gly Trp Ala Leu Asn Val Gly Glu Leu Glu Ala
        275                 280                 285

Val Tyr Lys Asp Cys Val Ala Asn Gly Asn Ala Thr Pro Arg Val Leu
    290                 295                 300

Val Val Ile Asn Pro Gly Asn Pro Thr Gly Gly Val Leu Glu Arg Thr
305                 310                 315                 320
```

Val Met Glu Glu Val Ala Lys Phe Cys Cys Asp His Gly Val Val Leu
325 330 335

Met Ala Asp Glu Val Tyr Gln Glu Asn Ile Tyr Thr Ala Thr Lys Arg
340 345 350

Phe Glu Ser Phe Arg Lys Ile Val Leu Glu Leu Pro Pro Pro Tyr Asn
355 360 365

Thr Asp Thr Val Leu Val Ser Leu His Ser Val Ser Lys Gly Ile Ile
370 375 380

Gly Glu Cys Gly Arg Arg Gly Gly Tyr Phe Thr Leu Thr Asn Ala Pro
385 390 395 400

Pro Glu Leu Val Glu Gln Val Met Lys Leu Cys Ser Ile Asn Leu Cys
405 410 415

Ser Asn Val Asn Gly Gln Leu Met Thr Ala Leu Met Cys Ser Pro Pro
420 425 430

Lys Pro Gly Asp Ala Ser Phe Asp His Tyr Thr Ala Glu Tyr Ser Gly
435 440 445

Ile Phe Glu Ser Leu Lys Arg Arg Ala Asp Leu Leu Ala Lys Glu Leu
450 455 460

Asn Asn Ile Arg Gly Phe Lys Ser Gln Ser Val Glu Gly Ala Met Tyr
465 470 475 480

Ala Phe Pro Thr Ile Glu Leu Pro Pro Lys Tyr Val Lys His Asn Asp
485 490 495

Glu Met Asn Ser Lys Glu Gly Arg Gln Leu Ala Pro Asp Ala Arg Trp
500 505 510

Ala Leu Glu Leu Leu Glu Ser Thr Gly Ile Val Val Val Pro Gly Ser
515 520 525

Gly Phe Gly Gln Gln Pro Gly Thr Leu His Phe Arg Thr Thr Ile Leu
530 535 540

Pro Pro Glu Ala His Met Glu Arg Val Val Lys Ala Leu Arg Gln Phe
545 550 555 560

Gln Glu Gly Ile Trp Ala Lys Tyr Ala
565

<210> 47
<211> 1494
<212> DNA
<213> Leishmania major

<400> 47
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atggaggcgg aatacgccgt gcgggggctg atcccggcgc gcgcggatga gatcaaggcg 120

gacttggcta caggccacgg cacctactcg ttcgaaagcc tcgtgtactg caacatcggc 180

aacccgcagt cagtggggca gatgccgcta acgttctacc gacaagtgat ggtgctcgtc 240

gatgcgccgt tcctgctgga ggatgcggaa atcgttgcgc ggctgccaga ggacgccgtt 300

gcacgcgcgc gcaggtacct ttcggagatc gggacgggca ccggcgcgta cacagagtct 360

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gtgagcccgg ctgcgacggt gaacgatatc tgtctgacag acggcgcgag catgggtgcg 480

aagctgttcc tgcagctcct tgtgggcggc gcgagcgatg ctgtgatgat cccggttccg 540

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tttttgagct tccgcgaggt tgtgcttggg atgcctgagc cgtactgctc ggagacgatg 900

cttgtgtcac tgcactcgac atcgaaaggg gtgattggtg aatgcgggcg gcgcggcggg 960

tatttctgca tgacgaacct gcctgctgcg ctgcgccagc aggttgtgaa gctgtgctcg 1020

atcaacctgt gtgcaaacgt gaacgggcag ttgatgactg cgctgatgtg ctcgccgccg 1080

cgcgagggcg aagcgagcta cgcgctgcac cggcgcgagt acgacgagat ctttacgggc 1140

atgaaggagc gcgctgagct gctggcgcgc gagcttgggg ctgtgcgcgg gctctcgtgc 1200

caaccggtgg agggcgcaat gtacgcgttc ccgagaattg tgttgcctga gcggtacgcc 1260

cagcggaacg aggagctgaa cgcgaaggag ggtcggcagc ttgcgctgga cgcgcggtgg 1320

gcgctggagc tgctggagtc gagcgggatc gttgttgtgc ccgggtctgg gttcgggcag 1380

gaacccggga cgctgcactt tcggatcacg attctcccgc ctcttgaaca gattgatcgg 1440

atggtgcgtg cgatccgcga gttccaggac cggatctacg agcagtacgc ttaa 1494

<210> 48
<211> 497
<212> PRT
<213> Leishmania major

<400> 48

Met Leu Arg His Ala Ala Arg Cys Phe Ser Pro Arg Gln Cys Tyr Val
1 5 10 15

Ser Pro Arg Val Met Glu Ala Glu Tyr Ala Val Arg Gly Leu Ile Pro
20 25 30

Ala Arg Ala Asp Glu Ile Lys Ala Asp Leu Ala Thr Gly His Gly Thr
35 40 45

Tyr Ser Phe Glu Ser Leu Val Tyr Cys Asn Ile Gly Asn Pro Gln Ser
50 55 60

Val Gly Gln Met Pro Leu Thr Phe Tyr Arg Gln Val Met Val Leu Val
65 70 75 80

Asp Ala Pro Phe Leu Leu Glu Asp Ala Glu Ile Val Ala Arg Leu Pro
85 90 95

Glu Asp Ala Val Ala Arg Ala Arg Arg Tyr Leu Ser Glu Ile Gly Thr
100 105 110

Gly Thr Gly Ala Tyr Thr Glu Ser Phe Gly Phe Arg Phe Ala Arg Ala
115 120 125

Ala Val Ala Ala His Ile Asn Glu Leu Asp His Gly Val Ser Pro Ala
130 135 140

Ala Thr Val Asn Asp Ile Cys Leu Thr Asp Gly Ala Ser Met Gly Ala
145 150 155 160

Lys Leu Phe Leu Gln Leu Leu Val Gly Gly Ala Ser Asp Ala Val Met
165 170 175

Ile Pro Val Pro Gln Tyr Pro Leu Tyr Ser Ala Gln Ile Ala Leu Leu
180 185 190

Gly Gly Val Lys Val Pro Tyr Gly Leu His Glu Ser Glu Gly Trp Val
195 200 205

Met Lys Leu Ser Asp Leu Val Ala Ala Tyr Glu Arg Cys Val Thr Glu
210 215 220

Ser Gly Ala Thr Pro Arg Leu Phe Val Cys Ile Asn Pro Gly Asn Pro
225 230 235 240

Thr Gly Asn Val Leu Glu Arg Cys Val Met Glu Asp Val Val Arg Phe
245 250 255

Cys His Glu Arg Gly Met Leu Leu Leu Ala Asp Glu Val Tyr Gln Glu
260 265 270

Asn Val Tyr Asp Thr Arg Arg Arg Phe Leu Ser Phe Arg Glu Val Val
275 280 285

Leu Gly Met Pro Glu Pro Tyr Cys Ser Glu Thr Met Leu Val Ser Leu
290 295 300

His Ser Thr Ser Lys Gly Val Ile Gly Glu Cys Gly Arg Arg Gly Gly
305 310 315 320

Tyr Phe Cys Met Thr Asn Leu Pro Ala Ala Leu Arg Gln Gln Val Val
325 330 335

Lys Leu Cys Ser Ile Asn Leu Cys Ala Asn Val Asn Gly Gln Leu Met
340 345 350

Thr Ala Leu Met Cys Ser Pro Pro Arg Glu Gly Glu Ala Ser Tyr Ala
355 360 365

Leu His Arg Arg Glu Tyr Asp Glu Ile Phe Thr Gly Met Lys Glu Arg
370 375 380

Ala Glu Leu Leu Ala Arg Glu Leu Gly Ala Val Arg Gly Leu Ser Cys
385 390 395 400

Gln Pro Val Glu Gly Ala Met Tyr Ala Phe Pro Arg Ile Val Leu Pro
405 410 415

Glu Arg Tyr Ala Gln Arg Asn Glu Glu Leu Asn Ala Lys Glu Gly Arg
420 425 430

Gln Leu Ala Leu Asp Ala Arg Trp Ala Leu Glu Leu Leu Glu Ser Ser
435 440 445

Gly Ile Val Val Val Pro Gly Ser Gly Phe Gly Gln Glu Pro Gly Thr
450 455 460

Leu His Phe Arg Ile Thr Ile Leu Pro Pro Leu Glu Gln Ile Asp Arg
465 470 475 480

Met Val Arg Ala Ile Arg Glu Phe Gln Asp Arg Ile Tyr Glu Gln Tyr
485 490 495

Ala

<210> 49
<211> 1455
<212> DNA
<213> Entamoeba histolytica

<400> 49
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agaggaaaat tagtattaga ggcaaatgag attcaaaaag aaattgaaga agcaagaaaa 120

aaaggaaaaa ataatcctta tccatttgag aaagtagttt attgtaatat tggtaatcca 180

cagatatgta accaacagcc attaacatat ccaaggcaga ttatctcaat agttgaatat 240

cctgagcttt taaatcatac aaccctttt ccgaaagatg ttatcaccca tgctaaaaaa 300

attattaata gtcttggttg tactggaaca agtggtgcat atactaattc tatgggagtt 360

attcaattca gaaaatcaat ttgtaaattt ataaaacata gagatggaac tgctccatcc 420

cctgatgacg tatttataac cgatggagca tctactggaa taaaaatgat tttaaatatg 480

ttgatttcac atcctcttca tggaattatg attcctattc cacaataccc attatacagt 540

gcttcaatat ctcaattcgg aggttttcaa attaattact ttctagatga atcaaaaaaa 600

tggtcaacag atatgacatc cgtaagaaaa gtttatgaac aagcggttga aaaaggtatt 660

caagtgaaag gatttgtttg tattaaccca ggtaatccaa ctggacaagt tcttacagtc 720

caaaatatga aagaaattat agaattttgc tatgaaaaaa aaatttgttt attagctgat 780

gaagtatatc aagagaatat ctacggtgaa ataccattta catcattcag aaaggtattg 840

aagtcaatga gggatgaggt gaaaaatagt gttgagctaa tctcattttt tagtgtttca 900

aaaggatttt atggtgaatg tggaaagcga ggtggatatt tccagataga aaatattaat 960

tcatttgctc gttctcagat gtataaaata gcatctacca atttatgttc aaatgtagtt 1020

ggtcaagaga tggttgaaat aatttgcaac ccaccaaaag aaggtgatga atcttatcca 1080

aaatacatga atgaaaaaat gtctatttta aactctttga aaagaaaagc caagttactc 1140

tattctgttc taaatgagtg tgaaggaatt tcttgtaatg aagctatggg tgctctttat 1200

cttttcccaa agattacatt cccaaacaaa tatattgatg agtgtaaaag aaaggatcaa 1260

aaaccagatg aattgtattg tttaaggatg ttaaaaagta taggggtgtg tgttgttcca 1320

ggatctggtt ttggtcaaaa agataatacg tatcatttta gaattgccat tctaccacca 1380

gaaaatgaaa tacagaatat tgccgtcaaa ataaaaactt ttcatacatc ttttatgaag 1440

gactattgtc actaa 1455

<210> 50
<211> 484
<212> PRT
<213> Entamoeba histolytica

<400> 50

Met Lys Ala Phe Ser Arg Gln Ser Ile Asn Pro Cys Ile Ile Ala Thr
1 5 10 15

Gln Tyr Ala Val Arg Gly Lys Leu Val Leu Glu Ala Asn Glu Ile Gln
20 25 30

Lys Glu Ile Glu Glu Ala Arg Lys Lys Gly Lys Asn Asn Pro Tyr Pro
35 40 45

Phe Glu Lys Val Val Tyr Cys Asn Ile Gly Asn Pro Gln Ile Cys Asn
50 55 60

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Gln Gln Pro Leu Thr Tyr Pro Arg Gln Ile Ile Ser Ile Val Glu Tyr
65                  70                  75                  80

Pro Glu Leu Leu Asn His Thr Thr Leu Phe Pro Lys Asp Val Ile Thr
                85                  90                  95

His Ala Lys Lys Ile Ile Asn Ser Leu Gly Cys Thr Gly Thr Ser Gly
            100                 105                 110

Ala Tyr Thr Asn Ser Met Gly Val Ile Gln Phe Arg Lys Ser Ile Cys
        115                 120                 125

Lys Phe Ile Lys His Arg Asp Gly Thr Ala Pro Ser Pro Asp Asp Val
    130                 135                 140

Phe Ile Thr Asp Gly Ala Ser Thr Gly Ile Lys Met Ile Leu Asn Met
145                 150                 155                 160

Leu Ile Ser His Pro Leu His Gly Ile Met Ile Pro Ile Pro Gln Tyr
                165                 170                 175

Pro Leu Tyr Ser Ala Ser Ile Ser Gln Phe Gly Gly Phe Gln Ile Asn
            180                 185                 190

Tyr Phe Leu Asp Glu Ser Lys Lys Trp Ser Thr Asp Met Thr Ser Val
        195                 200                 205

Arg Lys Val Tyr Glu Gln Ala Val Glu Lys Gly Ile Gln Val Lys Gly
    210                 215                 220

Phe Val Cys Ile Asn Pro Gly Asn Pro Thr Gly Gln Val Leu Thr Val
225                 230                 235                 240

Gln Asn Met Lys Glu Ile Ile Glu Phe Cys Tyr Glu Lys Lys Ile Cys
                245                 250                 255
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Leu Leu Ala Asp Glu Val Tyr Gln Glu Asn Ile Tyr Gly Glu Ile Pro
260 265 270

Phe Thr Ser Phe Arg Lys Val Leu Lys Ser Met Arg Asp Glu Val Lys
275 280 285

Asn Ser Val Glu Leu Ile Ser Phe Phe Ser Val Ser Lys Gly Phe Tyr
290 295 300

Gly Glu Cys Gly Lys Arg Gly Gly Tyr Phe Gln Ile Glu Asn Ile Asn
305 310 315 320

Ser Phe Ala Arg Ser Gln Met Tyr Lys Ile Ala Ser Thr Asn Leu Cys
325 330 335

Ser Asn Val Val Gly Gln Glu Met Val Glu Ile Ile Cys Asn Pro Pro
340 345 350

Lys Glu Gly Asp Glu Ser Tyr Pro Lys Tyr Met Asn Glu Lys Met Ser
355 360 365

Ile Leu Asn Ser Leu Lys Arg Lys Ala Lys Leu Leu Tyr Ser Val Leu
370 375 380

Asn Glu Cys Glu Gly Ile Ser Cys Asn Glu Ala Met Gly Ala Leu Tyr
385 390 395 400

Leu Phe Pro Lys Ile Thr Phe Pro Asn Lys Tyr Ile Asp Glu Cys Lys
405 410 415

Arg Lys Asp Gln Lys Pro Asp Glu Leu Tyr Cys Leu Arg Met Leu Lys
420 425 430

Ser Ile Gly Val Cys Val Val Pro Gly Ser Gly Phe Gly Gln Lys Asp
435 440 445

Asn Thr Tyr His Phe Arg Ile Ala Ile Leu Pro Pro Glu Asn Glu Ile
450 455 460

Gln Asn Ile Ala Val Lys Ile Lys Thr Phe His Thr Ser Phe Met Lys
465 470 475 480

Asp Tyr Cys His

<210> 51
<211> 1452
<212> DNA
<213> Entamoeba histolytica

<400> 51
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cgtggtaaaa ttgctattgt ttcagaagaa attgataatg ctattaaaaa agcaaaagca 120

gaaggtaaac caaatcctta tccatttgaa aaagttgtta aatgtaatag tggtaatcct 180

caattattaa atcaaaaacc attaactttt gttagagaaa ttacttctat ggtagaatat 240

cctcctctta cagaacatcc agaacttttc catgctgatg ctgttgctcg tgctaaagaa 300

attattaaag ctactggttg taatggaaca actggtgctt actcaccatc taaaggtctt 360

gcttatgtta gacaaacaat tgcacgtttc ttagaagaaa gagataatgt tccaatgtcc 420

ccagaagata tttatttaac tgatggtgct tctattgcta ttaagattgt tatgcaatta 480

atgctttcac atccacttca tggtattatg attccaaatc cacaatatcc attatatggt 540

gcttgtattc aacaattagg aggaaaaaca tgtcattata atttaaacga agataattat 600

tggttaccag acattaatga tattaaggaa caatatgaaa aatatcagaa tgaaggaatt 660

aaaattaagg cattagttgt tattaatcca ggaaatccat gtggagaagt tttaccagtt 720

gacactataa aagaaattat tagattctgt aacgaaaaga agatttgttt aatggctgat 780

gaagtatatc aagaaaatat ttggactgat gttccattca actcatttag aaaaattctt 840

gctacaatgg aaccagaaat tgcacatgga cttgaattaa tttctttcca ttctatttca 900

aaaggattct atggagaatg tggtaagaga ggaggaatgt ttgcatgtac caatattcca 960

gaatttgctc gtttaatgat gtataaaatt atttctacta ctttatgttc taatgttgta 1020

ggacaagttg taatgtctat aatttgtaat cttccaaaag aaggagaccc atcctatcca 1080

ttatttaaac aagaaagaga tgaaatcctt ggctctttaa aacgtaaagc agaatattta 1140

tgtgatattt tcaataagtg tgaaggtatg tcttgtaata gagctgctgg agctatgtat 1200

cttttcccaa gaattacatt accagaaaaa ttcataaaag aatgtcatga aagacatgaa 1260

gatccaaatg aaacatattg tattgaaatg ttaaaaaaga ctggaattgc tgttgtaaaa 1320

gggtctggat ttggtcagaa aaagggtaca tatcatttta gaattgcttt gttaccacca 1380

gaaaatgaaa ttgaagaagt tggaaaaaga attcaagtat tccataattc ttttattcaa 1440

caatacaagt aa 1452

<210> 52
<211> 483
<212> PRT
<213> Entamoeba histolytica

<400> 52

Met Arg Ser Phe Ala Ser Glu Asn Ile Ser Pro Asp Val Val Ala Phe
1 5 10 15

Gln Phe Ala Val Arg Gly Lys Ile Ala Ile Val Ser Glu Glu Ile Asp
20 25 30

Asn Ala Ile Lys Lys Ala Lys Ala Glu Gly Lys Pro Asn Pro Tyr Pro
35 40 45

Phe Glu Lys Val Val Lys Cys Asn Ser Gly Asn Pro Gln Leu Leu Asn
50 55 60

Gln Lys Pro Leu Thr Phe Val Arg Glu Ile Thr Ser Met Val Glu Tyr
65 70 75 80

Pro Pro Leu Thr Glu His Pro Glu Leu Phe His Ala Asp Ala Val Ala
85 90 95

Arg Ala Lys Glu Ile Ile Lys Ala Thr Gly Cys Asn Gly Thr Thr Gly
100 105 110

Ala Tyr Ser Pro Ser Lys Gly Leu Ala Tyr Val Arg Gln Thr Ile Ala
115 120 125

Arg Phe Leu Glu Glu Arg Asp Asn Val Pro Met Ser Pro Glu Asp Ile
130 135 140

Tyr Leu Thr Asp Gly Ala Ser Ile Ala Ile Lys Ile Val Met Gln Leu
145 150 155 160

Met Leu Ser His Pro Leu His Gly Ile Met Ile Pro Asn Pro Gln Tyr
165 170 175

Pro Leu Tyr Gly Ala Cys Ile Gln Gln Leu Gly Gly Lys Thr Cys His
180 185 190

Tyr Asn Leu Asn Glu Asp Asn Tyr Trp Leu Pro Asp Ile Asn Asp Ile
195 200 205

Lys Glu Gln Tyr Glu Lys Tyr Gln Asn Glu Gly Ile Lys Ile Lys Ala
210 215 220

Leu Val Val Ile Asn Pro Gly Asn Pro Cys Gly Glu Val Leu Pro Val
225 230 235 240

Asp Thr Ile Lys Glu Ile Ile Arg Phe Cys Asn Glu Lys Lys Ile Cys
245 250 255

Leu Met Ala Asp Glu Val Tyr Gln Glu Asn Ile Trp Thr Asp Val Pro
260 265 270

Phe Asn Ser Phe Arg Lys Ile Leu Ala Thr Met Glu Pro Glu Ile Ala
275 280 285

His Gly Leu Glu Leu Ile Ser Phe His Ser Ile Ser Lys Gly Phe Tyr
290 295 300

Gly Glu Cys Gly Lys Arg Gly Gly Met Phe Ala Cys Thr Asn Ile Pro
305 310 315 320

Glu Phe Ala Arg Leu Met Met Tyr Lys Ile Ile Ser Thr Thr Leu Cys
325 330 335

Ser Asn Val Val Gly Gln Val Val Met Ser Ile Ile Cys Asn Leu Pro
340 345 350

Lys Glu Gly Asp Pro Ser Tyr Pro Leu Phe Lys Gln Glu Arg Asp Glu
355 360 365

Ile Leu Gly Ser Leu Lys Arg Lys Ala Glu Tyr Leu Cys Asp Ile Phe
370 375 380

Asn Lys Cys Glu Gly Met Ser Cys Asn Arg Ala Ala Gly Ala Met Tyr
385 390 395 400

Leu Phe Pro Arg Ile Thr Leu Pro Glu Lys Phe Ile Lys Glu Cys His
405 410 415

Glu Arg His Glu Asp Pro Asn Glu Thr Tyr Cys Ile Glu Met Leu Lys
420 425 430

Lys Thr Gly Ile Ala Val Val Lys Gly Ser Gly Phe Gly Gln Lys Lys
435 440 445

Gly Thr Tyr His Phe Arg Ile Ala Leu Leu Pro Pro Glu Asn Glu Ile
450 455 460

Glu Glu Val Gly Lys Arg Ile Gln Val Phe His Asn Ser Phe Ile Gln
465 470 475 480

Gln Tyr Lys

<210> 53
<211> 1482
<212> DNA
<213> Trypanosoma cruzi

<400> 53
atgtctgggt cacgaaagga aattcgcatc aacccccgtg tggtggcggc agagtatgcg 60

gtgcgtggga tgctccccat gcgtgcggac gagatcaggg cggccctggc gacaccggag 120

gggaaggcca agtaccccct ctccagcatt gtgtactgca acattgggaa cccgcaggca 180

ctggaacaga agccgctgac gttcttccgg caggtgatgt cgctgattga cgcgccgttc 240

ctgctggaga acgagaaggt tacgtcgcag ttcccggcgg atgcggtggc gcgtgcgagg 300

gagtatcttc gccacatcgg cgatcgcacg ggcgcctaca cggactctgc gggctacgcc 360

tttgtccgtg acatcgtggc gcggcaaatc aatgaacgcg accacgagat aaagccgctg 420

gtggacgcat cctctatttt tctgacggac ggcgcgagct cgggcgtgcg tcttttgctg 480

caggttctcg tgggtgacgc gagtgatgcg gtgatggttc ccattccgca gtacccgctg 540

tacacggcgc agcttacgct tcttggcggc acgcccgcga tgtactacct gtgtgagaag 600

gataactggg cactgaacgt ggaggagctg gcgtcggtgt acgacgagtg cgtggcgaag 660

aataatgcga ccccgcgcgt gctcgttgtg atcaaccctg ggaacccgac tggcggcgtg 720

ctggatcgcg acgtgatgga ggccgtggcg aaattctgct gcgaccgcgg cattgtgctg 780

atggcggacg aggtgtacca ggagaacgtg tacgcggcgg gaaagcgttt cttgagcttc 840

cgggaagtgg tgcttgggct gccggcgccg tacaacacgg acacggtgct ggcctcgctg 900

cactcgacgt cgaagggcat cattggtgag tgcgggcgcc gcggcgggta cttctgcctc 960

acaaacttcc ccgcgccggt tcgggagcag gtgttaaaga tgtgctccat ggttccgtgc 1020

agcagcgtga atgggcagtt gatgacggca ctgatgtgct cgccaccgcg gcccggtgac 1080

gcgagctatg agtcatactg ggcggagtac aatgggatct ttgcgagtct aaagaagcgc 1140

gccctgctgc ttgcgaagga gctgagcacg attcgcggtt tttcttgcca gccggtggaa 1200

ggggcgatgt acgcgtttcc gacgattgag ctgccggaga agtactttca gcacaatgag 1260

gagctgaacg cgaaggaggg gcgaaagctt gggcccgaca cgcgatgggc gttggagctt 1320

ctggagagca gcggggttgt tgttgtggcc ggctctgggt ttggtcagca gcccaacacg 1380

ctgcacttcc gcacgacgat cctgccgccg gagcagcaga tggaacggat ggtgaaggcg 1440

atgcgcacat tccaggaggg catttgggca aagtacgggt aa 1482

<210> 54
<211> 493
<212> PRT
<213> Trypanosoma cruzi

<400> 54

Met Ser Gly Ser Arg Lys Glu Ile Arg Ile Asn Pro Arg Val Val Ala
1 5 10 15

Ala Glu Tyr Ala Val Arg Gly Met Leu Pro Met Arg Ala Asp Glu Ile
20 25 30

Arg Ala Ala Leu Ala Thr Pro Glu Gly Lys Ala Lys Tyr Pro Phe Ser
35 40 45

Ser Ile Val Tyr Cys Asn Ile Gly Asn Pro Gln Ala Leu Glu Gln Lys
50 55 60

Pro Leu Thr Phe Phe Arg Gln Val Met Ser Leu Ile Asp Ala Pro Phe
65 70 75 80

Leu Leu Glu Asn Glu Lys Val Thr Ser Gln Phe Pro Ala Asp Ala Val
85 90 95

Ala Arg Ala Arg Glu Tyr Leu Arg His Ile Gly Asp Arg Thr Gly Ala
100 105 110

Tyr Thr Asp Ser Ala Gly Tyr Ala Phe Val Arg Asp Ile Val Ala Arg
115 120 125

Gln Ile Asn Glu Arg Asp His Glu Ile Lys Pro Leu Val Asp Ala Ser
130 135 140

Ser Ile Phe Leu Thr Asp Gly Ala Ser Ser Gly Val Arg Leu Leu Leu
145 150 155 160

Gln Val Leu Val Gly Asp Ala Ser Asp Ala Val Met Val Pro Ile Pro
165 170 175

Gln Tyr Pro Leu Tyr Thr Ala Gln Leu Thr Leu Leu Gly Gly Thr Pro
180 185 190

Ala Met Tyr Tyr Leu Cys Glu Lys Asp Asn Trp Ala Leu Asn Val Glu
195 200 205

Glu Leu Ala Ser Val Tyr Asp Glu Cys Val Ala Lys Asn Asn Ala Thr
210 215 220

Pro Arg Val Leu Val Val Ile Asn Pro Gly Asn Pro Thr Gly Gly Val
225 230 235 240

Leu Asp Arg Asp Val Met Glu Ala Val Ala Lys Phe Cys Cys Asp Arg
245 250 255

Gly Ile Val Leu Met Ala Asp Glu Val Tyr Gln Glu Asn Val Tyr Ala
260 265 270

Ala Gly Lys Arg Phe Leu Ser Phe Arg Glu Val Val Leu Gly Leu Pro
275 280 285

Ala Pro Tyr Asn Thr Asp Thr Val Leu Ala Ser Leu His Ser Thr Ser
290 295 300

Lys Gly Ile Ile Gly Glu Cys Gly Arg Arg Gly Gly Tyr Phe Cys Leu
305 310 315 320

Thr Asn Phe Pro Ala Pro Val Arg Glu Gln Val Leu Lys Met Cys Ser
325 330 335

Met Val Pro Cys Ser Ser Val Asn Gly Gln Leu Met Thr Ala Leu Met
340 345 350

Cys Ser Pro Pro Arg Pro Gly Asp Ala Ser Tyr Glu Ser Tyr Trp Ala
355 360 365

Glu Tyr Asn Gly Ile Phe Ala Ser Leu Lys Lys Arg Ala Leu Leu Leu
370 375 380

Ala Lys Glu Leu Ser Thr Ile Arg Gly Phe Ser Cys Gln Pro Val Glu
385 390 395 400

Gly Ala Met Tyr Ala Phe Pro Thr Ile Glu Leu Pro Glu Lys Tyr Phe
405 410 415

Gln His Asn Glu Glu Leu Asn Ala Lys Glu Gly Arg Lys Leu Gly Pro
420 425 430

Asp Thr Arg Trp Ala Leu Glu Leu Leu Glu Ser Ser Gly Val Val Val
435 440 445

Val Ala Gly Ser Gly Phe Gly Gln Gln Pro Asn Thr Leu His Phe Arg
450 455 460

Thr Thr Ile Leu Pro Pro Glu Gln Gln Met Glu Arg Met Val Lys Ala
465 470 475 480

Met Arg Thr Phe Gln Glu Gly Ile Trp Ala Lys Tyr Gly
485 490

<210> 55
<211> 1494
<212> DNA
<213> Trypanosoma cruzi

<400> 55
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gcagagtatg cggtgcgtgg gatgctccca atgcgtgcgg acgagatcag ggcggccctg 120

gcgacaccgg aggggaaggc caagtatccc ttccccagca ttgtgtactg caacattggg 180

aacccgcagg cactggaaca gaagccgctg acgttcttcc ggcaggtgat gtcgctgatt 240

gacgcgccgt tcctgctgga aaacgagaag gttacgtcgc agtacccggc ggatgcggtg 300

gcgcgtgcga gggagtatct tcgccacatc ggcgatcgca cgggcgccta cacggactct 360

gcgggctacg cctttgtccg tgacatcgtg gcgcggcaaa tcaatgaacg cgaccacgag 420

ataaagccgc tggtggacgc atcctctatt tttctgacgg acggcgcgag ctcgggcgtg 480

cgtcttttgc tgcaggttct cgtgggtgac gcgagtgatg cggtgatggt tcccattccg 540

cagtacccgc tgtacacggc gcagcttacg cttcttggcg gcacgcccgc gatgtactac 600

ctgtgtgaga aggataactg ggcactgaac gtggaggagc tggcgtcggt gtacgacgag 660

tgcgtggcga agaataatgc gactccgcgc gtgctcgttg tgatcaaccc tgggaacccg 720

actggcggcg tgctggatcg cgacgtgatg gaggctgtgg cgaaattctg ctgcgaccgc 780

ggcattgtgc tgatggcgga cgaggtgtac caggagaacg tgtacgcggc gggaaagcgt 840

ttcttgagct tccgggaagt ggtgcttggg ctgccggcgc cgtacaacac ggacacggtg 900

ctggcctcgc tgcactcgac gtcgaagggc atcattggtg agtgcgggcg ccgcggcggg 960

tacttctgcc tcacaaactt ccccgcgccg gttcgggagc aggtgttaaa gatgtgctcc 1020

atggttccgt gcagcagcgt gaatgggcag ttgatgacgg cactgatgtg ctcgccaccg 1080

cggcccggtg acgcgagcta tgagtcatac tgggcggagt acaatgggat ctttgcgagt 1140

ctaaagaagc gcgccctgct gcttgcgaag gagctgagca cgattcgcgg tttttcttgc 1200

cagccggtgg aaggggcgat gtacgcgttt ccgacgattg agctgccgga gaagtacttt 1260

cagcacaatg aggagctgaa cgcgaaggag gggcgaaagc ttgggcccga cacgcgatgg 1320

gcgttggagc ttctggagag cagcggggtt gttgttgtgg ccggctctgg gtttggtcag 1380

cagcccaaca cgctgcactt ccgcacgacg atcctgccgc cggagcagca gatggaacgg 1440

atggtgaagg cgatgcgcac attccaggag ggcatttggg caaagtacgg gtaa 1494

<210> 56
<211> 497
<212> PRT
<213> Trypanosoma cruzi

<400> 56

Met Leu Arg Lys Thr Leu Phe Gly Phe Arg Ala Ile Arg Ile Asn Pro
1 5 10 15

Arg Val Val Ala Ala Glu Tyr Ala Val Arg Gly Met Leu Pro Met Arg
20 25 30

Ala Asp Glu Ile Arg Ala Ala Leu Ala Thr Pro Glu Gly Lys Ala Lys
35 40 45

Tyr Pro Phe Pro Ser Ile Val Tyr Cys Asn Ile Gly Asn Pro Gln Ala
50 55 60

Leu Glu Gln Lys Pro Leu Thr Phe Phe Arg Gln Val Met Ser Leu Ile
65 70 75 80

Asp Ala Pro Phe Leu Leu Glu Asn Glu Lys Val Thr Ser Gln Tyr Pro
85 90 95

Ala Asp Ala Val Ala Arg Ala Arg Glu Tyr Leu Arg His Ile Gly Asp
100 105 110

Arg Thr Gly Ala Tyr Thr Asp Ser Ala Gly Tyr Ala Phe Val Arg Asp
115 120 125

Ile Val Ala Arg Gln Ile Asn Glu Arg Asp His Glu Ile Lys Pro Leu
130 135 140

Val Asp Ala Ser Ser Ile Phe Leu Thr Asp Gly Ala Ser Ser Gly Val
145 150 155 160

Arg Leu Leu Leu Gln Val Leu Val Gly Asp Ala Ser Asp Ala Val Met
165 170 175

Val Pro Ile Pro Gln Tyr Pro Leu Tyr Thr Ala Gln Leu Thr Leu Leu
180 185 190

Gly Gly Thr Pro Ala Met Tyr Tyr Leu Cys Glu Lys Asp Asn Trp Ala
195 200 205

Leu Asn Val Glu Glu Leu Ala Ser Val Tyr Asp Glu Cys Val Ala Lys
210 215 220

Asn Asn Ala Thr Pro Arg Val Leu Val Val Ile Asn Pro Gly Asn Pro
225 230 235 240

Thr Gly Gly Val Leu Asp Arg Asp Val Met Glu Ala Val Ala Lys Phe
245 250 255

Cys Cys Asp Arg Gly Ile Val Leu Met Ala Asp Glu Val Tyr Gln Glu
260 265 270

Asn Val Tyr Ala Ala Gly Lys Arg Phe Leu Ser Phe Arg Glu Val Val
275 280 285

Leu Gly Leu Pro Ala Pro Tyr Asn Thr Asp Thr Val Leu Ala Ser Leu
290 295 300

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His Ser Thr Ser Lys Gly Ile Ile Gly Glu Cys Gly Arg Arg Gly Gly
305                 310                 315                 320

Tyr Phe Cys Leu Thr Asn Phe Pro Ala Pro Val Arg Glu Gln Val Leu
                325                 330                 335

Lys Met Cys Ser Met Val Pro Cys Ser Ser Val Asn Gly Gln Leu Met
            340                 345                 350

Thr Ala Leu Met Cys Ser Pro Pro Arg Pro Gly Asp Ala Ser Tyr Glu
        355                 360                 365

Ser Tyr Trp Ala Glu Tyr Asn Gly Ile Phe Ala Ser Leu Lys Lys Arg
    370                 375                 380

Ala Leu Leu Leu Ala Lys Glu Leu Ser Thr Ile Arg Gly Phe Ser Cys
385                 390                 395                 400

Gln Pro Val Glu Gly Ala Met Tyr Ala Phe Pro Thr Ile Glu Leu Pro
                405                 410                 415

Glu Lys Tyr Phe Gln His Asn Glu Glu Leu Asn Ala Lys Glu Gly Arg
            420                 425                 430

Lys Leu Gly Pro Asp Thr Arg Trp Ala Leu Glu Leu Leu Glu Ser Ser
        435                 440                 445

Gly Val Val Val Val Ala Gly Ser Gly Phe Gly Gln Gln Pro Asn Thr
    450                 455                 460

Leu His Phe Arg Thr Thr Ile Leu Pro Pro Glu Gln Gln Met Glu Arg
465                 470                 475                 480

Met Val Lys Ala Met Arg Thr Phe Gln Glu Gly Ile Trp Ala Lys Tyr
                485                 490                 495
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Gly

<210> 57
<211> 1482
<212> DNA
<213> Trypanosoma cruzi

<400> 57
atgtctgggt cacgaaagga attcgcatc aacccccgtg tggtggcggc agagtatgcg 60

gtgcgtggga tgctccccat gcgtgcggac gagatcaggg cggccctggc gacaccggag 120

gggaaggcca agtacccctt ctccagcatt gtgtactgca acattgggaa cccgcaggca 180

ctggaacaga agccgctgac gttcttccgg caggtgatgt cgctgattga cgcgccgttc 240

ctgctggaga acgagaaggt tacgtcgcag ttcccggcgg atgcggtggc gcgtgcgagg 300

gagtatcttc gccacatcgg cgatcgcacg ggcgcctaca cggactctgc gggctacgcc 360

tttgtccgtg acatcgtggc gcggcaaatc aatgaacgcg accacgagat aaagccgctg 420

gtggacgcat cctctatttt tctgacggac ggcgcgagct cgggcgtgcg tcttttgctg 480

caggttctcg tgggtgacgc gagtgatgcg gtgatggttc ccattccgca gtacccgctg 540

tacacggcgc agcttacgct tcttggcggc acgcccgcga tgtactacct gtgtgagaag 600

gataactggg cactgaatgt ggaggagctg gcgtcggtgt acgacgagtg cgtggcgaag 660

aataatgcga ccccgcgcgt gctcgttgtg atcaaccctg ggaacccgac tggcggcgtg 720

ctggatcgcg acgtgatgga ggctgtggcg aaattctgct gcgaccgcgg cattgtgctg 780

atggcggacg aggtgtacca ggagaacgtg tacgcggcgg gaaagcgttt cttgagcttc 840

cgggaagtgg tgcttgggct gccggcgccg tacaacacgg acacggtgct ggcctcgctg 900

cactcgacgt cgaagggcat cattggtgag tgcgggcgcc gcggcgggta cttctgcctc 960

acaaacttcc ccgcgccggt gcgggagcag gtggtaaaga tgtgctccat ggttccgtgc 1020

agcagcgtga atgggcagtt gatgacggca ctgatgtgct cgccaccgcg gcccggtgac 1080

gcgagctatg agtcatactg ggcggagtac aatgggatct ttgcgagtct aaagaagcgc 1140

gccctgctgc ttgcgaagga gctgggcacg attcgcggtt tttcttgcca gccggtggaa 1200

ggggcgatgt acgcgtttcc gacgattgag ctgccggaga agtactttca gcacaatgcg 1260

gagctgaacg cgaaggaggg gcgaaagctt gggcccgaca cgcgatgggc gttggagctt 1320

ctggagagca gcggggttgt tgttgtgccc ggctctgggt ttggtcagcg gcccaacacg 1380

ctgcacttcc gcacgacgat cctgccgccg gagcagcaga tggaacggat ggtgaaggcg 1440

atgcgcacat tccaggaggg catttgggca aagtacgggt aa 1482

<210> 58
<211> 493
<212> PRT
<213> Trypanosoma cruzi

<400> 58

Met Ser Gly Ser Arg Lys Glu Ile Arg Ile Asn Pro Arg Val Val Ala
1 5 10 15

Ala Glu Tyr Ala Val Arg Gly Met Leu Pro Met Arg Ala Asp Glu Ile
20 25 30

Arg Ala Ala Leu Ala Thr Pro Glu Gly Lys Ala Lys Tyr Pro Phe Ser
35 40 45

Ser Ile Val Tyr Cys Asn Ile Gly Asn Pro Gln Ala Leu Glu Gln Lys
50 55 60

Pro Leu Thr Phe Phe Arg Gln Val Met Ser Leu Ile Asp Ala Pro Phe
65 70 75 80

Leu Leu Glu Asn Glu Lys Val Thr Ser Gln Phe Pro Ala Asp Ala Val
85 90 95

Ala Arg Ala Arg Glu Tyr Leu Arg His Ile Gly Asp Arg Thr Gly Ala
100 105 110

Tyr Thr Asp Ser Ala Gly Tyr Ala Phe Val Arg Asp Ile Val Ala Arg
115 120 125

Gln Ile Asn Glu Arg Asp His Glu Ile Lys Pro Leu Val Asp Ala Ser
130 135 140

Ser Ile Phe Leu Thr Asp Gly Ala Ser Ser Gly Val Arg Leu Leu Leu
145 150 155 160

Gln Val Leu Val Gly Asp Ala Ser Asp Ala Val Met Val Pro Ile Pro
165 170 175

Gln Tyr Pro Leu Tyr Thr Ala Gln Leu Thr Leu Leu Gly Gly Thr Pro
180 185 190

Ala Met Tyr Tyr Leu Cys Glu Lys Asp Asn Trp Ala Leu Asn Val Glu
195 200 205

Glu Leu Ala Ser Val Tyr Asp Glu Cys Val Ala Lys Asn Asn Ala Thr
210 215 220

Pro Arg Val Leu Val Val Ile Asn Pro Gly Asn Pro Thr Gly Gly Val
225 230 235 240

Leu Asp Arg Asp Val Met Glu Ala Val Ala Lys Phe Cys Cys Asp Arg
245 250 255

Gly Ile Val Leu Met Ala Asp Glu Val Tyr Gln Glu Asn Val Tyr Ala
260 265 270

Ala Gly Lys Arg Phe Leu Ser Phe Arg Glu Val Val Leu Gly Leu Pro
275 280 285

Ala Pro Tyr Asn Thr Asp Thr Val Leu Ala Ser Leu His Ser Thr Ser
290 295 300

Lys Gly Ile Ile Gly Glu Cys Gly Arg Arg Gly Gly Tyr Phe Cys Leu
305 310 315 320

Thr Asn Phe Pro Ala Pro Val Arg Glu Gln Val Val Lys Met Cys Ser
325 330 335

Met Val Pro Cys Ser Ser Val Asn Gly Gln Leu Met Thr Ala Leu Met
340 345 350

Cys Ser Pro Pro Arg Pro Gly Asp Ala Ser Tyr Glu Ser Tyr Trp Ala
355 360 365

Glu Tyr Asn Gly Ile Phe Ala Ser Leu Lys Lys Arg Ala Leu Leu Leu
370 375 380

Ala Lys Glu Leu Gly Thr Ile Arg Gly Phe Ser Cys Gln Pro Val Glu
385 390 395 400

Gly Ala Met Tyr Ala Phe Pro Thr Ile Glu Leu Pro Glu Lys Tyr Phe
405 410 415

Gln His Asn Ala Glu Leu Asn Ala Lys Glu Gly Arg Lys Leu Gly Pro
420 425 430

Asp Thr Arg Trp Ala Leu Glu Leu Leu Glu Ser Ser Gly Val Val Val
435 440 445

Val Pro Gly Ser Gly Phe Gly Gln Arg Pro Asn Thr Leu His Phe Arg
450 455 460

Thr Thr Ile Leu Pro Pro Glu Gln Gln Met Glu Arg Met Val Lys Ala
465 470 475 480

Met Arg Thr Phe Gln Glu Gly Ile Trp Ala Lys Tyr Gly
485 490

<210> 59
<211> 1494
<212> DNA
<213> Trypanosoma cruzi

<400> 59
atgctacgca aaacccttttt tggattcagg gccattcgca tcaacccccg tgtggtggcg 60

gcagagtatg cggtgcgtgg gatgctcccc atgcgtgcgg acgagatcag ggcggccctg 120

gcgacaccgg aggggaaggc caagtacccc ttctccagca ttgtgtactg caacattggg 180

aacccgcagg cactggaaca gaagccgctg acgttcttcc ggcaggtgat gtcgctgatt 240

gacgcgccgt tcctgctgga gaacgagaag gttacgtcgc agttcccggc ggatgcggtg 300

gcgcgtgcga gggagtatct tcgccacatc ggcgatcgca cgggcgccta cacggactct 360

gcgggctacg cctttgcccg tgacatcgtg gcgcggcaaa tcaatgaacg cgaccacgag 420

ataaagccgc tggtggacgc atcctctatt tttctgacgg acggcgcgag ctcgggcgtg 480

cgtcttttgc tgcaggttct cgtgggtgac gcgagtgatg cggtgatggt tcccattccg 540

cagtacccgc tgtacacggc gcagcttact cttcttggcg gcacgcccgc gatgtactac 600

ctgtgtgaga aggataactg ggcactgaac gtggaggagc tggcgtcggt gtacgacgag 660

tgcgtggcga agaataatgc gaccccgcgc gtgctcgttg tgatcaaccc cgggaacccg 720

actggcggcg tgctggatcg cgaagtgatg gaggccgtgg cgaaattctg ctgcgaccgc 780

ggcattgtgc tgatggcgga cgaggtgtac caggagaacg tgtacgcggc gggaaagcgt 840

ttcttgagct tccgggaagt ggtgcttggg ctgccggcgc cgtacaacac ggacacggtg 900

ctggcctcgc tgcactcgac gtcgaagggc atcattggtg agtgcgggcg ccgcggcggg 960

tacttctgcc tcacaaactt ccccgcgccg gtgcgggagc aggtggtaaa gatgtgctcc 1020

atggttccgt gcagcagcgt gaatgggcag ttgatgacgg cactgatgtg ctcgccaccg 1080

cggcccggtg acgcgagcta tgagtcatac tgggcggagt acaatgggat ctttgcgagt 1140

ctaaagaagc gcgccctgct gcttgcgaag gagctgggca cgattcgcgg tttttcttgc 1200

cagccggtgg aaggggcgat gtacgcgttt ccgacgattg agctgccgga gaagtacttt 1260

cagcacaatg cggagctgaa cgcgaaggag gggcgaaagc ttgggcccga cacgcgatgg 1320

gcgttggagc ttctggagag cagcggggtt gttgttgtgc ccggctctgg gtttggtcag 1380

cggcccaaca cgctgcactt ccgcacgacg atcctgccgc cggagcagca gatggaacgg 1440

atggtgaagg cgatgcgcac attccaggag ggcatttggg caaagtacgg gtaa 1494

<210> 60
<211> 497
<212> PRT
<213> Trypanosoma cruzi

<400> 60

Met Leu Arg Lys Thr Leu Phe Gly Phe Arg Ala Ile Arg Ile Asn Pro
1 5 10 15

Arg Val Val Ala Ala Glu Tyr Ala Val Arg Gly Met Leu Pro Met Arg
20 25 30

Ala Asp Glu Ile Arg Ala Ala Leu Ala Thr Pro Glu Gly Lys Ala Lys
35 40 45

Tyr Pro Phe Ser Ser Ile Val Tyr Cys Asn Ile Gly Asn Pro Gln Ala
50 55 60

Leu Glu Gln Lys Pro Leu Thr Phe Phe Arg Gln Val Met Ser Leu Ile
65 70 75 80

Asp Ala Pro Phe Leu Leu Glu Asn Glu Lys Val Thr Ser Gln Phe Pro
85 90 95

Ala Asp Ala Val Ala Arg Ala Arg Glu Tyr Leu Arg His Ile Gly Asp
100 105 110

Arg Thr Gly Ala Tyr Thr Asp Ser Ala Gly Tyr Ala Phe Ala Arg Asp
115 120 125

Ile Val Ala Arg Gln Ile Asn Glu Arg Asp His Glu Ile Lys Pro Leu
130 135 140

Val Asp Ala Ser Ser Ile Phe Leu Thr Asp Gly Ala Ser Ser Gly Val
145 150 155 160

Arg Leu Leu Leu Gln Val Leu Val Gly Asp Ala Ser Asp Ala Val Met
165 170 175

Val Pro Ile Pro Gln Tyr Pro Leu Tyr Thr Ala Gln Leu Thr Leu Leu
180 185 190

Gly Gly Thr Pro Ala Met Tyr Tyr Leu Cys Glu Lys Asp Asn Trp Ala
195 200 205

Leu Asn Val Glu Glu Leu Ala Ser Val Tyr Asp Glu Cys Val Ala Lys
210 215 220

Asn Asn Ala Thr Pro Arg Val Leu Val Val Ile Asn Pro Gly Asn Pro
225 230 235 240

Thr Gly Gly Val Leu Asp Arg Glu Val Met Glu Ala Val Ala Lys Phe
245 250 255

Cys Cys Asp Arg Gly Ile Val Leu Met Ala Asp Glu Val Tyr Gln Glu
260 265 270

Asn Val Tyr Ala Ala Gly Lys Arg Phe Leu Ser Phe Arg Glu Val Val
275 280 285

Leu Gly Leu Pro Ala Pro Tyr Asn Thr Asp Thr Val Leu Ala Ser Leu
290 295 300

His Ser Thr Ser Lys Gly Ile Ile Gly Glu Cys Gly Arg Arg Gly Gly
305 310 315 320

Tyr Phe Cys Leu Thr Asn Phe Pro Ala Pro Val Arg Glu Gln Val Val
325 330 335

Lys Met Cys Ser Met Val Pro Cys Ser Ser Val Asn Gly Gln Leu Met
340 345 350

Thr Ala Leu Met Cys Ser Pro Pro Arg Pro Gly Asp Ala Ser Tyr Glu
355 360 365

Ser Tyr Trp Ala Glu Tyr Asn Gly Ile Phe Ala Ser Leu Lys Lys Arg
370 375 380

Ala Leu Leu Leu Ala Lys Glu Leu Gly Thr Ile Arg Gly Phe Ser Cys
385 390 395 400

Gln Pro Val Glu Gly Ala Met Tyr Ala Phe Pro Thr Ile Glu Leu Pro
405 410 415

Glu Lys Tyr Phe Gln His Asn Ala Glu Leu Asn Ala Lys Glu Gly Arg
420 425 430

Lys Leu Gly Pro Asp Thr Arg Trp Ala Leu Glu Leu Leu Glu Ser Ser
435 440 445

Gly Val Val Val Val Pro Gly Ser Gly Phe Gly Gln Arg Pro Asn Thr
450 455 460

Leu His Phe Arg Thr Thr Ile Leu Pro Pro Glu Gln Gln Met Glu Arg
465 470 475 480

Met Val Lys Ala Met Arg Thr Phe Gln Glu Gly Ile Trp Ala Lys Tyr
485 490 495

Gly

<210> 61
<211> 1869
<212> DNA
<213> Cricetulus griseus

<400> 61
atggccacca aggagaagct gcagtgtctg aaagacttcc acaaagacat cctgaagcct 60

tctccaggga agagcccagg cacacggcct gaggatgagg ctgaggggaa gccccctcag 120

agggagaagt ggtccagcaa gattgacttt gtgctgtctg tggccggagg cttcgtgggt 180

ttgggcaacg tttggcgttt cccgtacctc tgctacaaaa atggtggagg tgctttcctc 240

ataccgtatt ttattttcct gtttgggagt ggcctgcctg tgtttttcct ggaggtcata 300

ataggccagt acacctcaga agggggaatc acctgctggg agaagatctg ccccttgttc 360

tctggcattg gctacgcatc catcgtcatc gtgtccctcc tgaatgtgta ctacattgtc 420

atcctggcct gggccacata ctacctattt cactccttcc agacagagct tccctgggcc 480

cactgcaacc acagctggaa cacaccacat tgcatggagg acaccctgcg taggaatgag 540

agtctctggg tctcccttag cgcctccaac ttcacctcgc ctgtcatcga gttctgggag 600

cgcaatgtac tcagcctgtc ttccggaatc gacgaaccag gcgctctgaa atgggacctt 660

gcgctctgcc tcctcttagt ctggcttgtc tgtttttttct gcatatggaa gggtgttcga 720

tccacaggca aggttgtcta cttcaccgcc actttcccgt ttgccatgct tctggtgctg 780

ctggtccgtg gactgaccct gccgggtgct ggcgaaggca tcaaattcta cctgtaccct 840

gacatcagcc gccttgagga cccacaggtg tggatcgacg ccggaaccca gatattcttt 900

tcctatgcca tctgcctggg ggccatgacc tcactgggaa gctacaacaa gtacaagtat 960

aactcgtaca gggactgtat gctgctggga tgcctgaaca gtggtaccag ttttgtgtct 1020

ggcttcgcag ttttttccat cctgggcttc atggcacaag agcaaggggt ggacattgct 1080

gatgtggctg agtcaggtcc tggcttggcc ttcattgcct atccaaaagc tgtgactatg 1140

atgccgctgc ccacctttg gtccattctg ttttttatta tgctcctctt gcttggactg 1200

gacagccagt ttgttgaagt cgaaggacag atcacatcct tggttgatct ttacccgtcc 1260

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tggatatatg gtggtgataa cttatatgac ggtattgagg acatgattgg ctatcggcct 1500

gggccctgga tgaagtacag ctgggctgtc atcactccag ttctctgtgc tggatgtttc 1560

atcttctctc ttgtcaagta tgtacccctg acctacaaca aagtctacgt gtatcctgat 1620

tgggcaattg ggctgggctg gggcctggcc ctatcctcca tggtgtgtat ccccttggtc 1680

attgccatcc tcctctgccg gacggaggga ccgttccgcg tgagaatcca atacctgata 1740

acccccaggg agcccaaccg ctgggctgtg gagcgtgagg gggccacacc cttccactcc 1800

cgcacaagcc tcgtcatgaa cggcgcactc atgaaaccca gtcacgtcat tgtggagacc 1860

atgatgtga 1869

<210> 62
<211> 622
<212> PRT
<213> Cricetulus griseus

<400> 62

Met Ala Thr Lys Glu Lys Leu Gln Cys Leu Lys Asp Phe His Lys Asp
1 5 10 15

Ile Leu Lys Pro Ser Pro Gly Lys Ser Pro Gly Thr Arg Pro Glu Asp
20 25 30

Glu Ala Glu Gly Lys Pro Pro Gln Arg Glu Lys Trp Ser Ser Lys Ile
35 40 45

Asp Phe Val Leu Ser Val Ala Gly Gly Phe Val Gly Leu Gly Asn Val
50 55 60

Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly Ala Phe Leu

125

65 70 75 80

Ile Pro Tyr Phe Ile Phe Leu Phe Gly Ser Gly Leu Pro Val Phe Phe
85 90 95

Leu Glu Val Ile Ile Gly Gln Tyr Thr Ser Glu Gly Gly Ile Thr Cys
100 105 110

Trp Glu Lys Ile Cys Pro Leu Phe Ser Gly Ile Gly Tyr Ala Ser Ile
115 120 125

Val Ile Val Ser Leu Leu Asn Val Tyr Tyr Ile Val Ile Leu Ala Trp
130 135 140

Ala Thr Tyr Tyr Leu Phe His Ser Phe Gln Thr Glu Leu Pro Trp Ala
145 150 155 160

His Cys Asn His Ser Trp Asn Thr Pro His Cys Met Glu Asp Thr Leu
165 170 175

Arg Arg Asn Glu Ser Leu Trp Val Ser Leu Ser Ala Ser Asn Phe Thr
180 185 190

Ser Pro Val Ile Glu Phe Trp Glu Arg Asn Val Leu Ser Leu Ser Ser
195 200 205

Gly Ile Asp Glu Pro Gly Ala Leu Lys Trp Asp Leu Ala Leu Cys Leu
210 215 220

Leu Leu Val Trp Leu Val Cys Phe Phe Cys Ile Trp Lys Gly Val Arg
225 230 235 240

Ser Thr Gly Lys Val Val Tyr Phe Thr Ala Thr Phe Pro Phe Ala Met
245 250 255

Leu Leu Val Leu Leu Val Arg Gly Leu Thr Leu Pro Gly Ala Gly Glu

260 265 270

Gly Ile Lys Phe Tyr Leu Tyr Pro Asp Ile Ser Arg Leu Glu Asp Pro
275 280 285

Gln Val Trp Ile Asp Ala Gly Thr Gln Ile Phe Phe Ser Tyr Ala Ile
290 295 300

Cys Leu Gly Ala Met Thr Ser Leu Gly Ser Tyr Asn Lys Tyr Lys Tyr
305 310 315 320

Asn Ser Tyr Arg Asp Cys Met Leu Leu Gly Cys Leu Asn Ser Gly Thr
325 330 335

Ser Phe Val Ser Gly Phe Ala Val Phe Ser Ile Leu Gly Phe Met Ala
340 345 350

Gln Glu Gln Gly Val Asp Ile Ala Asp Val Ala Glu Ser Gly Pro Gly
355 360 365

Leu Ala Phe Ile Ala Tyr Pro Lys Ala Val Thr Met Met Pro Leu Pro
370 375 380

Thr Phe Trp Ser Ile Leu Phe Phe Ile Met Leu Leu Leu Leu Gly Leu
385 390 395 400

Asp Ser Gln Phe Val Glu Val Glu Gly Gln Ile Thr Ser Leu Val Asp
405 410 415

Leu Tyr Pro Ser Phe Leu Arg Lys Gly Tyr Arg Arg Glu Val Phe Ile
420 425 430

Ala Ile Leu Cys Ser Ile Ser Tyr Leu Leu Gly Leu Ser Met Val Thr
435 440 445

Glu Gly Gly Met Tyr Val Phe Gln Leu Phe Asp Tyr Tyr Ala Ala Ser

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    450                 455                 460

Gly Val Cys Leu Leu Trp Val Ala Phe Phe Glu Cys Phe Val Ile Ala
465                 470                 475                 480

Trp Ile Tyr Gly Gly Asp Asn Leu Tyr Asp Gly Ile Glu Asp Met Ile
                485                 490                 495

Gly Tyr Arg Pro Gly Pro Trp Met Lys Tyr Ser Trp Ala Val Ile Thr
            500                 505                 510

Pro Val Leu Cys Ala Gly Cys Phe Ile Phe Ser Leu Val Lys Tyr Val
        515                 520                 525

Pro Leu Thr Tyr Asn Lys Val Tyr Val Tyr Pro Asp Trp Ala Ile Gly
    530                 535                 540

Leu Gly Trp Gly Leu Ala Leu Ser Ser Met Val Cys Ile Pro Leu Val
545                 550                 555                 560

Ile Ala Ile Leu Leu Cys Arg Thr Glu Gly Pro Phe Arg Val Arg Ile
                565                 570                 575

Gln Tyr Leu Ile Thr Pro Arg Glu Pro Asn Arg Trp Ala Val Glu Arg
            580                 585                 590

Glu Gly Ala Thr Pro Phe His Ser Arg Thr Ser Leu Val Met Asn Gly
        595                 600                 605

Ala Leu Met Lys Pro Ser His Val Ile Val Glu Thr Met Met
    610                 615                 620
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<210> 63
<211> 1866
<212> DNA
<213> Rattus norvegicus

<400> 63

atggccacca aggagaagct tcaatgtctg aaagacttcc acaaagacat cctgaagcct 60

tctccaggga agagcccagg cacgcggcct gaggatgagg ctgatgggaa gccccctcag 120

agggagaagt ggtccagcaa gatcgacttt gtgctgtctg tggccggagg cttcgtgggt 180

ttgggcaatg tctggcgttt cccgtacctc tgctacaaaa atggtggagg tgcattcctc 240

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ataggccagt acacctcaga agggggcatc acctgctggg agaagatctg ccccttgttc 360

tctggcattg gctacgcgtc catcgtcatc gtgtccctcc tgaatgtgta ctacatcgtc 420

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gcgctctgcc tcctcttagt ctggctcgtc tgtttttttct gcatctggaa gggtgttcgg 720

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gatgtggctg agtcaggtcc tggcttggcc ttcattgcct acccaaaagc tgtgaccatg 1140

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gacagccagt ttgttgaagt cgaaggacag atcacatcct tggttgatct ttacccgtcc 1260

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ggaccctgga tgaagtacag ctgggctgtc atcactccag ctctctgtgt tggatgtttc 1560

atcttctctc tcgtcaagta tgtaccccctg acctacaaca aagtctaccg gtaccctgat 1620

tgggcaatcg ggctgggctg gggcctggcc ctttcctcca tggtgtgtat cccottggtc 1680

attgtcatcc tcctctgccg gacggaggga ccgctccgcg tgagaatcaa atacctgata 1740

acccccaggg agcccaaccg ctgggctgtg gagcgtgaag gggctacgcc ctttcactcc 1800

agagcaaccc tcatgaacgg tgcactcatg aaacccagtc acgtcattgt ggagaccatg 1860

atgtga 1866

<210> 64
<211> 621
<212> PRT
<213> Rattus norvegicus

<400> 64

Met Ala Thr Lys Glu Lys Leu Gln Cys Leu Lys Asp Phe His Lys Asp
1 5 10 15

Ile Leu Lys Pro Ser Pro Gly Lys Ser Pro Gly Thr Arg Pro Glu Asp
20 25 30

Glu Ala Asp Gly Lys Pro Pro Gln Arg Glu Lys Trp Ser Ser Lys Ile
35 40 45

Asp Phe Val Leu Ser Val Ala Gly Gly Phe Val Gly Leu Gly Asn Val
50 55 60

Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly Ala Phe Leu
65 70 75 80

Ile Pro Tyr Phe Ile Phe Leu Phe Gly Ser Gly Leu Pro Val Phe Phe
85 90 95

Leu Glu Val Ile Ile Gly Gln Tyr Thr Ser Glu Gly Gly Ile Thr Cys
100 105 110

Trp Glu Lys Ile Cys Pro Leu Phe Ser Gly Ile Gly Tyr Ala Ser Ile
115 120 125

Val Ile Val Ser Leu Leu Asn Val Tyr Tyr Ile Val Ile Leu Ala Trp
130 135 140

Ala Thr Tyr Tyr Leu Phe Gln Ser Phe Gln Lys Asp Leu Pro Trp Ala
145 150 155 160

His Cys Asn His Ser Trp Asn Thr Pro Gln Cys Met Glu Asp Thr Leu
165 170 175

Arg Arg Asn Glu Ser His Trp Val Ser Leu Ser Ala Ala Asn Phe Thr
180 185 190

Ser Pro Val Ile Glu Phe Trp Glu Arg Asn Val Leu Ser Leu Ser Ser
195 200 205

Gly Ile Asp His Pro Gly Ser Leu Lys Trp Asp Leu Ala Leu Cys Leu
210 215 220

Leu Leu Val Trp Leu Val Cys Phe Phe Cys Ile Trp Lys Gly Val Arg
225 230 235 240

Ser Thr Gly Lys Val Val Tyr Phe Thr Ala Thr Phe Pro Phe Ala Met
245 250 255

Leu Leu Val Leu Leu Val Arg Gly Leu Thr Leu Pro Gly Ala Gly Glu
260 265 270

Gly Ile Lys Phe Tyr Leu Tyr Pro Asn Ile Ser Arg Leu Glu Asp Pro
275 280 285

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Gln Val Trp Ile Asp Ala Gly Thr Gln Ile Phe Phe Ser Tyr Ala Ile
    290                 295                 300

Cys Leu Gly Ala Met Thr Ser Leu Gly Ser Tyr Asn Lys Tyr Lys Tyr
305                 310                 315                 320

Asn Ser Tyr Arg Asp Cys Met Leu Leu Gly Cys Leu Asn Ser Gly Thr
                325                 330                 335

Ser Phe Val Ser Gly Phe Ala Ile Phe Ser Ile Leu Gly Phe Met Ala
            340                 345                 350

Gln Glu Gln Gly Val Asp Ile Ala Asp Val Ala Glu Ser Gly Pro Gly
        355                 360                 365

Leu Ala Phe Ile Ala Tyr Pro Lys Ala Val Thr Met Met Pro Leu Pro
    370                 375                 380

Thr Phe Trp Ser Ile Leu Phe Phe Ile Met Leu Leu Leu Leu Gly Leu
385                 390                 395                 400

Asp Ser Gln Phe Val Glu Val Glu Gly Gln Ile Thr Ser Leu Val Asp
                405                 410                 415

Leu Tyr Pro Ser Phe Leu Arg Lys Gly Tyr Arg Arg Glu Ile Phe Ile
            420                 425                 430

Ala Ile Val Cys Ser Ile Ser Tyr Leu Leu Gly Leu Thr Met Val Thr
        435                 440                 445

Glu Gly Gly Met Tyr Val Phe Gln Leu Phe Asp Tyr Tyr Ala Ala Ser
    450                 455                 460

Gly Val Cys Leu Leu Trp Val Ala Phe Phe Glu Cys Phe Val Ile Ala
465                 470                 475                 480
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Trp Ile Tyr Gly Gly Asp Asn Leu Tyr Asp Gly Ile Glu Asp Met Ile
485 490 495

Gly Tyr Arg Pro Gly Pro Trp Met Lys Tyr Ser Trp Ala Val Ile Thr
500 505 510

Pro Ala Leu Cys Val Gly Cys Phe Ile Phe Ser Leu Val Lys Tyr Val
515 520 525

Pro Leu Thr Tyr Asn Lys Val Tyr Arg Tyr Pro Asp Trp Ala Ile Gly
530 535 540

Leu Gly Trp Gly Leu Ala Leu Ser Ser Met Val Cys Ile Pro Leu Val
545 550 555 560

Ile Val Ile Leu Leu Cys Arg Thr Glu Gly Pro Leu Arg Val Arg Ile
565 570 575

Lys Tyr Leu Ile Thr Pro Arg Glu Pro Asn Arg Trp Ala Val Glu Arg
580 585 590

Glu Gly Ala Thr Pro Phe His Ser Arg Ala Thr Leu Met Asn Gly Ala
595 600 605

Leu Met Lys Pro Ser His Val Ile Val Glu Thr Met Met
610 615 620

<210> 65
<211> 1866
<212> DNA
<213> Mus musculus

<400> 65
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tctccaggga agagcccagg cacacggcct gaagatgagg cggacgggaa gccccctcag 120

agggagaagt ggtccagcaa gatcgacttt gtgctgtctg tggccggagg cttcgtgggt 180

ttgggcaacg tctggcgttt cccgtacctc tgctacaaaa atggtggagg tgcgttcctc 240

ataccgtatt ttatttttcct gtttgggagc ggcctgcctg tgtttttctt ggaggtcatc 300

ataggccagt acacatcaga agggggcatc acctgctggg agaagatctg tcctttgttc 360

tctggcattg gctacgcatc catcgtcatt gtgtccctcc tgaacgtgta ctacatcgtc 420

atcctggcct gggccacata ctacctattc cactctttcc agaaggatct tccctgggcc 480

cactgcaacc atagctggaa cacaccacag tgcatggagg acaccctgcg taggaacgag 540

agtcactggg tctcccttag cactgccaac ttcacctcac ccgtcatcga gttctgggag 600

cgcaatgtgc tcagcctgtc ctccggaatc gacaacccag gcagtctgaa atgggacctc 660

gcgctctgcc tcctcttagt ctggctcgtc tgtttttttct gcatctggaa gggtgttcga 720

tccacaggca aggttgtcta cttcaccgct actttcccgt ttgccatgct tctggtgctg 780

ctggtccgtg gactgaccct gccaggtgct ggtgaaggca tcaaattcta cctgtaccct 840

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tcctacgcaa tctgcctggg ggccatgacc tcactgggaa gctataacaa gtacaagtat 960

aactcgtaca gggactgtat gctgctggga tgcctgaaca gtggtaccag ttttgtgtct 1020

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gatgtggctg agtcaggtcc tggcttggcc ttcattgcct acccaaaagc tgtaaccatg 1140

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gacagccagt ttgttgaagt cgaaggacag atcacatcct tggttgatct ttacccgtcc 1260

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ctgctggggc tgacgatggt gacggagggt ggcatgtatg tgtttcaact ctttgactac 1380

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tggatatatg gcggtgataa cttatatgac ggtattgagg acatgattgg ctatcggcct 1500

gggccctgga tgaagtacag ctgggctgtc atcactccag ctctttgtgt tggatgtttc 1560

gtcttctcgc ttgtcaagta tgtaccccctg acctacaaca aagtgtaccg gtacccggat 1620

tgggcaattg ggctgggctg gggcctggcc ctttcctcca tgctgtgtat ccccttggtc 1680

attgtcatcc tcctctgccg gacggaggga ccgctccgcg tgagaatcaa atacctgata 1740

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cgagtaaccc tcatgaacgg cgcactcatg aaacccagtc acgtcattgt ggagaccatg 1860

atgtga 1866

<210> 66
<211> 621
<212> PRT
<213> Mus musculus

<400> 66

Met Ala Thr Lys Glu Lys Leu Gln Cys Leu Lys Asp Phe His Lys Asp
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Ile Leu Lys Pro Ser Pro Gly Lys Ser Pro Gly Thr Arg Pro Glu Asp
20 25 30

Glu Ala Asp Gly Lys Pro Pro Gln Arg Glu Lys Trp Ser Ser Lys Ile
35 40 45

Asp Phe Val Leu Ser Val Ala Gly Gly Phe Val Gly Leu Gly Asn Val
50 55 60

Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly Ala Phe Leu
65 70 75 80

Ile Pro Tyr Phe Ile Phe Leu Phe Gly Ser Gly Leu Pro Val Phe Phe
85 90 95

Leu Glu Val Ile Ile Gly Gln Tyr Thr Ser Glu Gly Gly Ile Thr Cys
100 105 110

Trp Glu Lys Ile Cys Pro Leu Phe Ser Gly Ile Gly Tyr Ala Ser Ile

135

115 120 125

Val Ile Val Ser Leu Leu Asn Val Tyr Tyr Ile Val Ile Leu Ala Trp
130 135 140

Ala Thr Tyr Tyr Leu Phe His Ser Phe Gln Lys Asp Leu Pro Trp Ala
145 150 155 160

His Cys Asn His Ser Trp Asn Thr Pro Gln Cys Met Glu Asp Thr Leu
165 170 175

Arg Arg Asn Glu Ser His Trp Val Ser Leu Ser Thr Ala Asn Phe Thr
180 185 190

Ser Pro Val Ile Glu Phe Trp Glu Arg Asn Val Leu Ser Leu Ser Ser
195 200 205

Gly Ile Asp Asn Pro Gly Ser Leu Lys Trp Asp Leu Ala Leu Cys Leu
210 215 220

Leu Leu Val Trp Leu Val Cys Phe Phe Cys Ile Trp Lys Gly Val Arg
225 230 235 240

Ser Thr Gly Lys Val Val Tyr Phe Thr Ala Thr Phe Pro Phe Ala Met
245 250 255

Leu Leu Val Leu Leu Val Arg Gly Leu Thr Leu Pro Gly Ala Gly Glu
260 265 270

Gly Ile Lys Phe Tyr Leu Tyr Pro Asp Ile Ser Arg Leu Gly Asp Pro
275 280 285

Gln Val Trp Ile Asp Ala Gly Thr Gln Ile Phe Phe Ser Tyr Ala Ile
290 295 300

Cys Leu Gly Ala Met Thr Ser Leu Gly Ser Tyr Asn Lys Tyr Lys Tyr

305 310 315 320

Asn Ser Tyr Arg Asp Cys Met Leu Leu Gly Cys Leu Asn Ser Gly Thr
325 330 335

Ser Phe Val Ser Gly Phe Ala Ile Phe Ser Ile Leu Gly Phe Met Ala
340 345 350

Gln Glu Gln Gly Val Asp Ile Ala Asp Val Ala Glu Ser Gly Pro Gly
355 360 365

Leu Ala Phe Ile Ala Tyr Pro Lys Ala Val Thr Met Met Pro Leu Pro
370 375 380

Thr Phe Trp Ser Ile Leu Phe Phe Ile Met Leu Leu Leu Leu Gly Leu
385 390 395 400

Asp Ser Gln Phe Val Glu Val Glu Gly Gln Ile Thr Ser Leu Val Asp
405 410 415

Leu Tyr Pro Ser Phe Leu Arg Lys Gly Tyr Arg Arg Glu Ile Phe Ile
420 425 430

Ala Ile Leu Cys Ser Ile Ser Tyr Leu Leu Gly Leu Thr Met Val Thr
435 440 445

Glu Gly Gly Met Tyr Val Phe Gln Leu Phe Asp Tyr Tyr Ala Ala Ser
450 455 460

Gly Val Cys Leu Leu Trp Val Ala Phe Phe Glu Cys Phe Val Ile Ala
465 470 475 480

Trp Ile Tyr Gly Gly Asp Asn Leu Tyr Asp Gly Ile Glu Asp Met Ile
485 490 495

Gly Tyr Arg Pro Gly Pro Trp Met Lys Tyr Ser Trp Ala Val Ile Thr

500 505 510

Pro Ala Leu Cys Val Gly Cys Phe Val Phe Ser Leu Val Lys Tyr Val
515 520 525

Pro Leu Thr Tyr Asn Lys Val Tyr Arg Tyr Pro Asp Trp Ala Ile Gly
530 535 540

Leu Gly Trp Gly Leu Ala Leu Ser Ser Met Leu Cys Ile Pro Leu Val
545 550 555 560

Ile Val Ile Leu Leu Cys Arg Thr Glu Gly Pro Leu Arg Val Arg Ile
565 570 575

Lys Tyr Leu Ile Thr Pro Arg Glu Pro Asn Arg Trp Ala Val Glu Arg
580 585 590

Glu Gly Ala Thr Pro Phe His Ser Arg Val Thr Leu Met Asn Gly Ala
595 600 605

Leu Met Lys Pro Ser His Val Ile Val Glu Thr Met Met
610 615 620

<210> 67
<211> 1863
<212> DNA
<213> Homo sapiens

<400> 67
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agggagaagt ggtctagcaa gatcgacttt gtgctctctg tggctggcgg cttcgtgggc 180

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ataccgtatt ttattttcct gtttgggagc ggcctgcctg tgtttttctt ggagatcatc 300

ataggccagt acacctctga agggggcatc acctgctggg aaaagatctg ccccttgttc 360

tctggtatcg gctatgcctc cgttgtaatt gtgtcctcc tgaatgtcta ctacatcgtc 420

atcctggcct gggccacata ctacctgttc cagtccttcc agaaggagct gccctgggca 480

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atcgtcatcc gcctctgcca gactgagggg ccgttccttg tgagagtcaa gtacctgctg 1740

accccaaggg aacccaaccg ctgggctgtg gagcgcgagg gagccacacc ttacaactct 1800

cgcaccgtca tgaacggcgc tctcgtgaaa ccgacccaca tcattgtgga gaccatgatg 1860

tga 1863

<210> 68
<211> 620
<212> PRT
<213> Homo sapiens

<400> 68

Met Ala Thr Lys Glu Lys Leu Gln Cys Leu Lys Asp Phe His Lys Asp
1 5 10 15

Ile Leu Lys Pro Ser Pro Gly Lys Ser Pro Gly Thr Arg Pro Glu Asp
20 25 30

Glu Ala Glu Gly Lys Pro Pro Gln Arg Glu Lys Trp Ser Ser Lys Ile
35 40 45

Asp Phe Val Leu Ser Val Ala Gly Gly Phe Val Gly Leu Gly Asn Val
50 55 60

Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly Ala Phe Leu
65 70 75 80

Ile Pro Tyr Phe Ile Phe Leu Phe Gly Ser Gly Leu Pro Val Phe Phe
85 90 95

Leu Glu Ile Ile Ile Gly Gln Tyr Thr Ser Glu Gly Gly Ile Thr Cys
100 105 110

Trp Glu Lys Ile Cys Pro Leu Phe Ser Gly Ile Gly Tyr Ala Ser Val
115 120 125

Val Ile Val Ser Leu Leu Asn Val Tyr Tyr Ile Val Ile Leu Ala Trp
130 135 140

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Ala Thr Tyr Tyr Leu Phe Gln Ser Phe Gln Lys Glu Leu Pro Trp Ala
145                 150                 155                 160

His Cys Asn His Ser Trp Asn Thr Pro His Cys Met Glu Asp Thr Met
                165                 170                 175

Arg Lys Asn Lys Ser Val Trp Ile Thr Ile Ser Ser Thr Asn Phe Thr
            180                 185                 190

Ser Pro Val Ile Glu Phe Trp Glu Arg Asn Val Leu Ser Leu Ser Pro
        195                 200                 205

Gly Ile Asp His Pro Gly Ser Leu Lys Trp Asp Leu Ala Leu Cys Leu
    210                 215                 220

Leu Leu Val Trp Leu Val Cys Phe Phe Cys Ile Trp Lys Gly Val Arg
225                 230                 235                 240

Ser Thr Gly Lys Val Val Tyr Phe Thr Ala Thr Phe Pro Phe Ala Met
                245                 250                 255

Leu Leu Val Leu Leu Val Arg Gly Leu Thr Leu Pro Gly Ala Gly Ala
            260                 265                 270

Gly Ile Lys Phe Tyr Leu Tyr Pro Asp Ile Thr Arg Leu Glu Asp Pro
        275                 280                 285

Gln Val Trp Ile Asp Ala Gly Thr Gln Ile Phe Phe Ser Tyr Ala Ile
    290                 295                 300

Cys Leu Gly Ala Met Thr Ser Leu Gly Ser Tyr Asn Lys Tyr Lys Tyr
305                 310                 315                 320

Asn Ser Tyr Arg Asp Cys Met Leu Leu Gly Cys Leu Asn Ser Gly Thr
                325                 330                 335
```

Ser Phe Val Ser Gly Phe Ala Ile Phe Ser Ile Leu Gly Phe Met Ala
340 345 350

Gln Glu Gln Gly Val Asp Ile Ala Asp Val Ala Glu Ser Gly Pro Gly
355 360 365

Leu Ala Phe Ile Ala Tyr Pro Lys Ala Val Thr Met Met Pro Leu Pro
370 375 380

Thr Phe Trp Ser Ile Leu Phe Phe Ile Met Leu Leu Leu Leu Gly Leu
385 390 395 400

Asp Ser Gln Phe Val Glu Val Glu Gly Gln Ile Thr Ser Leu Val Asp
405 410 415

Leu Tyr Pro Ser Phe Leu Arg Lys Gly Tyr Arg Arg Glu Ile Phe Ile
420 425 430

Ala Phe Val Cys Ser Ile Ser Tyr Leu Leu Gly Leu Thr Met Val Thr
435 440 445

Glu Gly Gly Met Tyr Val Phe Gln Leu Phe Asp Tyr Tyr Ala Ala Ser
450 455 460

Gly Val Cys Leu Leu Trp Val Ala Phe Phe Glu Cys Phe Val Ile Ala
465 470 475 480

Trp Ile Tyr Gly Gly Asp Asn Leu Tyr Asp Gly Ile Glu Asp Met Ile
485 490 495

Gly Tyr Arg Pro Gly Pro Trp Met Lys Tyr Ser Trp Ala Val Ile Thr
500 505 510

Pro Val Leu Cys Val Gly Cys Phe Ile Phe Ser Leu Val Lys Tyr Val
515 520 525

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Pro Leu Thr Tyr Asn Lys Thr Tyr Val Tyr Pro Asn Trp Ala Ile Gly
    530                 535                 540

Leu Gly Trp Ser Leu Ala Leu Ser Ser Met Leu Cys Val Pro Leu Val
545                 550                 555                 560

Ile Val Ile Arg Leu Cys Gln Thr Glu Gly Pro Phe Leu Val Arg Val
                565                 570                 575

Lys Tyr Leu Leu Thr Pro Arg Glu Pro Asn Arg Trp Ala Val Glu Arg
            580                 585                 590

Glu Gly Ala Thr Pro Tyr Asn Ser Arg Thr Val Met Asn Gly Ala Leu
        595                 600                 605

Val Lys Pro Thr His Ile Ile Val Glu Thr Met Met
    610                 615                 620
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