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INOUE, E. ET AL.: 'Synaptic activity prompts γ-secretase-mediated cleavage of EphA4 and dendritic spine formation' J. CELL BIOL. vol. 185, no. 3, 04 May 2009, pages 551 - 564, XP055112350
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DESCRIPTION

TECHNICAL FIELD

[0001] The present invention relates to a screening method using gelatinase (MMP-2 or MMP-9)-mediated EphA4 cleavage reaction as an indicator.

BACKGROUND ART

[0002] Eph receptor A4 (EphA4) is a member of the receptor tyrosine kinase family and is a molecule regulating postsynaptic morphogenesis. It is known that knockout of EphA4 or expression of an EphA4 dominant-negative mutant causes a reduction in the number of spines, which are small thorn-like protrusions found on dendrites, and also makes their shape slender (Non-patent Document 1). It is generally proposed that the processes of memory and learning are reflected in the number and/or morphology of spines.

[0003] Recent studies have clarified that this EphA4 undergoes γ -secretase-mediated cleavage and the cleaved intracellular fragment activates a small GTP-binding protein, Rac, to thereby promote spine formation (Patent Documents 1 and 2, and Non-patent Document 2). Substrates of γ -secretase are first cleaved in their ectodomains by another protease and then cleaved by γ -secretase. It is known that cleavage of the EphA4 ectodomain is induced in a neuronal activity-dependent manner (Non-patent Document 2). On the other hand, in this series of cleavage processes, the first ectodomain cleavage reaction is known to be a rate-limiting step.

[0004] The MMP (matrix metalloproteinase) family, which includes enzymes cleaving off the ectodomain of EphA4, is divided into the classical MMP family and the ADAM family, and there are nearly 50 members in total. Many substrates of γ -secretase, such as Notch and APP, are known to be cleaved by ADAM protease (Non-patent Document 3). Among molecules classified as classical MMPs in the MMP family, MMP-2 and MMP-9 belonging to the gelatinase family are known to be highly expressed in the central nervous system, activated in a neuronal activity-dependent manner, and involved in spine formation (Non-patent Document 4).

[0005] However, there is no report at all of the relationship between the gelatinase family and EphA4, and it has never been clarified whether EphA4 is cleaved by gelatinase family molecules.

Prior Art Documents

Patent Documents

[0006]

Patent Document 1: WO2008/150010

Patent Document 2: WO2009/069808

Non-patent Documents

[0007]

Non-patent Document 1: Murai KK, Nguyen LN, Irie F, Yamaguchi Y, Pasquale EB. Control of hippocampal dendritic spine morphology through ephrin-A3/EphA4 signaling. *Nat Neurosci.* 2003 Feb; 6(2):153-60.

Non-patent Document 2: Inoue E, Deguchi-Tawarada M, Togawa A, Matsui C, Arita K, Katahira-Tayama S, Sato T, Yamauchi E, Oda Y, Takai Y. Synaptic activity prompts gamma-secretase-mediated cleavage of EphA4 and dendritic spine formation. *J Cell*

Biol. 2009 May 4; 185(3):551-64.

Non-patent Document 3: Landman N, Kim TW. Got RIP? Presenilin-dependent intramembrane proteolysis in growth factor receptor signaling. Cytokine Growth Factor Rev. 2004 Oct; 15(5):337-51.

Non-patent Document 4: Ethell IM, Ethell DW. Matrix metalloproteinases in brain development and remodeling: synaptic functions and targets. J Neurosci Res. 2007 Oct; 85(13):2813-23.

Non-patent Document 5: K.-T. Lin et al., "Ephrin-B2-induced cleavage of EphB2 receptor is mediated by matrix metalloproteinases to trigger cell repulsion", Journal of Biological Chemistry, vol. 283, no. 43 (2008), pp. 28969-28979.

Non-patent Document 6: Sbai O. et al., "Vesicular trafficking and secretion of matrix metalloproteinases-2, -9 and tissue inhibitor of metalloproteinases-1 in neuronal cells", Molecular and Cellular Neuroscience, 2008, vol. 39, no. 4, pages 549-568.

Non-patent document 6 discloses differential trafficking of MMP and TIMP-1-containing vesicles in neuronal cells and suggests that these vesicles could play a role in neuronal and synaptic plasticity.

SUMMARY OF THE INVENTION

PROBLEM TO BE SOLVED BY THE INVENTION

[0008] The object of the present invention is to provide a screening method using gelatinase family molecule (MMP-2, MMP-9)-mediated EphA4 cleavage reaction as an indicator.

MEANS TO SOLVE THE PROBLEM

[0009] As a result of extensive and intensive efforts made to achieve the above object, the inventors of the present invention have found that EphA4 ectodomain cleavage reaction, which is induced in hippocampal primary cultured neurons in a neuronal activity-dependent manner, is completely inhibited by a gelatinase (MMP-2, MMP-9)-selective inhibitor, mmp-2/9 Inhibitor II. Based on this finding, the inventors have further found that it is possible to screen a compound which enhances or reduces EphA4 cleavage mediated by γ -secretase or a compound which enhances or reduces spine formation mediated by the γ -secretase-processed EphA4 intracellular fragment. These findings led to the completion of the present invention.

[0010] Namely, the present invention provides an in vitro method for screening a substance that affects gelatinase-mediated EphA4 cleavage, which comprises the steps of:

1. (a) allowing a first biological composition containing gelatinase to be contacted with a second biological composition containing EphA4 in the presence and absence of a candidate substance;
2. (b) measuring the presence or amount of the EphA4 ectodomain and/or endodomain fragment; and
3. (c) selecting the candidate substance as a substance that affects gelatinase-mediated EphA4 cleavage if the results of the step (b) measured in the presence of the candidate substance are changed in comparison with the results of the step (b) measured in the absence of the candidate substance.

[0011] In the present invention, γ -secretase may further be present during the above step (a).

[0012] In the present invention, the above step (c) comprises identifying the candidate substance as a substance that promotes gelatinase-mediated EphA4 cleavage if the EphA4 endodomain and/or ectodomain fragment measured in the presence of the candidate substance during the above step (b) is increased in comparison with the EphA4 endodomain and/or ectodomain fragment measured in the absence of the candidate substance during the above step (b). In this case, the substance that stimulates gelatinase-mediated EphA4 cleavage can further be evaluated as a substance that promotes γ -secretase-mediated EphA4 cleavage reaction. Alternatively, the substance that promotes gelatinase-mediated EphA4 cleavage can further be evaluated as a substance that promotes spine formation reaction mediated by the EphA4 intracellular fragment.

[0013] On the other hand, the above step (c) comprises identifying the candidate substance as a substance that inhibits gelatinase-mediated EphA4 cleavage if the EphA4 endodomain and/or ectodomain fragment measured in the presence of the candidate substance during the above step (b) is decreased in comparison with the EphA4 endodomain and/or ectodomain fragment measured in the absence of the candidate substance during the above step (b). In this case, the substance that inhibits gelatinase-mediated EphA4 cleavage can further be evaluated as a substance that inhibits γ -secretase-mediated EphA4 cleavage reaction. Alternatively, the substance that inhibits gelatinase-mediated EphA4 cleavage can further be evaluated as a substance that inhibits spine formation reaction mediated by the EphA4 intracellular fragment.

[0014] The present invention further provides the use of gelatinase for cleaving the ectodomain of EphA4.

[0015] The present invention further provides the use of an assay kit for measurement of gelatinase-mediated EphA4 cleavage or the use of an assay kit for measurement of spine formation, which comprises a first biological composition containing gelatinase and a second biological composition containing EphA4.

[0016] The assay kits of the present invention may further comprise a biological composition containing γ -secretase.

EFFECTS OF THE INVENTION

[0017] The present invention provides a screening method using EphA4 cleavage reaction as an indicator. The present invention enables the screening of a substance that promotes or inhibits EphA4 cleavage reaction. The present invention enables the screening of a substance that enhances or reduces spine formation.

[0018] The present invention will be described in more detail below.

BRIEF DESCRIPTION OF THE DRAWINGS

[0019]

Figure 1 schematically shows cleavage processing of EphA4 and spine formation.

Figure 2 shows the results of EphA4 ectodomain cleavage reaction.

DESCRIPTION OF EMBODIMENTS

[0020] The present invention will be described in more detail below.

1. Overview

[0021] The present invention is directed to a method for screening a substance that affects gelatinase-mediated EphA4 cleavage. This method has now been completed based on the finding that gelatinase cleaves EphA4.

[0022] Figure 1 schematically shows cleavage processing of EphA4 and spine formation.

[0023] As shown in Figure 1, once neuronal activity has occurred and neurotransmitters have acted on the NMDA receptor (NMDAR), which is a glutamate receptor, MMP (matrix metalloproteinase)-mediated EphA4 cleavage reaction will be induced and the cleaved endodomain fragment (i.e., a fragment including a transmembrane domain and an intracellular domain) will further be cleaved by γ -secretase to produce an EphA4 intracellular domain (EICD). This EICD has the ability to form and stabilize spines.

[0024] Although many types of MMPs are expressed in the brain, the present invention has clarified that among these MMPs, MMP-2 or MMP-9 (collectively referred to as gelatinase) cleaves EphA4.

[0025] In view of the foregoing, a substance that promotes the activity of gelatinase is a substance that promotes a series of the following processing steps:

1. (i) promotion of gelatinase-mediated EphA4 cleavage reaction, as a result of which EphA4 is cleaved into the ectodomain fragment and the endodomain fragment (i.e., a fragment including a transmembrane domain and an EICD), followed by
2. (ii) γ -secretase-mediated cleavage of the EphA4 endodomain fragment, and
3. (iii) production of the EICD.

[0026] Thus, a substance that suppresses the activity of gelatinase can be regarded as a substance that suppresses the above processing steps.

[0027] As described above, the action of gelatinase is to cleave EphA4 into the ectodomain and endodomain fragments. The gelatinase-cleaved ectodomain fragment of EphA4 is released into the extracellular environment. Thus, when EphA4 is treated with gelatinase together with a candidate substance and the released fragments are collected and analyzed by ELISA it is possible to quantify changes in cleavage efficiency and thereby to screen a substance that affects the action of gelatinase. Likewise, the gelatinase-cleaved endodomain fragment of EphA4 allows quantification of changes in cleavage efficiency and thereby screening of a substance that affects the action of gelatinase, when the cells are collected and analyzed for fragments contained therein (including the cell membrane fraction) by ELISA. Moreover, the gelatinase-cleaved endodomain fragment of EphA4 further undergoes γ -secretase-mediated cleavage to produce an intracellular domain (EICD). Thus, when a fusion gene is prepared in advance to have a transcription factor linked to the C-terminal end of EphA4 (i.e., the end of the endodomain fragment) and is allowed to be expressed in neurons, the γ -secretase-cleaved EICD-transcription factor fusion molecule migrates into the nucleus and thereby allows enhanced expression of a reporter gene whose expression is designed to be controlled by the transcription factor. As a result, EICD production can be quantified.

[0028] Thus, when gelatinase is allowed to act on neurons in the presence of a candidate substance, it is possible to examine whether the candidate substance will affect the activity of gelatinase by measuring the presence or amount of the EphA4 ectodomain fragment or the presence or amount of the EphA4 endodomain fragment, particularly the intracellular domain EICD.

[0029] The inventors of the present invention have demonstrated, ahead of others, that EphA4 ectodomain cleavage reaction, which is induced in hippocampal primary cultured neurons in a neuronal activity-dependent manner, is completely inhibited by a gelatinase (MMP-2, MMP-9)-selective inhibitor, mmp-2/9 Inhibitor II. Moreover, the inventors have also found, ahead of others, that gelatinase-mediated cleavage reaction can be quantified by ELISA assay using an antibody specific for the EphA4 ectodomain or by Western blot assay using an antibody specific for the EphA4 endodomain fragment.

[0030] Namely, the inventors of the present invention have shown that EphA4 ectodomain cleavage reaction, which determines the efficiency of γ -secretase-mediated cleavage reaction in EphA4, is suppressed by gelatinase inhibitors. In light of this finding, the inventors have shown that a screening method based on gelatinase-mediated cleavage reaction of EphA4 is effective.

[0031] Enhancers and inhibitors of gelatinase-mediated cleavage reaction of EphA4 obtained by the screening method of the present invention are respectively involved in activation and deactivation of gelatinase, and these enhancers and inhibitors are substances (e.g., compounds) that act on EphA4 to respectively activate or deactivate the gelatinase-catalyzed enzymatic reaction.

[0032] Further, in light of the fact that EphA4 ectodomain cleavage reaction is a factor determining the efficiency of γ -secretase-mediated cleavage reaction, enhancers and inhibitors of gelatinase-mediated cleavage reaction of EphA4 can be regarded not only as substances (e.g., compounds) that respectively enhance or reduce γ -secretase-mediated EphA4 cleavage, but also as substances (e.g., compounds) that respectively enhance or reduce spine formation via the γ -secretase-processed EphA4 intracellular fragment.

2. Screening methods

[0033] As described in the section "1. Overview" above, when gelatinase is allowed to act on EphA4 in neurons in the presence of a candidate substance, it is possible to examine whether the candidate substance will affect the activity of gelatinase by measuring the presence or amount of the EphA4 ectodomain fragment or the presence or amount of the EphA4 endodomain

fragment (particularly EICD).

[0034] Thus, the present invention is directed to a method for screening a substance that affects gelatinase-mediated EphA4 cleavage, which comprises the steps of:

1. (a) allowing a first biological composition containing gelatinase
to be contacted with a second biological composition containing EphA4 in the presence and absence of a candidate substance;
2. (b) measuring the presence or amount of the EphA4 ectodomain and/or endodomain fragment; and
3. (c) selecting the candidate substance as a substance that affects gelatinase-mediated EphA4 cleavage if the results of the step (b) measured in the presence of the candidate substance are changed in comparison with the results of the step (b) measured in the absence of the candidate substance.

[0035] As used herein, the term "contact" is intended to mean that the first biological composition and the second biological composition are placed in an environment where they can be reacted with each other under given conditions, as exemplified by mixing of the second biological composition into the first biological composition, mixing of the first biological composition into the second biological composition, culturing of a mixture of these compositions, co-culturing of a transformant carrying a gelatinase-encoding gene with a transformant carrying an EphA4-encoding gene, co-expression of a gelatinase-encoding gene with an EphA4-encoding gene.

[0036] The first biological composition contains gelatinase, while the second biological composition contains EphA4. Upon contacting these two compositions with each other, EphA4 cleavage reaction will proceed by the action of gelatinase. In a case where this reaction system is a cell-free or cell-based system containing γ -secretase, when the reaction between the first biological composition and the second biological composition is allowed to proceed in the presence of a candidate substance, cleavage fragments of EphA4 are produced by the action of gelatinase and then γ -secretase-mediated cleavage reaction occurs in the EphA4 endodomain fragment to produce EICD if the candidate substance is a substance that promotes the action of gelatinase. Since gelatinase-catalyzed enzymatic reaction will proceed even in the absence of a candidate substance, when a reaction system free from the candidate substance is used as a control, the candidate substance can be evaluated as a substance that promotes the action of gelatinase if the amount of the ectodomain fragment, the endodomain fragment or both thereof is increased in comparison with the control, or alternatively, the candidate substance can be evaluated as a substance that inhibits the action of gelatinase if the amount of the ectodomain fragment, the endodomain fragment or both thereof is decreased in comparison with the control. As a result, the cleaved ectodomain fragment and/or the produced endodomain fragment (particularly EICD) can be used as an indicator to evaluate whether or not the candidate substance promotes the action of gelatinase.

[0037] Thus, in one embodiment of the method of the present invention, the candidate substance is identified as a substance that promotes gelatinase-mediated EphA4 cleavage if the EphA4 endodomain and/or ectodomain fragment measured in the presence of the candidate substance during the above step (b) is increased in comparison with that measured in the absence of the candidate substance, whereas the candidate substance is identified as a substance that inhibits gelatinase-mediated EphA4 cleavage if the EphA4 endodomain and/or ectodomain fragment measured in the presence of the candidate substance during the above step (b) is decreased in comparison with that measured in the absence of the candidate substance. Moreover, the substance that promotes gelatinase-mediated EphA4 cleavage can further be evaluated as a substance that enhances γ -secretase-mediated EphA4 cleavage reaction, whereas the substance that inhibits gelatinase-mediated EphA4 cleavage can be evaluated as a substance that inhibits γ -secretase-mediated EphA4 cleavage reaction.

[0038] Likewise, the substance that promotes gelatinase-mediated EphA4 cleavage can further be evaluated as a substance that enhances spine formation reaction mediated by the EphA4 intracellular fragment, whereas the substance that inhibits gelatinase-mediated EphA4 cleavage can be evaluated as a substance that inhibits spine formation reaction mediated by the EphA4 intracellular fragment.

[0039] The presence or amount of the cleaved ectodomain fragment and/or the endodomain fragment (particularly EICD) may be measured, e.g., by ELISA or Western blotting using antibodies against these fragments (details will be described later).

[0040] As used herein, the term "gelatinase" refers to a molecule classified as a classical MMP in the MMP family and includes MMP-2 and MMP-9. In the present invention, gelatinase may be a polypeptide of any animal origin, a recombinant polypeptide or

a synthetic polypeptide. Moreover, although gelatinase is preferably in its full-length form, a biologically active fragment (partial sequence) thereof or a mutated sequence of the full-length sequence or a partial fragment thereof may also be possible as long as it has matrix metalloproteinase activity. A mutant or biologically active fragment (e.g., partial sequence) of gelatinase may be a polypeptide substantially functionally equivalent to gelatinase, which comprises an amino acid sequence with deletion, substitution, insertion and/or addition of one or more (preferably one or several) amino acids in the full-length or partial sequence of gelatinase or with any combination of these modifications.

[0041] As described above, gelatinase or a biologically active fragment thereof has the ability to cleave off the ectodomain of EphA4 and hence is used as an ectodomain cleavage agent for EphA4.

[0042] As used herein, the term "EphA4" refers to a known polypeptide serving as a regulatory factor for synapse formation and/or maintenance (Murai KK et al., Nat Neurosci. 2003 Feb; 6(2):153-60). For example, EphA4 intended in the present invention includes human EphA4 (NM_004438.3, BC026327, NP_004429.1, BAG35298.1), rhesus monkey (*Macaca mulatta*) EphA4 (XM_001106493.1, XM_001106620, XM_001106561, XM_001106876, XM_001106943, XM_001106806, XP_001106430.1), chimpanzee (*Pan troglodytes*) EphA4 (XM_001164636.1, XM_001164828, XM_526042, XM_001164899, XM_001164862, XM_001164676), rat EphA4 (XM_244186), mouse EphA4 (NM_007936.3, BC052164, X65138, BC004782, AK132203, AAH04782.1, NP_031962.2), gray short-tailed opossum (*Monodelphis domestica*) EphA4 (XM_001365826), domestic dog (*Canis familiaris*) EphA4 (XM_536084), avian (*Gallus gallus*) EphA4 (NM_204781, CAA79509.1), *Xenopus laevis* EphA4 (NM_001085992, L26099, NM_001096714, NP_001079461.1), zebrafish (*Danio rerio*) EphA4 (NM_001005919, XM_001342436), horse (*Equus caballus*) EphA4 (XP_001494588.1), pig (*Sus scrofa*) EphA4 (NP_001128439.1), platypus (*Ornithorhynchus anatinus*) EphA4 (XP_001506050.1) and so on. Preferred is mammalian EphA4. EphA4 structurally comprises a γ -secretase cleavage site, a transmembrane domain and a kinase active site, and its ligand is among the Ephrin A family (Aoto, J et al., Brain Res. 2006 11).

[0043] In the present invention, EphA4 may be any of the above animal-derived polypeptide, recombinant polypeptide and synthetic polypeptide. In the present invention, EphA4 is preferably in its full-length form, but a partial sequence thereof or a mutated sequence thereof may also be possible as long as it comprises at least the gelatinase-mediated cleavage site and γ -secretase-mediated cleavage site of EphA4. A mutant of EphA4 may be a polypeptide substantially functionally equivalent to EphA4, which comprises an amino acid sequence with deletion, substitution, insertion and/or addition of one or more (preferably one or several) amino acids in the full-length or partial sequence of EphA4 or with any combination of these modifications. Such a "polypeptide substantially functionally equivalent to EphA4" is intended to mean a polypeptide having the activity of EphA4, such as gelatinase- or γ -secretase-dependent cleavage activity.

[0044] As used herein, the term " γ -secretase" refers to a protease formed from presenilin (presenilin 1 or 2) and three types of cofactor proteins (nicastrin, Aph-1 and Pen-2). In the present invention, each protein constituting γ -secretase may be a polypeptide of any animal origin, a recombinant polypeptide or a synthetic polypeptide. Moreover, although each protein constituting γ -secretase is preferably in its full-length form, a partial sequence thereof or a mutated sequence thereof may also be possible as long as γ -secretase has proteolytic activity. A mutant of each protein constituting γ -secretase may be a polypeptide substantially functionally equivalent to γ -secretase formed therefrom, which comprises an amino acid sequence with deletion, substitution, insertion and/or addition of one or more (preferably one or several) amino acids in the full-length or partial sequence of each constituent protein or with any combination of these modifications. Such a "polypeptide substantially functionally equivalent to γ -secretase" is intended to mean a polypeptide having the activity of γ -secretase, such as proteolytic activity to cleave proteins (e.g., EphA4 whose ectodomain is cleaved off).

[0045] Table 1 shows the correspondence between nucleotide sequence and amino acid sequence for EphA4 derived from various animals, while Table 2 shows the correspondence between nucleotide sequence and amino acid sequence for human gelatinase. Likewise, Table 3 shows the correspondence between nucleotide sequence and amino acid sequence for γ -secretase derived from various animals.

[Table 1]

Origin or Type	Accession No.	Nucleotide sequence	Amino acid sequence
Rat (<i>Rattus norvegicus</i>)	XM_244186.3	SEQ ID NO: 1	SEQ ID NO: 2
Rat EphA4-HA	XM_244186	SEQ ID NO: 3	SEQ ID NO: 4
Human (<i>Homo sapiens</i>)	NM_004438	SEQ ID NO: 5	SEQ ID NO: 6
	BC026327	SEQ ID NO: 7	SEQ ID NO: 8
	NP_004429.1	SEQ ID NO: 9	SEQ ID NO: 10

Origin or Type	Accession No.	Nucleotide sequence	Amino acid sequence
	BAG35298.1	SEQ ID NO: 11	SEQ ID NO: 12
Mouse (<i>Mus musculus</i>)	NM_007936	SEQ ID NO: 13	SEQ ID NO: 14
	BC052164	SEQ ID NO: 15	SEQ ID NO: 16
	X65138	SEQ ID NO: 17	SEQ ID NO: 18
	BC004782	SEQ ID NO: 19	SEQ ID NO: 20
	AK132203	SEQ ID NO: 21	SEQ ID NO: 22
	AAH04782.1	SEQ ID NO: 23	SEQ ID NO: 24
	NP_031962.2	SEQ ID NO: 25	SEQ ID NO: 26
Gray short-tailed opossum (<i>Monodelphis domestica</i>)	XM_001365826	SEQ ID NO: 27	SEQ ID NO: 28
Domestic dog (<i>Canis familiaris</i>)	XM_536084.2	SEQ ID NO: 29	SEQ ID NO: 30
Chimpanzee (<i>Pan troglodytes</i>)	XM_001164636	SEQ ID NO: 31	SEQ ID NO: 32
	XM_001164828	SEQ ID NO: 33	SEQ ID NO: 34
	XM_526042.2	SEQ ID NO: 35	SEQ ID NO: 36
	XM_001164899	SEQ ID NO: 37	SEQ ID NO: 38
	XM_001164862	SEQ ID NO: 39	SEQ ID NO: 40
	XM_001164676	SEQ ID NO: 41	SEQ ID NO: 42
Rhesus monkey (<i>Macaca mulatta</i>)	XM_001106493	SEQ ID NO: 43	SEQ ID NO: 44
	XM_001106620	SEQ ID NO: 45	SEQ ID NO: 46
	XM_001106561	SEQ ID NO: 47	SEQ ID NO: 48
	XM_001106876.1	SEQ ID NO: 49	SEQ ID NO: 50
	XM_001106943	SEQ ID NO: 51	SEQ ID NO: 52
	XM_001106806	SEQ ID NO: 53	SEQ ID NO: 54
	XP_001106430.1	SEQ ID NO: 55	SEQ ID NO: 56
Avian (<i>Gallus gallus</i>)	NM_204781	SEQ ID NO: 57	SEQ ID NO: 58
	CAA79509.1	SEQ ID NO: 59	SEQ ID NO: 60
<i>Xenopus laevis</i>	NM_001085992	SEQ ID NO: 61	SEQ ID NO: 62
	L26099	SEQ ID NO: 63	SEQ ID NO: 64
	NM_001096714	SEQ ID NO: 65	SEQ ID NO: 66
	NP_001079461.1	SEQ ID NO: 67	SEQ ID NO: 68
Zebrafish (<i>Danio rerio</i>)	NM_001005919	SEQ ID NO: 69	SEQ ID NO: 70
	XM_001342436	SEQ ID NO: 71	SEQ ID NO: 72
Horse (<i>Equus caballus</i>)	XP_001494588.1	SEQ ID NO: 73	SEQ ID NO: 74
Pig (<i>Sus scrofa</i>)	NP_001128439.1	SEQ ID NO: 75	SEQ ID NO: 76
Platypus (<i>Ornithorhynchus anatinus</i>)	XP_001506050.1	SEQ ID NO: 77	SEQ ID NO: 78

[Table 2]

Origin or Type	Accession No.	Nucleotide sequence	Amino acid sequence
Human MMP-2 (<i>Homo sapiens</i>)	NM_001127891	SEQ ID NO: 79	SEQ ID NO: 80
Human MMP-9 (<i>Homo sapiens</i>)	NM_004994	SEQ ID NO: 81	SEQ ID NO: 82

[Table 3]

Origin or Type	Accession No.	Nucleotide sequence	Amino acid sequence
Mouse Presenilin 1 (<i>Mus musculus</i>)	NM_008943	SEQ ID NO: 83	SEQ ID NO: 84
Rat Presenilin 1 (<i>Rattus norvegicus</i>)	D82363	SEQ ID NO: 85	SEQ ID NO: 86
Human Presenilin 1 (<i>Homo sapiens</i>)	NM_000021	SEQ ID NO: 87	SEQ ID NO: 88

Origin or Type	Accession No.	Nucleotide sequence	Amino acid sequence
Mouse Presenilin 2 (<i>Mus musculus</i>)	NM_011183	SEQ ID NO: 89	SEQ ID NO: 90
Rat Presenilin 2 (<i>Rattus norvegicus</i>)	NM_031087	SEQ ID NO: 91	SEQ ID NO: 92
Human Presenilin 2 (<i>Homo sapiens</i>)	NM_000447	SEQ ID NO: 93	SEQ ID NO: 94
Mouse Nicastrin (<i>Mus musculus</i>)	NM_021607	SEQ ID NO: 95	SEQ ID NO: 96
Rat Nicastrin (<i>Rattus norvegicus</i>)	NM_174864	SEQ ID NO: 97	SEQ ID NO: 98
Human Nicastrin (<i>Homo sapiens</i>)	NM_015331	SEQ ID NO: 99	SEQ ID NO: 100
Mouse Aph-1 (<i>Mus musculus</i>)	NM_146104	SEQ ID NO: 101	SEQ ID NO: 102
Rat Aph-1 (<i>Rattus norvegicus</i>)	NM_001014255	SEQ ID NO: 103	SEQ ID NO: 104
Human Aph-1 (<i>Homo sapiens</i>)	NM_016022	SEQ ID NO: 105	SEQ ID NO: 106
Mouse Pen-2 (<i>Mus musculus</i>)	NM_025498	SEQ ID NO: 107	SEQ ID NO: 108
Rat Pen-2 (<i>Rattus norvegicus</i>)	NM_001008764	SEQ ID NO: 109	SEQ ID NO: 110
Human Pen-2 (<i>Homo sapiens</i>)	NM_172341	SEQ ID NO: 111	SEQ ID NO: 112

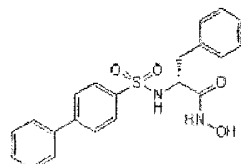
[0046] As used herein, the term "candidate substance" refers to a substance to be tested whether or not it has the ability to change the activity of gelatinase, preferably the activity of mammalian gelatinase, and such a substance may be of any type or origin. Examples include one or more substances selected from the group consisting of expression products of gene libraries, natural or synthetic small compounds (including compounds contained in libraries), nucleic acids (oligo DNAs, oligo RNAs), natural or synthetic peptides (including peptides contained in libraries), antibodies, substances released from bacteria (including substances released upon bacterial metabolism), extracts of cells (microorganisms, plant cells, animal cells), culture supernatants of cells (microorganisms, plant cells, animal cells), purified or partially purified peptides, extracts derived from various organisms (marine organisms, plants or animals), soil, and peptides contained in random phage peptide display libraries.

[0047] The above candidate substances may be either novel substances or known substances. Moreover, the above candidate substances may be modified by conventionally used chemical means, physical means and/or biochemical means. For example, they may be compounds modified to give structural analogs by being subjected to direct chemical modifications (e.g., acylation, alkylation, esterification, amidation) or random chemical modifications. The above candidate substances may also be compounds which are identified by pharmacophore search of compounds, computer-aided structure comparison programs, etc. These compounds may form salts, and the candidate compounds or salts thereof may further form solvates (including hydrates).

[0048] Further, the candidate substances may also be known gelatinase enhancers or gelatinase inhibitors involved in gelatinase processing, or structural analogs thereof. The above candidate substances may be compounds that can be designed on the basis of known compounds that promote or inhibit the activity of gelatinase through rational drug design. Examples of these compounds include NMDA, mmp-2/9 Inhibitor II

[0049] The structure of mmp-2/9 Inhibitor II (Merck) is shown below.

[Formula 1]



(2R)-[(4-Biphenyl)sulfonyl]amino-N-hydroxy-3-phenylpropionamide (BiPS)

[0050] In general, such a candidate substance may be incorporated into (e.g., added to) the reaction system at a concentration ranging from about 1 nM to 1 mM, usually about 10 μ M to 1 mM. To identify a substance that changes the EphA4 cleavage activity of gelatinase, each step described above is performed in the presence and absence of a candidate substance, and the EphA4 cleavage activity of gelatinase in the presence of the candidate substance is compared with the activity in the absence of the candidate substance, whereby a substance that changes the activity of gelatinase-mediated EphA4 cleavage is identified.

[0051] Some change in the amount or degree (presence) of EphA4 in the presence of a candidate substance is indicative of a change in the activity of gelatinase-mediated EphA4 cleavage in the presence of the candidate substance, which means that a substance serving as a modulator for gelatinase activity has been identified. For example, a substance that enhances the production of EphA4 cleavage products in comparison with its control is evaluated as an enhancer for the proteolytic activity of gelatinase. On the other hand, a substance that reduces the production of EphA4 cleavage products in comparison with its control is evaluated as an inhibitor for the proteolytic activity of gelatinase.

[0052] Gelatinase enhancers or modulators obtained by the method of the present invention have the potential to be useful for treatment of Alzheimer's disease (AD). Likewise, gelatinase inhibitors obtained by the method of the present invention have the potential to be useful for treatment of diseases associated with excessive formation of synapses, particularly spines.

[0053] As used herein, the term "ectodomain fragment" refers to an N-terminal fragment of EphA4, which will be released into the extracellular environment upon gelatinase-mediated cleavage (see Figure 1).

[0054] As used herein, the term "endodomain fragment" refers to a cleavage product of EphA4 after gelatinase-mediated cleavage, i.e., a C-terminal fragment of EphA4 except for the ectodomain fragment. The endodomain fragment includes a transmembrane domain and an intracellular domain, and it serves as a substrate of γ -secretase. A subfragment produced from the endodomain fragment upon γ -secretase-mediated cleavage is referred to as an EphA4 intracellular domain (EICD). Thus, EICD is a concept falling within the "endodomain fragment."

[0055] As used herein, the term "substitution" is preferably intended to mean conservative substitution, in which one or more (preferably one or several) amino acid residues are replaced with other chemically similar amino acid residues such that the activity of the resulting polypeptide is not substantially altered. Examples include cases where one hydrophobic residue is replaced with another hydrophobic residue and where one polar residue is replaced with another polar residue having the same charge. For each amino acid, its functionally similar amino acids allowing such substitution are known in the art. More specifically, examples of non-polar (hydrophobic) amino acids include alanine, valine, isoleucine, leucine, proline, tryptophan, phenylalanine, methionine and so on. Examples of polar (neutral) amino acids include glycine, serine, threonine, tyrosine, glutamine, asparagine, cysteine and so on. Examples of positively-charged (basic) amino acids include arginine, histidine, lysine and so on. Likewise, examples of negatively-charged (acidic) amino acids include aspartic acid, glutamic acid.

[0056] The number of amino acids which may be deleted, substituted, inserted and/or added as described above is, e.g., 1 to 30, preferably 1 to 20, more preferably 1 to 10, even more preferably 1 to 5, and particularly preferably 1 or 2.

[0057] Mutated amino acid sequences of the individual proteins constituting the above gelatinase, EphA4 and γ -secretase include amino acid sequences sharing a homology of preferably 80% or more, more preferably 85% or more, even more preferably 90% or more, still even more preferably 95% or more, particularly preferably 98% or more, and most preferably 99% or more with the amino acid sequences of their respective wild-type polypeptides. Polypeptides comprising amino acid sequences each having the above homology fall within mutated polypeptides to be used in the present invention, as long as they have substantially the same activity as EphA4 (e.g., the ability to cause a morphological change in postsynapses, particularly to cause an Ephrin A-dependent morphological change), substantially the same activity as gelatinase (e.g., the ability to cause cleavage of EphA4) or substantially the same activity as γ -secretase (e.g., the ability to cause cleavage of the EphA4 endodomain fragment). These polypeptides may be any of the above animal-derived polypeptides, recombinant polypeptides and synthetic polypeptides.

[0058] The above identity may be a numerical value calculated using any homology search program known to those skilled in the art, for example, may be calculated using default (initial setting) parameters in the homology algorithm BLAST (Basic Local Alignment Search Tool) program of the National Center for Biotechnology Information (NCBI), available at <http://www.ncbi.nlm.nih.gov/BLAST/>.

[0059] In the present invention, gelatinase to be used, EphA4 to be analyzed, and γ -secretase to be optionally used may be in the form of fusion polypeptides fused with other polypeptides, as exemplified by tagged or labeled polypeptides or otherwise modified polypeptides. These polypeptides may be obtained by gene recombination techniques, site-directed mutagenesis, treatment with mutagens (e.g., hydroxylamine), or automated peptide synthesis.

[0060] EphA4 derivatives each carrying at least gelatinase- and γ -secretase-mediated cleavage sites can all be used in the present invention. These polypeptides are particularly useful in detection and/or purification of EphA4.

[0061] As used herein, the term "biological composition" refers to any composition containing gelatinase or EphA4, as exemplified by a cell-free reconstituted system, an expression product obtained by genetic engineering procedures, a mammal or a part thereof, or a transgenic non-human mammal or a part thereof engineered to overexpress gelatinase or EphA4. The biological composition intended in the present invention may also be a composition containing γ -secretase.

[0062] In the context of the present invention, gelatinase and/or EphA4 may be either endogenous or exogenous. In the case of endogenous gelatinase and/or EphA4, any composition is possible as long as it contains gelatinase or EphA4 derived from a part of the above animal. A part of the above animal used for this purpose may be, for example, a tissue, cell, cell membrane fraction or purified membrane derived from the above animal. Examples of such a cell include cells in the central nervous system, neuronal cells (e.g., brain-derived neurons, cerebral cortex-derived neurons, cerebral cortex-derived primary cultured neurons, hippocampus-derived primary cultured neurons), glia cells.

[0063] Moreover, in these cells, gelatinase and/or EphA4 may be in the state of being contained in a mammal or a part thereof or may be the gelatinase or EphA4 fraction of a cell lysate prepared from the mammal. Such a cell lysate may be prepared from gelatinase- or EphA4-containing cells, e.g., by lysis with a hypotonic solution or a surfactant or by ultrasonic or physical homogenization, optionally followed by treatment with a purification means such as a column. In the case of exogenous gelatinase and/or EphA4, the intended composition may be gelatinase-expressing cells or EphA4-expressing cells obtained when the whole or a part of an expression vector carrying a gelatinase-encoding polynucleotide or an EphA4-encoding polynucleotide is used and expressed in host cells, or alternatively, may be the gelatinase fraction of a cell lysate derived from gelatinase-expressing cells or the gelatinase fraction of a cell lysate derived from EphA4-expressing cells. Such a cell lysate may be prepared from gelatinase- or EphA4-containing cells, e.g., by lysis with a hypotonic solution or a surfactant or by ultrasonic or physical homogenization, optionally followed by treatment with a purification means such as a column. The expression vectors used for this purpose may be those which are to be transformed or transfected into host cells to cause transient gene expression, or may be those which are to be integrated into the genome of host cells to ensure stable gene expression.

[0064] As used herein, the term "transformation" or "transfection" is intended to mean any technique which changes the DNA content of eukaryotic cells. Examples include calcium phosphate transfection, protoplast fusion transfection, electroporation transfection, DEAE-dextran transfection, liposome transfection, polybrene transfection, direct microinjection transfection (Sambrook, et al., Molecular Cloning 3:16.30-16.31 (1989)).

[0065] Expression vectors used for the above transformation or transfection are not limited in any way as long as they carry a gelatinase-encoding polynucleotide or an EphA4-encoding polynucleotide, and examples include plasmids which are obtained by inserting these polynucleotides into known expression vectors selected as appropriate depending on the type of host cell to be used. For example, promoters may be used in mammalian cells for the purpose of giving strong transcriptional activity, as exemplified by CMV immediate early promoter, retrovirus promoters (e.g., LTR from MLV or MMTV), SV40, RSV LTR, HIV-1 LTR and HIV-2 LTR promoters, adenovirus promoters (e.g., those from the E1A, E2A and MLP regions), as well as AAV LTR, cauliflower mosaic virus, HSV-TK and avian sarcoma virus promoters.

[0066] The thus transformed or transfected host cells are also not limited in any way as long as they contain a gelatinase-encoding polynucleotide or an EphA4-encoding polynucleotide. For example, they may be transformants which have the polynucleotides integrated into the chromosomes of the host cells, may be transformants which contain plasmids carrying the polynucleotides, or may be transformants which are not expressing gelatinase or EphA4. These transformants may be obtained upon transformation of desired host cells with the above plasmids or with the above polynucleotides per se.

[0067] Host cells to be transformed or transfected with the above expression vectors may be cells or cell lines capable of gene expression, as exemplified by known cultured cells. Examples include mammalian cells or cell lines, such as HEK293 cells, Chinese hamster ovary (CHO) cells, fibroblasts, primary endothelial cells (HUVEC cells), human glioma cells, Hela cells, COS cells, PC12 cells, lymphoblasts, melanoma cells, hybridoma cells, oocytes and embryonic stem cells; known microorganisms such as *E. coli* and yeast; as well as insect cells (e.g., BmN4 cells). Any of the above cells may be used as long as it is expressing at least one of gelatinase and EphA4, which may be either endogenous or exogenous.

[0068] Examples of the above expression vectors include pUC, pTV, pGEX, pKK or pTrcHis for *E. coli*, pEMBL or pYES2 for yeast, pcDNA3, pMAMneo or pBabe Puro for animal cells (CHO cells, HEK293 cells and COS cells), as well as vectors (e.g., pBK283) carrying the polyhedrin promoter of *Bombyx mori* nuclear polyhedrosis virus (BmNPV) for insect cells (BmN4 cells).

[0069] Although the above gelatinase- and/or EphA4-containing cells are not limited in any way, for example, gelatinase- and EphA4-expressing cells in which one of gelatinase and EphA4 is endogenous and the other is exogenous, or cells which express both exogenous gelatinase and exogenous EphA4 may also be obtained by being cultured under conditions allowing expression

of gelatinase and/or EphA4.

[0070] Alternatively, appropriate cells may be injected with gelatinase-encoding RNA and/or EphA4-encoding RNA and cultured under conditions allowing expression of gelatinase and/or EphA4 to thereby obtain desired cells.

[0071] The above cell membrane fraction may be obtained, e.g., by homogenizing the gelatinase- or EphA4-expressing cells of the present invention and then separating a fraction rich in cell membranes. Techniques for cell homogenization include, for example, cell crushing with a homogenizer, homogenization with a Waring blender or a Polytron, ultrasonic homogenization, or ejection of cells through a narrow nozzle under pressure with a French press. Likewise, techniques for cell membrane fractionation include, for example, centrifugal fractionation, such as differential centrifugation or density gradient centrifugation.

[0072] To purify the cell membrane fraction, known protein purification techniques can be used. These techniques comprise, as one of their steps, rough fractionation of cells into the polypeptide fraction and the non-polypeptide fraction. Once gelatinase or EphA4 has been separated from the other polypeptides, the desired gelatinase or EphA4 will be further purified by using chromatographic or electrophoretic techniques to ensure partial purification or complete purification (or to ensure a uniform state through purification).

[0073] Analysis techniques particularly suitable for preparation and purification of pure peptides include, for example, precipitation with ammonium sulfate, PEG, antibody and so on, or centrifugation following thermal denaturation. Moreover, it is also possible to use various chromatographic steps such as ion exchange chromatography, gel filtration chromatography, reversed-phase chromatography, hydroxylapatite chromatography, affinity chromatography, fast protein liquid chromatography (FPLC), high performance liquid chromatography (HPLC) or immobilized metal affinity chromatography (IMAC), as well as isoelectric focusing, gel electrophoresis, SDS (sodium dodecyl sulfate)-polyacrylamide gel electrophoresis (SDS-PAGE) which may be used either alone or in combination, as appropriate. In addition to these techniques, other techniques may also be used in combination.

[0074] Alternatively, purification may be accomplished as follows: gelatinase or EphA4 is tagged in advance and passed through a purification column, to which a protein recognizing this tag has been attached, whereby the desired gelatinase or EphA4 is adsorbed within the column, followed by passing an appropriate elution solvent through the column to desorb the gelatinase or EphA4. Various purification steps may be performed in different orders, or some of the steps may be skipped. One of the techniques preferred for evaluation of the fraction purity is as follows: the specific activity of a fraction is calculated and then compared with the specific activity of the original extract, whereby the level of purity is calculated for evaluation.

[0075] In the present invention, it is also possible to use γ -secretase or a biological composition containing γ -secretase, which is prepared in the same manner as described above for gelatinase or EphA4.

[0076] As used herein, the phrase "substance that affects gelatinase-mediated EphA4 cleavage" is intended to mean either a substance that inhibits the activity of gelatinase-mediated EphA4 cleavage (i.e., a gelatinase inhibitor) or a substance that promotes the activity of gelatinase-mediated EphA4 cleavage (i.e., a gelatinase enhancer). In the context of the present invention, the gelatinase inhibitor includes an antagonist, and the gelatinase enhancer includes an agonist. The gelatinase inhibitor and gelatinase enhancer also include substances that change the site for gelatinase-mediated EphA4 cleavage to produce EphA4 cleavage products having different peptide lengths.

[0077] The method of the present invention can be performed in an appropriate cell-based or cell-free system containing gelatinase and EphA4. In a cell-based system containing gelatinase and EphA4, cells to be used may be either endogenous gene-expressing cells or exogenous gene-containing cells. In the presence and absence of a candidate substance, cells containing gelatinase and EphA4 may be cultured in an appropriate medium and incubated under reaction conditions which allow EphA4 cleavage reaction through gelatinase activity. In the present invention, glutamate receptors present in the reaction system may be activated by neurotransmitters such as NMDA during contact.

[0078] In the case of an exogenous gene-containing cell-based system, the method of the present invention can be performed under culture conditions which allow expression of the gene. In an endogenous gene-expressing cell-based system, primary cultured neurons may be cultured, for example, under culture conditions of 5% CO₂ and 37°C in MEM (Invitrogen) medium supplemented with 5% FBS (Hyclone), 1 × B27 supplement (Invitrogen), 0.5 mM L-glutamine (Invitrogen), 25 µg/ml insulin (SIGMA) and 8 µM AraC (SIGMA). In an exogenous gene-containing system, HEK293 cell line may be cultured, for example, under culture conditions of 5% CO₂ and 37°C in 10% FBS (Hyclone)/DMEM (Invitrogen). In a cell-free system, a first biological composition containing gelatinase or a biologically active fragment thereof (e.g., a cell membrane fraction containing gelatinase)

and a second biological composition containing EphA4 (e.g., a cell membrane fraction containing EphA4) are incubated by being mixed together in the presence and absence of a candidate compound. These compositions may be mixed under reaction conditions which allow EphA4 cleavage reaction through gelatinase activity. Gelatinase or EphA4 may be the purified gelatinase or EphA4, or a biologically active fragment thereof, an analog thereof, or a mutant thereof.

[0079] For analysis of EphA4 cleavage, a parameter indicative of cleavage is measured for either or both of the N-terminal and C-terminal fragments of EphA4. To monitor gelatinase-mediated EphA4 cleavage or the subsequent γ -secretase-mediated endodomain cleavage, it is possible to use an anti-EphA4 antibody, such as an antibody capable of recognizing a fragment generated as a result of EphA4 cleavage, preferably an antibody capable of recognizing a fragment of the EphA4 ectodomain or an antibody capable of recognizing a fragment of the EphA4 endodomain, more preferably an antibody capable of recognizing a C-terminal region fragment (particularly EICD) of EphA4. For detection of tagged polypeptide cleavage products of EphA4, it is possible to use an antibody capable of recognizing the selected tag. For example, when an HA tag is attached to the C-terminal end of EphA4, an anti-HA tag antibody may be used for detection. In this case, it is possible to clarify the presence and concentration of the C-terminal end of EphA4 which is generated as a result of EphA4 cleavage.

[0080] Systems particularly useful as tagged polypeptides include the hemagglutinin (HA) system, the glutathione-S-transferase (GST) system, the maltose-binding protein system, the 6 $\times$ histidine system, the 8 $\times$ histidine system.

[0081] When EphA4 or tagged EphA4 is labeled, the quenched state of the label may be detected.

[0082] Alternatively, in the present invention, it is also possible to use an assay system designed such that a fusion gene is prepared to have a transcription factor linked to the C-terminal end of EphA4 and this fusion gene is allowed to be expressed in cells to thereby cause γ -secretase-mediated cleavage reaction. In this case, when γ -secretase acts on the EphA4 endodomain, the EICD-transcription factor fusion molecule migrates into the nucleus and thereby allows enhanced expression of a reporter gene. As a result, EICD production can be quantified.

[0083] In the present invention, examples of the above transcription factor include yeast GAL4, heat shock factors, hypoxia inducing factors and so on. Once the EICD-transcription factor fusion molecule has migrated into the nucleus, the transcription factor moiety will act on the response sequence for the transcription factor located upstream of the reporter gene, thereby resulting in enhanced expression of the reporter gene.

[0084] In the present invention, examples of such a reporter gene include genes for luciferase, heat stable alkaline phosphatase, GFP (green fluorescent protein) and so on. The expression levels of these reporter genes may be measured using a detector for fluorescence, luminescence, depending on the nature of each reporter gene.

[0085] Examples of the above label include biotin labels, radioactive labels, fluorescent labels, chemiluminescent labels and so on. Moreover, modifications may also be made to integrate any detectable moiety in addition to the label. In the present invention, EphA4 in each embodiment may be provided with one or two or more of these labels or modifications.

[0086] EphA4 in a preferred embodiment of the present invention is rat EphA4, for example, a polypeptide comprising the amino acid sequence shown in SEQ ID NO: 2. EphA4 in a more preferred embodiment of the present invention is an HA-tagged polypeptide of rat EphA4. For example, it is a polypeptide (SEQ ID NO: 4) further having an HA tag attached to the C-terminal end of rat EphA4. Of course, the whole or a part of the human EphA4 sequence, e.g., the amino acid sequence of SEQ ID NO: 6, 8, 10 or 12 may also be used as in the case of rat EphA4.

[0087] The present invention further provides a polynucleotide comprising a nucleotide sequence encoding EphA4 as described above. An example of such a polynucleotide encoding EphA4 is a polynucleotide encoding rat EphA4, for example, the polynucleotide of SEQ ID NO: 1. A polynucleotide encoding EphA4 in a more preferred embodiment of the present invention is a polynucleotide encoding an HA-tagged polypeptide of rat EphA4. For example, it is a polynucleotide (SEQ ID NO: 3) encoding a polypeptide further having an HA tag attached to the C-terminal end of rat EphA4. Of course, the whole or a part of the human EphA4 sequence, e.g., the nucleotide sequence of SEQ ID NO: 5, 7, 9 or 11 may also be used as in the case of rat EphA4.

[0088] Although the antibody against EphA4 is not limited in any way as long as it is an antibody capable of recognizing EphA4, preferred is an antibody capable of recognizing the EphA4 endodomain. For example, it is possible to use antibodies described in Tremblay et al., J. Comp. Neurol 501 691-702 or commercially available anti-rat EphA4 antibodies (Upstate, Zymed, Santacruz). Alternatively, those skilled in the art would be able to prepare such an antibody by immunization with an immunogen (antigen) in accordance with existing standard procedures for monoclonal antibody preparation. For example, the antigen is immunized into a non-human mammal, optionally together with Freund's adjuvant. Polyclonal antibodies can be obtained from the serum taken from

the immunized animal. On the other hand, monoclonal antibodies are prepared as follows: antibody-producing cells obtained from the immunized animal and myeloma cells having no ability to produce autoantibodies are used to prepare fused cells (hybridomas), and these hybridomas are cloned and screened to select clones which produce monoclonal antibodies having specific affinity to the antigen used for immunization of the mammal. Production of monoclonal antibodies from hybridomas may be accomplished by culturing the hybridomas *in vitro* or *in vivo* (e.g., in the peritoneal fluid of non-human mammals, preferably mice or rats, more preferably mice) and then isolating monoclonal antibodies from the resulting culture supernatant or the peritoneal fluid of the mammals. For isolation and purification of monoclonal antibodies, the above culture supernatant or peritoneal fluid may be subjected to saturated ammonium sulfate, euglobulin precipitation, caproic acid method, caprylic acid method, ion exchange chromatography (e.g., DEAE or DE52), affinity column chromatography on an anti-immunoglobulin column or a Protein A column, etc. These monoclonal antibodies also encompass those consisting of heavy chains and/or light chains having amino acid sequences with deletion, substitution or addition of one or several amino acids in the amino acid sequences of the heavy chains and/or light chains constituting the above antibodies.

[0089] The method of the present invention allows evaluation of a substance that affects gelatinase-mediated EphA4 cleavage by incubating gelatinase and EphA4 in the presence or absence of a candidate substance and using the number of spines in spine-forming cells as an indicator.

[0090] Namely, the method of the present invention may be accomplished in a cell-based system which allows observation of the processes occurring after contact between gelatinase and EphA4, i.e., gelatinase-mediated cleavage of the EphA4 ectodomain, the subsequent γ -secretase-mediated cleavage of the EphA4 endodomain, production of EICD, and spine formation through intracellular signaling. In this case, an "appropriate cell-based system containing gelatinase and EphA4" and spine-forming cells may be composed of either different or the same cells. The term "spine-forming cells" is intended to mean cells capable of spine formation, and examples include neurons with excitatory synapses in the central nervous system, etc.

[0091] As used herein, the term "spine" refers to a microstructure constituting a chemical synapse, i.e., a thorn-like protrusion (dendritic spine) formed on postsynaptic dendrites (see Hering et al., Nat Rev Neurosci. 2001 Dec; 2(12):880-8). In general, there are two types of synapses (i.e., dendritic filopodia and dendritic spines) in the mature brain, and it is proposed that spines are involved in the processes of memory and learning because of transition from dendritic filopodia to dendritic spines during memory and learning.

[0092] Examples of a preferred cell-based system in this embodiment include primary cultured neurons, cultured cells derived from brain slices, etc. To obtain these cell-based systems, reference may be made to the Example section described later for primary cultured neurons, while cultured cells derived from brain slices may be obtained as follows for the case of hippocampus, by way of example.

[0093] The whole brain is taken from a rat at 8 to 9 days of age after birth and introduced into a beaker containing GBSS solution (HBSS (SIGMA)/MEM (Invitrogen)/horse serum (SIGMA) = 1:2:1), followed by cooling the whole brain for about one minute. After cooling, the whole brain is collected from the beaker and mounted on a stage. The cerebellum and the rostral half of the cerebrum are cut off, and the remainder is then fixed on the stage with an adhesive. The hippocampus is sliced from the fixed tissue graft. The resulting sections (300 to 400 μ m) are each placed on a membrane on a well prepared in advance. The primary cultured cells cultured on the membrane may also be used (see Stoppini, L., Buchs, P.-A. and Muller, D. J. Neurosci. Methods. 37 (1991) 173-182, Gahwiler, B. H. Trends Neurosci. 11 (1988) 484-489, Sakaguti, T., Okada, M. and Kawasaki, K. Neurosci. Res. 20 (1994) 157-164).

[0094] Spines to be measured in the present invention are spines on synapses, preferably spines on synapses at the stage of dendritic filopodia or dendritic spines. Such synapses at the stage of dendritic filopodia or dendritic spines are synapses whose morphology is actually observed during memory or learning. Upon measuring spines on these synapses, it is possible to measure spines on synapses in the state of *functioning in vivo* or on synapses at the stage just before functioning.

[0095] For measurement of the number of spines, spines can be detected by using an antibody capable of recognizing a molecule expressed specifically in spines or an antibody capable of recognizing a tagged polypeptide of a molecule expressed specifically in spines, or by using spine-forming cells in which the cells per se are labeled.

[0096] In the case of using spine-forming cells in which the cells per se are labeled, spine detection is accomplished by searching for thorn-like protrusions on the spine-forming cells under a microscope capable of detecting the label. An example of a label used for this purpose is EGFP.

[0097] In the case of using an antibody capable of recognizing a molecule expressed specifically in spines, examples of such an antibody capable of recognizing a molecule expressed specifically in spines include anti-PSD-95 (Postsynaptic Density-95) antibody, anti-Glutamate Receptor 1 antibody, anti-Actin antibody, anti-Homer antibody, anti-Shank antibody.

[0098] Moreover, in the case of detecting a tagged version of a molecule expressed specifically in spines, an antibody against the selected tag may be used. When PSD-95 is selected as a molecule expressed specifically in spines and an EGFP tag is attached to the C-terminal end of PSD-95, an anti-EGFP tag antibody may be used for detection. In this case, it is possible to clarify the presence and concentration of the C-terminal end of PSD-95.

[0099] To identify a substance that changes the activity of gelatinase-mediated EphA4 cleavage, each step described above is performed in the presence and absence of a candidate substance, and the spine formation activity in the presence of the candidate substance is compared with the activity in the absence of the candidate substance, whereby a substance that changes the activity of gelatinase-mediated EphA4 cleavage is identified.

[0100] Some change in the number of spines in the presence of a candidate substance is indicative of a change in the activity of gelatinase-mediated EphA4 cleavage in the presence of the candidate substance, which means that a substance serving as a modulator for gelatinase activity has been identified. For example, a compound that increases the number of spines in comparison with its control is evaluated as a modulator for the proteolytic activity of gelatinase or as an enhancer for the proteolytic activity of gelatinase. On the other hand, a compound that reduces the number of spines in comparison with its control is evaluated as an inhibitor for the proteolytic activity of gelatinase.

[0101] The present invention also comprises a method for evaluating the morphology of postsynapses or the function of neurotransmission using a substance which has been identified as a result of screening. For example, evaluation of the morphology of postsynapses described above may be accomplished by a method for evaluating the number and/or morphology of spines (Pak D et al. Neuron 2001 31. 289-303). Likewise, evaluation of neurotransmission function may be accomplished, for example, by a method for evaluating an electrical change caused on the synaptic membrane using cultured cells or cultured slices (Saura et al., Neuron 2004 42 23-36).

[0102] The method of the present invention also comprises any high-throughput screening (HTS) method known to those skilled in the art, in which many candidate substances are tested at the same time (US5876946, US5902732, Jayawickreme and Kost, Curr. Opin. Biotechnol., 8, pp. 629-634, 1997, Houston and Banks, Curr. Opin. Biotechnol., 8, pp. 734-740, 1997).

[0103] The method of the present invention also comprises the use of known animal models. Compounds selected by the *in vitro* method of the present invention may be analyzed for their *in vivo* effects, e.g., by using a non-human model of EphA4 cleavage. For example, when transgenic mice modified to have the EphA4 gene are administered with a known gelatinase inhibitor, mmp-2/9 Inhibitor II, or with a compound selected by the method of the present invention, analysis may be conducted by evaluation of A β levels in their brain, cerebrospinal fluid and serum (J. Pharmacol. Exp. Ther. 305, 864-871, 2003), by pathological examination of changes in their brain (e.g., changes in A β production, the degree of brain atrophy) arising from changes in their γ -secretase activity, or by evaluation of their survival rate, the amount of their exercise or the amount of their food consumption.

[0104] Moreover, the method of the present invention also provides a method for secondary evaluation (screening) of whether or not a test compound affects spine formation by means of a method for evaluating the morphology of postsynapses or the function of neurotransmission. This method may be accomplished in an appropriate cell-based system.

3. Therapeutic compositions comprising substances obtained by the method of the present invention

[0105] A substance that promotes the activity of gelatinase-mediated EphA4 cleavage, a salt thereof or a solvate thereof, which is obtainable by the method of the present invention, promotes EICD production, and the EICD in turn promotes spine formation. Thus, the above substance, a salt thereof or a solvate thereof can be expected as an improver for cognitive functions and has the potential to be useful for treatment of, e.g., dementia, particularly AD.

[0106] On the other hand, for treatment of diseases associated with excessive formation of synapses, particularly excessive formation of spines, a substance that inhibits the activity of gelatinase-mediated EphA4 cleavage, a salt thereof or a solvate thereof would be useful.

[0107] As used herein, the term "treatment" is generally intended to mean achieving a desired pharmacological effect and/or a

desired physiological effect. For example, in the case of AD, a reduction or amelioration of clinical symptoms or pathological signs is indicative of treatment success.

[0108] In the context of the present invention, clinical symptoms of Alzheimer's disease (AD) include progressive disorientation, memory loss and aphasia, eventually leading to disablement, language attrition and akinesia. Pathological signs of AD include, for example, the occurrence of neurofibrillary degeneration, senile plaques and amyloid angiopathy.

[0109] Diagnosis of AD in patients may be accomplished by using various known methods. Typically, clinical and pathological evaluations are used in combination for AD diagnosis. For example, the progress or severity of AD may be determined by using Mini Mental State Examination (MMSE) (Mohs et al., (1996) *Int Psychogeriatr* 8:195-203), Alzheimer's Disease Assessment Scale-Cognitive Subscale (ADAS-cog) (Galasko et al., (1997) *Alzheimer Dis Assoc Disord*, 11 suppl 2:S33-9), Alzheimer's Disease Cooperative Study-Activities of Daily Living (ADCS-ADL) (McKhann et al., (1984) *Neurology* 34:939-944), criteria of the National Institute of Neurologic Communicative Disorders and the Stroke-Alzheimer's Disease and Related Disorders Association (NINCDS-ADRDA) (Folstein et al., (1975) *J Psychiatr Res* 12:189-198, McKhann et al., (1984) *Neurology* 34:939-944). Further, it is also possible to use any methods which allow estimation of the frequency of senile plaques and/or neurofibrillary degeneration based on evaluation of various regions in the brain (Braak et al., (1991) *Acta Neuropathol* 82:239-259; Khachaturian (1985) *Arch Neuro* 42:1097-1105; Mirra et al., (1991) *Neurology* 41:479-486; and Mirra et al., (1993) *Arch Pathol Lab Med* 117:132-144).

[0110] As used herein, the term "salt" refers to a pharmaceutically acceptable salt, and there is no particular limitation as long as pharmaceutically acceptable salts are formed with the above substances (e.g., compounds). More specifically, examples include halogenated hydroacid salts (e.g., hydrofluoride salt, hydrochloride salt, hydrobromide salt, hydroiodide salt), inorganic acid salts (e.g., sulfate salt, nitrate salt, perchlorate salt, phosphate salt, carbonate salt, bicarbonate salt), organic carboxylic acid salts (e.g., acetate salt, oxalate salt, maleate salt, tartrate salt, fumarate salt, citrate salt), organic sulfonic acid salts (e.g., methanesulfonate salt, trifluoromethanesulfonate salt, ethanesulfonate salt, benzenesulfonate salt, toluenesulfonate salt, camphorsulfonate salt), amino acid salts (e.g., aspartate salt, glutamate salt), quaternary amine salts, alkali metal salts (e.g., lithium salt, sodium salt, potassium salt), alkaline earth metal salts (e.g., magnesium salt, calcium salt).

[0111] A pharmaceutical composition, preferably a therapeutic agent for AD according to the present invention, which comprises a substance (e.g., compound) identified by the method of the present invention may be administered to patients in various modes by either oral route or parenteral route (e.g., intravenous injection, intramuscular injection, subcutaneous administration, intrarectal administration, percutaneous administration). Thus, such a pharmaceutical composition comprising the substance (e.g., compound) of the present invention can be formulated into an appropriate dosage form using a pharmaceutically acceptable carrier in accordance with conventionally used procedures depending on the route of administration, although it can be used alone.

[0112] Preferred dosage forms include, for example, tablets, powders, fine granules, granules, coated tablets, capsules, syrups and troches for oral formulations, as well as inhalants, suppositories, injections (including drops), ointments, eye drops, ophthalmic ointments, nose drops, ear drops, cataplasms, lotions and liposomes for parenteral formulations.

[0113] Examples of carriers for use in these formulations include commonly used excipients, binders, disintegrants, lubricants, coloring agents, correctives and, if necessary, stabilizers, emulsifiers, absorbefacients, surfactants, pH adjustors, antiseptics, antioxidants, extenders, humectants, surface active agents, dispersants, buffering agents, preservatives, solubilizers, soothing agents. In general, ingredients commonly used as source materials of pharmaceutical preparations may be blended and formulated in a routine manner. Examples of such non-toxic ingredients available for use include animal and vegetable oils (e.g., soybean oil, beef tallow, synthetic glycerides); hydrocarbons (e.g., liquid paraffin, squalane, hard paraffin); ester oils (e.g., octyldodecyl myristate, isopropyl myristate); higher alcohols (e.g., cetostearyl alcohol, behenyl alcohol); silicone resins; silicone oils; surfactants (e.g., polyoxyethylene fatty acid ester, sorbitan fatty acid ester, glycerine fatty acid ester, polyoxyethylene sorbitan fatty acid ester, polyoxyethylene hydrogenated castor oil, polyoxyethylene-polyoxypropylene block copolymer); water-soluble polymers (e.g., hydroxyethylcellulose, polyacrylate, carboxyvinyl polymer, polyethylene glycol, polyvinylpyrrolidone, methylcellulose); lower alcohols (e.g., ethanol, isopropanol); polyhydric alcohols (polyols) (e.g., glycerine, propylene glycol, dipropylene glycol, sorbitol, polyethylene glycol); saccharides (e.g., glucose, sucrose); inorganic powders (e.g., silicic anhydride, magnesium aluminum silicate, aluminum silicate); inorganic salts (e.g., sodium chloride, sodium phosphate); purified water.

[0114] Examples of excipients available for use include lactose, fructose, corn starch, sucrose, glucose, mannitol, sorbit, crystalline cellulose, silicon dioxide and so on. Examples of binders available for use include polyvinyl alcohol, polyvinyl ether, methylcellulose, ethylcellulose, gum arabic, tragacanth, gelatin, shellac, hydroxypropylmethylcellulose, hydroxypropylcellulose, polyvinylpyrrolidone, polypropylene glycol-polyoxyethylene block polymer, meglumine. Examples of disintegrants available for use include starch, agar, gelatin powder, crystalline cellulose, calcium carbonate, sodium bicarbonate, calcium citrate, dextrin, pectin,

carboxymethylcellulose calcium. Examples of lubricants available for use include magnesium stearate, talc, polyethylene glycol, silica, hydrogenated vegetable oils. Examples of coloring agents available for use include those which are approved to be added to pharmaceutical preparations. Examples of correctives available for use include cocoa powder, menthol, aromatic powder, peppermint oil, borneol, cinnamon powder. The above ingredients may be in the form of their salts or solvates thereof.

[0115] For example, oral formulations may be prepared as follows: the substance (e.g., compound) of the present invention is blended with an excipient and optionally with a binder, a disintegrant, a lubricant, a coloring agent, a corrective and so on, and then formulated in a routine manner into, e.g., powders, fine granules, granules, tablets, coated tablets, capsules, etc. In the case of tablets and granules, they may be coated as appropriate with, e.g., sugar coating or other coatings, if necessary. In the case of syrups or injectable formulations, they may be formulated in a routine manner together with, e.g., a pH adjustor, a solvent, an isotonicizing agent optionally in combination with a solubilizer, a stabilizer, etc. Likewise, in the case of external preparations, how to prepare them is not limited in any way and they may be prepared in a routine manner. Base ingredients to be used may be various source materials commonly used for pharmaceutical preparations, quasi drugs, cosmetics and so on, as exemplified by animal and vegetable oils, mineral oils, ester oils, waxes, higher alcohols, fatty acids, silicone oils, surfactants, phospholipids, alcohols, polyhydric alcohols, water-soluble polymers, clay minerals, purified water and so on, optionally in combination with pH adjustors, antioxidants, chelating agents, antiseptic and antifungal agents, colorants, flavorings, etc. If necessary, additional ingredients may further be blended, such as blood flow accelerators, antimicrobial agents, anti-inflammatory agents, cell activators, vitamins, amino acids, moisturizers, keratolytic agents, etc. In these cases, the ratio of the active ingredient to carriers may vary from 1% to 90% by weight. If compounds to be used in the present invention, peptides to be used in the present invention or polynucleotides to be used in the present invention are used for the above treatment, they are preferably purified to at least 90% or more, preferably 95% or more, more preferably 98% or more, and even more preferably 99% or more purity before use.

[0116] The effective dose of the pharmaceutical composition of the present invention comprising the substance (e.g., compound) of the present invention will vary depending on, e.g., the severity of symptoms, the age, sex and body weight of a patient, the mode of administration, the type of salt, the detailed type of disease, etc. In general, for adults (body weight: 60 kg), the daily dose for oral administration is about 30 μ g to 10 g, preferably 100 μ g to 5 g, and more preferably 100 μ g to 100 mg, given once or several times, while the daily dose for injection is about 30 μ g to 1 g, preferably 100 μ g to 500 mg, and more preferably 100 μ g to 30 mg, given once or several times. In light of the fact that the efficiency varies depending on the route of administration, it is predicted that the required dose will vary over a wide range. For example, oral administration is expected to require a higher dose than intravenous injection. For administration to children, the dose may be smaller than that for adults. These variations in the dose level can be adjusted by using standard empirical optimization procedures well appreciated in the art.

4. Kits

[0117] In the present invention, because of having EphA4 cleavage activity, gelatinase can be used for cleaving EphA4, particularly for cleaving the EphA4 ectodomain, as an enhancer for γ -secretase-mediated cleavage of the EphA4 endodomain fragment, or as a reagent for γ -secretase-mediated EICD production, in order to perform *in vitro* experiments or non-human animal experiments. In these cases, the present invention can be configured in the form of a kit comprising gelatinase in combination with at least one member selected from a buffer, a cell culture medium, an antibody against EphA4 or a fragment thereof, a fluorescent dye. Such a kit may also comprise an instruction manual which describes, e.g., test procedures for the enzyme activity of gelatinase and nuclear migration of EICD.

[0118] The present invention further provides the use of an assay kit for measurement of the level of gelatinase-mediated EphA4 cleavage and the use of an assay kit for measurement of spine formation.

[0119] The kits of the present invention each comprise gelatinase or a biological composition containing the same, and a biological composition containing EphA4. The kits of the present invention may comprise a biological composition containing γ -secretase. These kits may further comprise tools for use in immunoblotting and/or Western blotting techniques (e.g., reaction vessels, blotting membranes), reagents (e.g., buffer, culture medium, anti-EphA4 antibody), an instruction manual, etc.

EXAMPLES

[0120] The present invention will be further described in more detail by way of the following examples, which are not intended to limit the scope of the present invention.

Example 1**Effects of gelatinase-selective inhibitor on neuronal activity-dependent EphA4 ectodomain cleavage reaction**

[0121] With the aim of identifying proteases which cleave off the EphA4 ectodomain in a neuronal activity-dependent manner, analysis was first performed using a specific inhibitor of gelatinase family molecules (MMP-2, MMP-9) having important functions in the brain. Neurostimulation was performed with 50 μ M NMDA, and the inhibitor used was mmp-2/9 Inhibitor II ((2R)-[(4-biphenylsulfonyl)amino]-N-hydroxy-3-phenylpropionamide, Merck). For detection of cleavage reaction, two types of antibody-based assays were used, i.e., Western blot assay using an antibody capable of recognizing the EphA4 endodomain and ELISA assay using an antibody capable of recognizing the EphA4 ectodomain.

1. Experimental conditions and experimental procedures**(1) Culture of hippocampal neuronal cells**

[0122] Hippocampi were isolated from SD rats at 18 days of embryonic age (Charles River Laboratories, Inc.) and provided for culture. More specifically, fetuses were aseptically taken from pregnant rats. From these fetuses, brains were excised and soaked in 20% FBS (Hyclone)/HBSS (SIGMA). From the excised brains, hippocampi were collected under a stereoscopic microscope. The collected hippocampi were each enzymatically treated at 37°C for 10 minutes in an enzyme solution containing 0.25% trypsin (Invitrogen) and 0.5 mg/ml DNase (SIGMA) to thereby disperse the cells. In this case, the enzymatic reaction was stopped by addition of 20% FBS (Hyclone)/HBSS (SIGMA). The resulting cells were supplemented with 2 ml of HBSS (SIGMA). The cell pellet supplemented with HBSS (SIGMA) was gently pipetted to disperse the cells again. This neuronal cell suspension was diluted with a medium and seeded in a 35 mm dish at an initial cell density of 2×10^5 cells/dish. The medium used was Neurobasal (Invitrogen) medium supplemented with $1 \times$ B27 supplement (Invitrogen) and 0.5 mM L-glutamine (Invitrogen). The seeded cells were cultured in a 37°C incubator under 5% CO₂ and 95% air. After culture for 3 weeks, the medium was replaced with a 50 μ M NMDA-containing medium, and after 30 minutes, the cultured solution was collected for use in ELISA. On the other hand, the neuronal cells were collected with PBS and then quantified for their protein levels, and 10 μ g aliquots were subjected to SDS-PAGE, followed by Western blotting with an anti-EphA4 antibody capable of recognizing the endodomain.

Experimental results

[0123] The results obtained are shown in Figure 2.

[0124] As shown in Figure 2, when hippocampal neuronal cells were stimulated with 50 μ M NMDA, EphA4 cleavage reaction was induced and the EphA4 endodomain fragment was detected. Upon addition of 0 μ M, 1 μ M, 5 μ M, 10 μ M or 25 μ M mmp-2/9 Inhibitor II in addition to the above stimulation conditions, the cleavage reaction was inhibited in a concentration-dependent manner (Figure 2A). Moreover, this cleavage event was also detected by ELISA, which had been prepared with an antibody capable of recognizing the EphA4 ectodomain, and was completely inhibited with 5 μ M mmp-2/9 Inhibitor II (Figure 2B). These results indicated that proteases cleaving off the EphA4 ectodomain were gelatinase family molecules (MMP-2, MMP-9).

INDUSTRIAL APPLICABILITY

[0125] Compounds that promote gelatinase-mediated EphA4 cleavage reaction are capable of enhancing EICD production, promoting spine formation and exerting an improving effect on cognitive functions. Thus, assay systems which allow detection or quantification of MMP2/9-mediated EphA4 cleavage reaction are useful for screening of cognitive function improvers.

SEQUENCE LISTING

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 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
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 Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
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 Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
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 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
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 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
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 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
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 Ser Gln Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
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 Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
 595 600 605
 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
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 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
 625 630 635 640

Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
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 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
 675 680 685
 Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
 690 695 700
 Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
 705 710 715 720
 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
 725 730 735
 Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
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 Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser
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 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
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 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
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 Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
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 Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
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 Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Pro Glu Ser Ser
 885 890 895
 Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
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 Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
 915 920 925
 Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
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 His Met Ser Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
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<211> 3000

<212> DNA

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<220>

<221> CDS

<222> (1)..(2997)

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tgc gac gct gtc acc ggt tct agg gta tac ccg gcg aat gaa gtt act      96
Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
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tta ttg gat tcc aga tct gtt cag gga gag ctt ggg tgg ata gca agc      144
Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
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cct ctg gaa gga ggg tgg gag gaa gta agc att atg gat gag aaa aat      192
Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
      50      55      60

aca ccg atc cga acc tac cag gta tgc aac gtg atg gaa gcc agt cag      240
Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ala Ser Gln
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aac aac tgg ctg cga act gac tgg atc acc cga gaa ggg gcg cag agg      288
Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
      85      90      95

gtg tac att gaa att aag ttc act ctg agg gac tgc aac agt ctt ccg      336

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
      100      105      110

ggc gtc atg ggg act tgc aag gag acg ttt aac ctt tac tac tat gaa      384
Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
      115      120      125

tcg gac aac gac aag gag cgc ttc atc aga gag agc cag ttc ggc aag      432
Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Gly Lys
      130      135      140

atc gac acc atc gca gcg gat gag agc ttt aca cag gtg gac att ggg      480
Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
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gac aga atc atg aag ctc aac acc gag atc ccg gat gta ggg ccc ctg      528
Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
      165      170      175

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Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
      180      185      190

gcc ctg gtg tct gtt cgt gtg ttc tac aag aag tgt ccc ctc acc gtt      624
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
      195      200      205

cga aat cta gcc cag ttc ccc gat acc atc act ggg gct gat acc tct      672
Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
      210      215      220

tcc ctg gtg gaa gtt cga gcc tcc tgt gtc aac aac tca gaa gag aag      720
Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
      225      230      235      240

gat gtg cca aaa atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc      768
Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
      245      250      255

att ggc aac tgc cta tgc aat gct ggg cac gag gag cag aat ggt gaa      816
Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Gln Asn Gly Glu
      260      265      270

tgc caa gct tgc aaa att gga tat tac aaa gct ctc tcc acg gat gcc      864
Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
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acc tgt gcc aag tgt cca ccg cac agc tac tct gtc tgg gaa gga gcc      912
Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
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acg tcc tgc acc tgt gac cga gcc ttt ttc aga gct gac aac gat gcc      960
Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
      305      310      315      320

gcg tcc atg ccc tgc acc cgc cca cca tct gct ccc ctc aac ttg att      1008
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
      325      330      335

tct aat gtc aac gag acg tcg gtg aac ttg gaa tgg agc agt cct cag      1056
Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
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act gac ctc cta gca cac acc aat tao acg ttt gag atc tgg goa gtg Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val 405 410 415	1248
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gct aaa gaa gtt aca aga tac agt gtg gct ctg gct tgg ctg gaa cca Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro 450 455 460	1392
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aag gtc att gga gtt ggc gaa ttt gga gaa gtc tgc agt ggg cgt ctc Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu 625 630 635 640	1920
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gtg atc aaa gcc atc gag gaa ggg tac cgg cta ccc ccg cca atg gac Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp 835 840 845	2544
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ctc atc cgc aac ccc aac agc ctg aag agg aca ggg cca gag agt tcc			2688
Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Pro Glu Ser Ser			
	885	890	895
aga cca aac aca gcc ttg tta gat ccc agc tcc cct gaa ttc tcc gcc			2736
Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala			
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gta gta tca gtg ggt gac tgg ctg cag gcc atc aaa atg gac cgg tat			2784
Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr			
	915	920	925
aag gac aac ttc aca gcc gcc ggg tac acg aca cta gaa gct gtg gtt			2832
Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val			
	930	935	940
cac atg agc cag gat gac ctg gcg cga att ggc atc acc gca atc acg			2880
His Met Ser Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr			
	945	950	955
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His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met			
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cag cag atg cat gcc agg atg gtt cct gtc gcg gcc gca gac tac cca			2976
Gln Gln Met His Gly Arg Met Val Pro Val Ala Ala Ala Asp Tyr Pro			
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<212> PRT

<213> Rattus norvegicus

<400> 4

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Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser			
	35	40	45
Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn			
	50	55	60
Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ala Ser Gln			

65	70	75	80
Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg	85	90	95
Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro	100	105	110
Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu	115	120	125
Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Gly Lys	130	135	140
Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly	145	150	155
Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu	165	170	175
Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile	180	185	190
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val	195	200	205
Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser	210	215	220
Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys	225	230	235
Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro	245	250	255
Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Gln Asn Gly Glu	260	265	270
Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala	275	280	285
Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala	290	295	300
Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala	305	310	315
			320

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 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Arg Val Ser Ile
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 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
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Ser Gln Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
 580 585 590
 Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
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 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
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 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
 625 630 635 640
 Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
 660 665 670
 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
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 Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
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 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
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 Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
 785 790 795 800
 Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
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 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
 820 825 830

Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
835 840 845

Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
850 855 860

Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
865 870 875 880

Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Pro Glu Ser Ser
885 890 895

Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
900 905 910

Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
915 920 925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
930 935 940

His Met Ser Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
945 950 955 960

His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met
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Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr	

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Pro	Leu	Glu	Gly	Gly	Trp	Glu	Glu	Val	Ser	Ile	Met	Asp	Glu	Lys	Asn	
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Asn	Asn	Trp	Leu	Arg	Thr	Asp	Trp	Ile	Thr	Arg	Glu	Gly	Ala	Gln	Arg	
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Val	Tyr	Ile	Glu	Ile	Lys	Phe	Thr	Leu	Arg	Asp	Cys	Asn	Ser	Leu	Pro	
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Ser	Asp	Asn	Asp	Lys	Glu	Arg	Phe	Ile	Arg	Glu	Asn	Gln	Phe	Val	Lys	
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Ile	Asp	Thr	Ile	Ala	Ala	Asp	Glu	Ser	Phe	Thr	Gln	Val	Asp	Ile	Gly	
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Arg	Asn	Leu	Ala	Gln	Phe	Pro	Asp	Thr	Ile	Thr	Gly	Ala	Asp	Thr	Ser	
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Ser	Leu	Val	Glu	Val	Arg	Gly	Ser	Cys	Val	Asn	Asn	Ser	Glu	Glu	Lys	
		225				230				235					240	
gat	gtg	cca	aaa	atg	tac	tgt	ggg	gca	gat	ggt	gaa	tgg	ctg	gta	ccc	768
Asp	Val	Pro	Lys	Met	Tyr	Cys	Gly	Ala	Asp	Gly	Gln	Trp	Leu	Val	Pro	
				245				250						255		
att	ggc	aac	tgc	cta	tgc	aac	gct	ggg	cat	gag	gag	cgg	agc	gga	gaa	816
Ile	Gly	Asn	Cys	Leu	Cys	Asn	Ala	Gly	His	Glu	Glu	Arg	Ser	Gly	Glu	
			260				265					270				
tgc	caa	gct	tgc	aaa	att	gga	tat	tac	aag	gct	ctc	tcc	acg	gat	gcc	864

Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala	
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Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala	
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Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile	
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Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln	
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Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys	
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Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val	
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His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile	
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Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val	
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Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val	
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Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg	
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Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu	
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gct ggt tat aca gac aaa cag agg aga gac ttc ctg agt gag gcc agc Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser 660 665 670	2016
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ctc atc cgc aac ccc aac agc ttg aag agg aca ggg acg gag agc tcc Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser 885 890 895	2688
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<212> PRT

<213> Homo sapiens

<400> 6

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

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Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile 325 330 335		
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His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile 385 390 395 400		
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Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg 485 490 495		
Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His 500 505 510		

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 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
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 Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
 545 550 555 560
 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
 565 570 575
 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
 580 585 590
 Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
 595 600 605
 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
 610 615 620
 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
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 Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
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 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
 675 680 685
 Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
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 Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
 705 710 715 720
 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
 725 730 735
 Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 740 745 750
 Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser
 755 760 765

Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
770 775 780

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
785 790 795 800

Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
805 810 815

Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
820 825 830

Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
835 840 845

Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
850 855 860

Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
865 870 875 880

Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser
885 890 895

Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
900 905 910

Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
915 920 925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
930 935 940

His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
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cct ctg gaa gga ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn 50 55 60	192
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Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro	245	250	255	
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Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu	260	265	270	
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Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala	275	280	285	
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Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala	290	295	300	
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Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys	355	360	365	
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Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val	370	375	380	
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His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile	385	390	395	400
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Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln	435	440	445	
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Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu	465	470	475	480
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Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
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 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
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 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
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 Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
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 Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
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 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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 Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
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 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
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 Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
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 Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
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 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
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 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
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 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
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 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
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 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala

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Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val 370 375 380		
His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile 385 390 395 400		
Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val 405 410 415		
Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val 420 425 430		
Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln 435 440 445		
Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro 450 455 460		
Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu 465 470 475 480		
Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg 485 490 495		
Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His 500 505 510		
Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu 515 520 525		

Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
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 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
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 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
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 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
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 690 695 700
 Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
 705 710 715 720
 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
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 Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 740 745 750
 Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser
 755 760 765
 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
 770 775 780

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
785 790 795 800

Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
805 810 815

Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
820 825 830

Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
835 840 845

Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
850 855 860

Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
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Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser
885 890 895

Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
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Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
915 920 925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
930 935 940

His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
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His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met
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Gln Gln Met His Gly Arg Met Val Pro Val
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<210> 11

<211> 3017

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile Cys	
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Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro	
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Leu Glu Gly Gly Trp Glu Val Ser Ile Met Asp Glu Lys Asn Thr	
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Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln Asn	
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Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg Val	
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tat att gag att aaa ttc acc ttg agg gac tgc aat agt ctt ccg ggc	395
Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly	
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Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ser	
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Asp Asn Asp Lys Glu Arg Phe Val Arg Glu Asn Gln Phe Val Lys Ile	
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gac acc att gct gct gat gag agc ttc acc caa gtg gac att ggt gac	539
Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly Asp	
150 155 160	
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Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu Ser	
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Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala	
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Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val Arg	
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Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser Ser	
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caa gct tgc aaa att gga tat tac aag gct ctg tcc acg gat gcc acc Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala Thr 275 280 285			923
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cgg ccc aat ggg gta atc ctg gaa tat gaa gtc aag tat tat gag aag Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys 470 475 480			1499
gat cag aat gag cga agc tat cgt ata gtt cgg aca gct gcc agg aac			1547

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cag ctg gtg ggc atg ctt cgt ggc att ggg tct ggg atg aag tat tta Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu 725 730 735	2267

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<211> 986

<212> PRT

<213> Homo sapiens

<400> 12

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 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
 50 55 60
 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
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 Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
 100 105 110
 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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 Ser Asp Asn Asp Lys Glu Arg Phe Val Arg Glu Asn Gln Phe Val Lys
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 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
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 Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
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 Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
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 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
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 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
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Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
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 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
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 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
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 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
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 Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val
 420 425 430
 Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
 435 440 445
 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
 450 455 460
 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu

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Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu	515	520	525
Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala	530	535	540
Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val	545	550	555
Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr	565	570	575
Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly	580	585	590
Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala	595	600	605
Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu	610	615	620
Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu	625	630	635
Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys	645	650	655
Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser	660	665	670
Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val	675	680	685
Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn	690	695	700
Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val	705	710	715
			720

Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
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 Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 740 745 750
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 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
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 Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
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 Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
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 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
 820 825 830
 Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
 835 840 845
 Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
 850 855 860
 Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
 865 870 875 880
 Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser
 885 890 895
 Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
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 Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
 915 920 925
 Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
 930 935 940
 His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
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<210> 13

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<212> DNA

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<221> CDS

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Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr	
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Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser	
35 40 45	
cct ctg gaa gga ggg tgg gag gaa gtg agc att atg gat gag aaa aat	192
Pro Leu Glu Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn	
50 55 60	
aca ccg atc cga acc tac cag gtg tgc aac gtg atg gaa gcc agc cag	240
Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ala Ser Gln	
65 70 75 80	
aac aac tgg ctg cga act gac tgg atc acc cgc gaa ggg gcg cag agg	288
Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg	
85 90 95	
gtg tac att gaa att aag ttc act cta agg gac tgc aac agt ctt ccg	336
Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro	
100 105 110	
ggc gtc atg ggg act tgc aag gag acg ttt aac ctc tac tac tat gag	384
Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu	
115 120 125	
tcg gac aac gac aag gag cgc ttc atc aga gag agc cag ttt ggc aag	432
Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Gly Lys	
130 135 140	
atc gac acc atc gca gct gat gag agc ttc acg cag gtg gac att ggt	480
Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly	
145 150 155 160	
gac cga atc atg aaa ctc aac act gag atc cgg gat gta ggg cca ctg	528
Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu	
165 170 175	
agc aag aaa ggg ttt tac ctg gct ttt cag gat gtg ggt gct tgc atc	576
Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile	
180 185 190	

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gat gtg cca aaa atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro 245 250 255	768
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atc atg gga cag ttt gac cac cca aac ata atc cac ctg gaa ggc gtt Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val 675 680 685			2064
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Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn 690 695 700	
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<400> 14

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 35 40 45
 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
 50 55 60
 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ala Ser Gln
 65 70 75 80
 Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
 85 90 95
 Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
 100 105 110
 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
 115 120 125
 Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Gly Lys
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 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
 145 150 155 160
 Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
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Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
 180 185 190
 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205
 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
 210 215 220
 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
 225 230 235 240
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Gln Asn Gly Glu
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 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
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 Ser Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
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 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
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 Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
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 Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
 355 360 365
 Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
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 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Arg Val Ser Ile
 385 390 395 400
 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
 405 410 415
 Asn Gly Val Ser Lys Tyr Asn Pro Ser Pro Asp Gln Ser Val Ser Val
 420 425 430

Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
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 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
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 485 490 495
 Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
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 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
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 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
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 Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
 545 550 555 560
 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
 565 570 575
 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
 580 585 590
 Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
 595 600 605
 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
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 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
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 Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
 660 665 670
 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val

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Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr 725 730 735		
Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 740 745 750		
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser 755 760 765		
Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly 770 775 780		
Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys 785 790 795 800		
Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu 805 810 815		
Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp 820 825 830		
Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp 835 840 845		
Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu 850 855 860		
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Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr 915 920 925		
Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val 930 935 940		
His Met Ser Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr 945 950 955 960		
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<220>

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Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr	
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Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser	
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Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn	
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Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg	
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Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala 900 905 910			
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aag gac aac ttc acg gcc gcc ggg tac acg aca cta gaa gcc gtg gtt Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val 930 935 940			2832
cac atg agc cag gac gac ctg gcg aga att ggc atc acc gcc atc acg His Met Ser Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr 945 950 955 960			2880
cac cag aat aag att ttg agc agc gtc cag gcg atg cga acc cag atg His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met 965 970 975			2928
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<210> 16

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<212> PRT

<213> Mus musculus

<400> 16

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 35 40 45
 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
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 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ala Ser Gln
 65 70 75 80
 Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
 85 90 95
 Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
 100 105 110
 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
 115 120 125
 Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Gly Lys
 130 135 140
 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
 145 150 155 160
 Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
 165 170 175
 Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
 180 185 190
 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205
 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
 210 215 220
 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
 225 230 235 240
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Gln Asn Gly Glu
 260 265 270
 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
 275 280 285
 Ser Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
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 Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
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 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
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 Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
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 Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
 355 360 365
 Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
 370 375 380

His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Arg Val Ser Ile
 385 390 395 400
 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
 405 410 415
 Asn Gly Val Ser Lys Tyr Asn Pro Ser Pro Asp Gln Ser Val Ser Val
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 Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
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 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
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 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
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 Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
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 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
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 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
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 595 600 605
 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
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 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
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Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
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 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
 675 680 685
 Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
 690 695 700
 Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
 705 710 715 720
 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
 725 730 735
 Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 740 745 750
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 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
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 Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
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 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
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 Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
 835 840 845
 Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
 850 855 860
 Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
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 Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Ser Glu Ser Ser
 885 890 895
 Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
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 Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
 915 920 925
 Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
 930 935 940
 His Met Ser Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
 945 950 955 960
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 Gln Gln Met His Gly Arg Met Val Pro Val
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<210> 17

<211> 2961

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(2958)

<400> 17

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tgc gac gct gtc acc ggt tct agg gta tac ccc gcg aat gaa gtt act      96
Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
      20      25      30

tta ttg gat tcc aga tct gtt cag gga gag ctt ggg tgg ata gca agc      144
Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
      35      40      45

cct ctg gaa gga ggg tgg gag gaa gtg agc att atg gat gag aaa aat      192
Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
      50      55      60

aca ccg atc cga acc tac cag gtg tgc aac gtg atg gaa gcc agc cag      240
Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ala Ser Gln
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aac aac tgg ctg cga act gac tgg atc acc cgc gaa ggg gcg cag agg      288
Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
      85      90      95

gtg tac att gaa att aag ttc act cta agg gac tgc aac agt ctt ccg      336

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
      100      105      110

ggc gtc atg ggg act tgc aag gag acg ttt aac ctc tac tac tat gag      384
Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
      115      120      125

tcg gac aac gac aag gag cgc ttc atc aga gag agc cag ttt ggc aag      432
Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Gly Lys
      130      135      140

act gac acc atc gca gct gat gag agc ttc acg cag gtg gac att ggt      480
Thr Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
      145      150      155      160

gac cga atc atg aaa ctc aac act gag atc cgg gat gta ggg cca ctg      528
Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
      165      170      175

agc aag aaa ggg ttt tac ctg gct ttt cag gat gtg ggt gct tgc atc      576
Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
      180      185      190

gcc ctg gtg tct gtc cgt gtg ttc tac aag aag tgt cca ctc acc gtt      624
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
      195      200      205

cga aat cta gcc cag ttt cct gac acc att act ggg gct gat acc tct      672
Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
      210      215      220

tcc ctg gtg gaa gtt cga ggc tcc tgt gtc aac aac tca gaa gag aag      720
Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
      225      230      235      240

gat gtg cca aaa atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc      768
Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
      245      250      255

att ggc aac tgc cta tgc aac gct ggg cac gag gag cag aat ggt gaa      816
Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Gln Asn Gly Glu
      260      265      270

tgc caa gct tgc aaa att gga tat tac aaa gct ctt tcc acg gac gcc      864
Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
      275      280      285

tcc tgt gcc aag tgt cca ccg cac agc tac tct gtc tgg gaa gga gcc      912
Ser Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
      290      295      300

acg tcc tgc acc tgt gac cga ggc ttt ttc aga gct gac aac gat gca      960
Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
      305      310      315      320

gcc tcc atg ccc tgc acc cgc cca cca tct gct ccc ctc aac ttg att      1008
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
      325      330      335

tct aat gtc aac gag aca tcg gtg aac ttg gaa tgg agc agc cct cag      1056
Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
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aca gtg aca acc aac caa gca gca cca tca tcc att gct ttg gtc cag Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln 435 440 445	1344
gct aaa gaa gtt aca aga tat agc gta gct ctg gct tgg ctg gaa cca Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro 450 455 460	1392
gat cga cca aat gga gtc atc tta gaa tat gaa gtc aaa tat tat gaa Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu 465 470 475 480	1440
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gtg cga gcc agg acc gct gct ggc tac gga gac ttc agc gag ccc ctg Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu 515 520 525	1584
gaa gtc act act aat aca gtg cct tcc cgc atc att ggc gat gga gcc Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala 530 535 540	1632
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agc aaa gcg aaa caa gaa gca gat gaa gag aaa cat ttg aat caa ggt Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly 580 585 590	1776
gtt aga act tat gtg gat ccc ttt aca tac gaa gac ccc aac cag gca Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala 595 600 605	1824

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gct ggc tat act gac aag cag agg aga gac ttc ctg agt gag gcc agc Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser 660 665 670	2016
atc atg gga cag ttt gac cac cca aac ata atc cac ctg gaa ggc gtt Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val 675 680 685	2064
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tgc ccc att gcc ctc cat cag tta atg ctg gac tgc tgg cag aaa gag Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu 850 855 860	2592
aga agt gac agg cct aaa ttt ggg cag atc gtc aac atg ctg gac aaa Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys 865 870 875 880	2640
ctc atc cgc aat ccc aac agc ctg aag agg aca ggg tgc gag agt tcc Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Ser Glu Ser Ser 885 890 895	2688
aga cca aac aca gcc ttg tta gat ccc agc tcc cct gaa ttc tct gct Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala 900 905 910	2736
gta gta tca gtg ggc gac tgg ctg cag gcc atc aaa atg gac cgg tat Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr 915 920 925	2784
aag gac aac ttc acg gcc gcc ggg tac acg aca cta gaa gcc gtg gtt Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val 930 935 940	2832
cac atg agc cag gac gac ctg gcg aga att ggc atc acc gcc atc acg His Met Ser Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr 945 950 955 960	2880
cac cag aat aag att ttg agc agc gtc cag gcg atg cga acc cag atg His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met 965 970 975	2928
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<210> 18

<211> 986

<212> PRT

<213> Mus musculus

<400> 18

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Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
35     40     45

Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
50     55     60

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

Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
85     90     95

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
100    105    110

Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
115    120    125

Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Gly Lys
130    135    140

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

Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
165    170    175

Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
180    185    190

Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
195    200    205

Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
210    215    220

Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
225    230    235    240

Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
245    250    255

Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Gln Asn Gly Glu
260    265    270

Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
275    280    285

Ser Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
290    295    300

Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
305    310    315    320

Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
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 355 360 365
 Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
 370 375 380
 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Arg Val Ser Ile
 385 390 395 400
 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
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 Asn Gly Val Ser Lys Tyr Asn Pro Ser Pro Asp Gln Ser Val Ser Val
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 Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
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 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
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 Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
 485 490 495
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 Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
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 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
 565 570 575
 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
 580 585 590

Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
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 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
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 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
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 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
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 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
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 Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
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 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
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 850 855 860
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 Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Ser Glu Ser Ser
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 Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
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 Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
 915 920 925
 Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
 930 935 940
 His Met Ser Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
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Glu Gly Ala Gln Arg Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp	
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Cys Asn Ser Leu Pro Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn	
50 55 60	
ctc tac tat tat gag tcg gac aac gac aag gag cgc ttc atc aga gag	240
Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu	
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agc cag ttt ggc aag atc gac acc atc gca gct gat gag agc ttc acg	288
Ser Gln Phe Gly Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr	
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Gln Val Asp Ile Gly Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg	
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Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp	
115 120 125	
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Val Gly Ala Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys	
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Cys Pro Leu Thr Val Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr	
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Gly Ala Asp Thr Ser Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn	
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Asn Ser Glu Glu Lys Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly	
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Leu Ser Thr Asp Ala Ser Cys Ala Lys Cys Pro Pro His Ser Tyr Ser	
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Val Trp Glu Gly Ala Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg	
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aac atg ctg gac aaa ctc atc cgc aat ccc aac agc ctg aag agg aca Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr 820 825 830	2496
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Glu Gly Ala Gln Arg Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp
35           40           45

Cys Asn Ser Leu Pro Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn
50           55           60

Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu
65           70           75           80

Ser Gln Phe Gly Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr
85           90           95

Gln Val Asp Ile Gly Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg
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Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp
115          120          125

Val Gly Ala Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys
130          135          140

Cys Pro Leu Thr Val Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr
145          150          155          160

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

Asn Ser Glu Glu Lys Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly
180          185          190

Glu Trp Leu Val Pro Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu
195          200          205

Glu Gln Asn Gly Glu Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala
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Val Trp Glu Gly Ala Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg
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Pro Leu Asn Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu
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Trp Ser Ser Pro Gln Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn
290          295          300

Val Val Cys Lys Lys Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro
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Cys Gly Ser Gly Val His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr
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Thr Arg Val Ser Ile Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe
340          345          350

Glu Ile Trp Ala Val Asn Glu Val Ser Lys Tyr Asn Pro Ser Pro Asp

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Ala Trp Leu Glu Pro Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu
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Val Lys Tyr Tyr Glu Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val
420          425          430

Arg Thr Ala Ala Arg Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr
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Ser Tyr Val Phe His Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp
450          455          460

Phe Ser Glu Pro Leu Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile
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Ile Gly Asp Gly Ala Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly
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Ser Val Val Leu Val Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg
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Arg Arg Ser Lys Tyr Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys
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His Leu Asn Gln Gly Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu
530          535          540

Asp Pro Asn Gln Ala Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser
545          550          555          560

Cys Ile Lys Ile Glu Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val
565          570          575

Cys Ser Gly Arg Leu Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala
580          585          590

Ile Lys Thr Leu Lys Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe
595          600          605

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 His Leu Glu Gly Val Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr
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 645 650 655
 Gly Arg Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly
 660 665 670
 Ser Gly Met Lys Tyr Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu
 675 680 685
 Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser
 690 695 700
 Asp Phe Gly Met Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr
 705 710 715 720
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 725 730 735
 Ile Ala Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly
 740 745 750
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 Pro Pro Pro Met Asp Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp
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 865 870 875 880
 Leu Glu Ala Val Val His Met Ser Gln Asp Asp Leu Ala Arg Ile Gly
 885 890 895
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gca agc cct ctg gaa gga ggg tgg gag gaa gtg agc att atg gat gag Ala Ser Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu 50 55 60	192
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Ala Val Asn Gly Val Ser Lys Tyr Asn Pro Ser Pro Asp Gln Ser Val	420	425	430	
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Tyr Glu Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala	485	490	495	
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Ala Arg Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val	500	505	510	
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Phe His Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu	515	520	525	
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Pro Leu Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp	530	535	540	
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Ser Gln Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala 85 90 95		
Gln Arg Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser 100 105 110		
Leu Pro Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr 115 120 125		
Tyr Glu Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe 130 135 140		
Gly Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp 145 150 155 160		
Ile Gly Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly 165 170 175		
Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala 180 185 190		
Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu 195 200 205		
Thr Val Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp 210 215 220		
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Val Pro Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Gln Asn 260 265 270		
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 Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser
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 Pro Gln Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys
 355 360 365
 Lys Lys Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser
 370 375 380
 Gly Val His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Arg Val
 385 390 395 400
 Ser Ile Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp
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 Tyr Glu Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala
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 Ala Arg Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val
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 Phe His Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu
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 Pro Leu Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp
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Met Asp Glu Lys Asn Thr Pro Ile	
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Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ala Ser Gln Asn Asn Trp	
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Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg Val Tyr Ile	
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gaa att aag ttc act cta agg gac tgc aac agt ctt ccg ggc gtc atg	317
Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Val Met	
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Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ser Asp Asn	
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75 80 85	
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Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn
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agc aac ttg gtc tgc aag gtg tct gac ttt ggc atg tcc agg gtg ctg      2285
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Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys
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Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile
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gcc ctc cat cag tta atg ctg gac tgc tgg cag aaa gag aga agc gac      2573
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795                                     800                                     805

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Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg
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Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val His Met Ser
875                                     880                                     885

cag gac gac ctg gcg aga att ggc atc acc gcc atc acg cac cag aat      2861
Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn
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Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Met
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His Gly Arg Met Val Pro Val
925

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Cys Asn Ser Leu Pro Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn
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Ser Gln Phe Gly Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr
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195     200     205

Glu Gln Asn Gly Glu Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala
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Pro Leu Asn Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu
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Trp Ser Ser Pro Gln Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn
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Cys Gly Ser Gly Val His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr
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Glu Ile Trp Ala Val Asn Glu Val Ser Lys Tyr Asn Pro Ser Pro Asp
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 Phe Ser Glu Pro Leu Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile
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 Cys Ser Gly Arg Leu Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala
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Gly Arg Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly
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Ser Gly Met Lys Tyr Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu
675              680              685
Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser
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705              710              715              720
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785              790              795              800
Cys Trp Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val
805              810              815
Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr
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835              840              845
Pro Glu Phe Ser Ala Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile
850              855              860
Lys Met Asp Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr
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Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr	
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Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Glu	
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 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ala Ser Gln
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 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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 Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
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Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
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His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Arg Val Ser Ile
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Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala 530 535 540		
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Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly 580 585 590		
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Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser 660 665 670		
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 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
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785 790 795 800	
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Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu	
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Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp	
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gtt ata aaa gcc att gaa gaa ggc tac cgg cta cct cca cca atg gac	2544
Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp	
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Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu	
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Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys	
865 870 875 880	
ctc att cgc aac ccc aac agc ttg aag agg acg ggt act gag agc tcc	2688
Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser	
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Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala	
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gtg gta tct gta ggt gat tgg ctt cag gcc att aaa atg gac cgg tat	2784
Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr	
915 920 925	
aag gac aac ttc aca gct gcc ggt tac acc acc ctc gag gct gtg gtg	2832
Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val	
930 935 940	
cac atg aac cag gac gac ctg gcg aga atc ggt atc acg gcc gtc acg	2880
His Met Asn Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Val Thr	
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cac cag aat aag atc ttg aac agc gtc cag gca atg cgg acc caa atg	2928
His Gln Asn Lys Ile Leu Asn Ser Val Gln Ala Met Arg Thr Gln Met	
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Gln Gln Met His Gly Arg Met Val Pro Val	
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<213> Monodelphis domestica

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 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
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 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ser Ser Gln
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 Asn Asn Trp Leu Arg Thr Asp Trp Ile Pro Arg Glu Gly Ala Gln Arg
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 Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
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 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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 Ser Asn Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Ala Lys
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 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
 145 150 155 160
 Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
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 Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
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 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
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 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
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 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
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 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Ser Thr Lys Val Ser Ile
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 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
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 Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
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 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
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 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
 625 630 635 640
 Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys

645	650	655
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Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val 675 680 685		
Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn 690 695 700		
Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val 705 710 715 720		
Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr 725 730 735		
Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 740 745 750		
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser 755 760 765		
Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly 770 775 780		
Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys 785 790 795 800		
Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu 805 810 815		
Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp 820 825 830		
Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp 835 840 845		
Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu 850 855 860		
Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys 865 870 875 880		
Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser 885 890 895		
Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala 900 905 910		
Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr 915 920 925		
Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val 930 935 940		
His Met Asn Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Val Thr 945 950 955 960		
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ccc aac aac agc cca aag cca cga gat gtc acg ccc gcg gga cag att      96
Pro Asn Asn Ser Pro Lys Pro Arg Asp Val Thr Pro Ala Gly Gln Ile
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cac tcg gtg aca ggc agt gac agt cag agc cca aca agg atg cca gtg      144
His Ser Val Thr Gly Ser Asp Ser Gln Ser Pro Thr Arg Met Pro Val
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cca cca gat gtt gcc gaa gct cat aaa ctg ggt cag cac aac cac gct      192
Pro Pro Asp Val Ala Glu Ala His Lys Leu Gly Gln His Asn His Ala
50     55     60

gtt gca aga ggt tcc gaa caa ata acc tta ttg gat tcc aga tct gtt      240
Val Ala Arg Gly Ser Glu Gln Ile Thr Leu Leu Asp Ser Arg Ser Val
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cag gga gaa ctt ggg tgg ata gcg agc cct ctg gaa gga ggg tgg gag      288
Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro Leu Glu Gly Gly Trp Glu
85     90     95

gaa gtg agt atc atg gat gaa aaa aac aca cca atc cga acc tac caa      336
Glu Val Ser Ile Met Asp Glu Lys Asn Thr Pro Ile Arg Thr Tyr Gln
100    105    110

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Val Cys Asn Val Met Glu Pro Ser Gln Asn Asn Trp Leu Arg Thr Asp
115    120    125

tgg atc acc cga gaa ggg gcg cag agg gtg tac att gaa atc aag ttc      432
Trp Ile Thr Arg Glu Gly Ala Gln Arg Val Tyr Ile Glu Ile Lys Phe
130    135    140

aca ttg aga gac tgc aac agc ctt cca ggt gtc atg ggc act tgc aag      480
Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Val Met Gly Thr Cys Lys
145    150    155    160

gag acg ttc aac ctc tac tac tat gaa tca gac aac gac aaa gag cgt      528
Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp Lys Glu Arg
165    170    175

ttt atc cga gag agc cag ttt gcc aag att gac acc atc gct gct gac      576
Phe Ile Arg Glu Ser Gln Phe Ala Lys Ile Asp Thr Ile Ala Ala Asp
180    185    190

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Glu Ser Phe Thr Gln Val Asp Ile Gly Asp Arg Ile Met Lys Leu Asn
195    200    205

acc gag atc cgg gat gta ggg ccg ttg agc aaa aag ggg ttt tat ctg      672
Thr Glu Ile Arg Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu
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Phe Tyr Lys Lys Cys Pro Leu Thr Val Arg Asn Leu Ala Gln Phe Pro
245    250    255

gac acc atc acg ggg gct gat acg tet tcc ctg gtg gag gtt cga ggc      816
Asp Thr Ile Thr Gly Ala Asp Thr Ser Ser Leu Val Glu Val Arg Gly
260    265    270

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Ser Cys Val Asn Asn Ser Glu Glu Lys Asp Val Pro Lys Met Tyr Cys
275    280    285

ggg gca gat ggt gaa tgg ctg gta ccc att ggc aac tgc cta tgc aat      912
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290    295    300

gct ggg cac gaa gag cga aat gga gaa tgc caa gcc tgc aaa att ggg      960
Ala Gly His Glu Glu Arg Asn Gly Glu Cys Gln Ala Cys Lys Ile Gly
305    310    315    320

tat tac aag gcc ctc tcc acg gat gcg gcc tgt gcc aag tgc ccg ccc      1008
Tyr Tyr Lys Ala Leu Ser Thr Asp Ala Ala Cys Ala Lys Cys Pro Pro
325    330    335

cac agc tat tcg gtc tgg gaa gga gcc aca tcg tgt acc tgt gac cga      1056
His Ser Tyr Ser Val Trp Glu Gly Ala Thr Ser Cys Thr Cys Asp Arg
340    345    350

ggc ttt ttc aga gcc gac aac gac gcc gcc tcc atg ccc tgc acc cgc      1104
Gly Phe Phe Arg Ala Asp Asn Asp Ala Ala Ser Met Pro Cys Thr Arg
355    360    365

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ccc tat tgg gat atg tcc aat caa gac gtg att aaa gcc att gag gaa			2640

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35 40 45

Pro Pro Asp Val Ala Glu Ala His Lys Leu Gly Gln His Asn His Ala
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 Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu Asp Asp Pro

805 810 815

Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr
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Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu
865 870 875 880

Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala Leu His Gln
885 890 895

Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe
900 905 910

Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser
915 920 925

Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Pro Asn Thr Ala Leu Leu
930 935 940

Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val Gly Asp Trp
945 950 955 960

Leu Gln Ala Ile Lys Met Asp Arg Tyr Lys Asp Asn Phe Thr Ala Ala
965 970 975

Gly Tyr Thr Thr Leu Glu Ala Val Val His Met Asn Gln Glu Asp Leu
980 985 990

Ala Arg Ile Gly Ile Thr Ala Val Thr His Gln Asn Lys Ile Leu Ser
995 1000 1005

Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Ile His Gly Arg
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Met Val Pro Val
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tta ttg gat tcc aga tct gtt cag gga gaa ctt ggg tgg ata gca agc Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser 35 40 45	144
cct ctg gaa gga ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat Pro Leu Glu Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn 50 55 60	192
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gac aga atc atg aag ctg aac acc gag atc cgg gat gta ggg cca tta Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu 165 170 175	528
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gcc ctg gta tca gtc cgt gtg ttc tat aaa aag tgt cca ctc aca gtc Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val 195 200 205	624
cgc aat ctg gcc cag ttt cct gac acc atc aca ggg gct gat acg tct Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser 210 215 220	672

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725	730	735	
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cac cag aat aag att ttg agc agt gtc cag gca atg cga acc caa atg His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met 965 970 975			2928
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 Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
 85 90 95
 Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
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 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
 115 120 125
 Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
 130 135 140
 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
 145 150 155 160
 Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
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 Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
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 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205

Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
 210 215 220
 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
 225 230 235 240
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
 260 265 270
 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
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 Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
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 Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
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 355 360 365
 Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
 370 375 380
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 405 410 415
 Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val
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 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
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 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
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 565 570 575
 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
 580 585 590
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 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
 625 630 635 640
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 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
 660 665 670
 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
 675 680 685
 Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
 690 695 700
 Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
 705 710 715 720

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Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
740                      745                      750

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755                      760                      765

Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
770                      775                      780

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
785                      790                      795                      800

Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
805                      810                      815

Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
820                      825                      830

Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
835                      840                      845

Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
850                      855                      860

Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
865                      870                      875                      880

Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser
885                      890                      895

Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
900                      905                      910

Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
915                      920                      925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
930                      935                      940

His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
945                      950                      955                      960

His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met
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Gln Gln Met His Gly Arg Met Val Pro Val
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<211> 2964

<212> DNA

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Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr	
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Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser	
35 40 45	
cct ctg gaa gga ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat	192
Pro Leu Glu Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn	
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aca cca atc cga acc tac caa gtg tgc aat gtg atg gaa ccc agc cag	240
Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln	
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Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg	
85 90 95	
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Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro	
100 105 110	
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Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Glu	
115 120 125	
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Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala	
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acc tcg tgc acc tgt gac cga ggc ttt ttc aga gct gac aac gat gct	960
Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala	
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gcc tct atg ccc tgc acc cgt cca ccg tct gct ccc ctg aac ttg att	1008
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340 345 350	
aat aca ggt ggc cgc cag gac att tcc tat aat gtg gta tgc aag aaa	1104
Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys	
355 360 365	
tgt gga gct ggt gac ccc agc aag tgc cga ccc tgt gga agt ggg gtc	1152
Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val	
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His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile	
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Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val	
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Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val	
420 425 430	

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agt aaa gcc aaa caa gaa gcg gat gaa gag aaa cat ttg aat caa ggt Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly 580 585 590	1776
gta aga aca tat gtg gac ccc ttt acg tac gaa gat ccc aac caa gca Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala 595 600 605	1824
gtt cga gag ttt gcc aaa gaa att gac gca tcc tgc att aag att gaa Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu 610 615 620	1872
aaa gtt ata gga gtt ggt gaa ttt ggt gag gta tgc agt ggg cgt ctc Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu 625 630 635 640	1920
aaa gtg cct ggc aag aga gag atc tgt gtg gct atc aag act ctg aaa Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys 645 650 655	1968
gct ggt tat aca gac aaa cag agg aga gac ttc ctg agt gag gcc agc Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser 660 665 670	2016
atc atg gga cag ttt gac cat ccg aac atc att cac ttg gaa ggc gtg Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val 675 680 685	2064

gtc act aaa tgt aaa cca gta atg atc ata aca gag tac atg gag aat Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn 690 695 700	2112
ggc tcc ttg gat gca ttc ctc agg aaa aat gat ggc aga ttt aca gtc Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val 705 710 715 720	2160
att cag ctg gtg ggc atg ctt cgt ggc att ggg tct ggg atg aag tat Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr 725 730 735	2208
tta tct gat atg agc tat gtg cat cgt gat ctg gcc gca cgg aac atc Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 740 745 750	2256
ctg gtg aac agc aac ttg gtc tgc aaa gtg tct gat ttt ggc atg tcc Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser 755 760 765	2304
cga gtg ctt gag gat gat ccg gaa gca gct tac acc acc agg ttg ggt Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Leu Gly 770 775 780	2352
ggc aag att cct atc cgg tgg act gcg cca gaa gca att gcc tat cgt Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg 785 790 795 800	2400
aaa ttc aca tca gca agt gat gta tgg agc tat gga atc gtt atg tgg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp 805 810 815	2448
gaa gtg atg tgc tac ggg gag agg ccc tat tgg gat atg tcc aat caa Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln 820 825 830	2496
gat gtg att aaa gcc att gag gaa ggc tat cgg tta ccc cct cca atg Asp Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Met 835 840 845	2544
gac tgc ccc att gca ctc cac cag ctg atg cta gac tgc tgg cag aag Asp Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys 850 855 860	2592
gag agg agc gac agg cct aaa ttt ggg cag att gtc aac atg ttg gac Glu Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp 865 870 875 880	2640
aaa ctc atc cgc aac ccc aac agc ttg aag agg aca ggg acg gag agc Lys Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser 885 890 895	2688
tcc aga cct aac act gcc ttg ttg gat cca agc tcc cct gaa ttc tct Ser Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser 900 905 910	2736
gct gtg gta tca gtg ggc gat tgg ctc cag gcc att aaa atg gac cgg Ala Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg 915 920 925	2784
tat aag gat aac ttc aca gct gct ggt tat acc aca cta gag gct gtg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val 930 935 940	2832
gtg cac gtg aac cag gag gac ctg gca aga att ggt atc aca gcc atc Val His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile 945 950 955 960	2880
acg cac cag aat aag att ttg agc agt gtc cag gca atg cga acc caa Thr His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln 965 970 975	2928
atg cag cag atg cac gcc aga atg gtt ccc gtc tga Met Gln Gln Met His Gly Arg Met Val Pro Val 980 985	2964

<210> 34

<211> 987

<212> PRT

<213> Pan troglodytes

<400> 34

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

165	170	175
Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile 180	185	190
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val 195	200	205
Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser 210	215	220
Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys 225	230	235
Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro 245	250	255
Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu 260	265	270
Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala 275	280	285
Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala 290	295	300
Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala 305	310	315
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile 325	330	335
Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln 340	345	350
Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys 355	360	365
Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val 370	375	380
His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile 385	390	395
Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val 405	410	415

Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val
 420 425 430
 Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
 435 440 445
 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
 450 455 460
 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
 465 470 475 480
 Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
 485 490 495
 Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
 500 505 510
 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
 515 520 525
 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
 530 535 540
 Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
 545 550 555 560
 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
 565 570 575
 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
 580 585 590
 Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
 595 600 605
 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
 610 615 620
 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
 625 630 635 640
 Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
 660 665 670

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Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
675                               680                               685

Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
690                               695                               700

Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
705                               710                               715                               720

Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
725                               730                               735

Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
740                               745                               750

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser
755                               760                               765

Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Leu Gly
770                               775                               780

Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg
785                               790                               795                               800

Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp
805                               810                               815

Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln
820                               825                               830

Asp Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met
835                               840                               845

Asp Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys
850                               855                               860

Glu Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp
865                               870                               875                               880

Lys Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser
885                               890                               895

Ser Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser
900                               905                               910

Ala Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg
915                               920                               925

Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val
930                               935                               940

Val His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile
945                               950                               955                               960

Thr His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln
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Met Gln Gln Met His Gly Arg Met Val Pro Val
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<210> 35

<211> 2784

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)..(2781)

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Met Glu Pro Ser Gln Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg	
20 25 30	
gaa ggg gct cag agg gtg tat att gag att aaa ttc acc ttg agg gac	144
Glu Gly Ala Gln Arg Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp	
35 40 45	
tgc aat agt ctt cag ggc gtc atg ggg act tgc aag gag acg ttt aac	192
Cys Asn Ser Leu Pro Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn	
50 55 60	
ctg tac tac tat gaa tca gac aac gac aaa gag cgt ttc atc aga gag	240
Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu	
65 70 75 80	
aac cag ttt gtc aaa att gac acc att gct gct gat gag agc ttc acc	288
Asn Gln Phe Val Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr	
85 90 95	
caa gtg gac att ggt gac aga atc atg aag ctg aac acc gag atc cgg	336
Gln Val Asp Ile Gly Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg	
100 105 110	
gat gta ggg cca tta agc aaa aag ggg ttt tac ctg gct ttt cag gat	384
Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp	
115 120 125	
gtg ggg gcc tgc atc gcc ctg gta tca gtc cgt gtg ttc tat aaa aag	432
Val Gly Ala Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys	
130 135 140	
tgt cca ctc aca gtc cgc aat ctg gcc cag ttt cct gac acc atc aca	480
Cys Pro Leu Thr Val Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr	
145 150 155 160	
ggg gct gat acg tot tcc ctg gtg gaa gtt cga ggc tcc tgt gtc aac	528
Gly Ala Asp Thr Ser Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn	
165 170 175	
aac tca gaa gag aag gat gtg cca aaa atg tac tgt ggg gca gat ggt	576
Asn Ser Glu Glu Lys Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly	
180 185 190	
gaa tgg ctg gta ccc att ggc aac tgc cta tgc aac gct ggg cat gag	624
Glu Trp Leu Val Pro Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu	
195 200 205	
gag cgg agc gga gaa tgc caa gct tgc aaa att gga tat tac aag gct	672
Glu Arg Ser Gly Glu Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala	
210 215 220	
ctc tcc acg gat gcc acc tgt gcc aag tgc cca ccc cac agc tac tot	720
Leu Ser Thr Asp Ala Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser	
225 230 235 240	
gtc tgg gaa gga gcc acc tcg tgc acc tgt gac cga ggc ttt ttc aga	768
Val Trp Glu Gly Ala Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg	
245 250 255	
gct gac aac gat gct gcc tot atg ccc tgc acc cgt cca cgg tot gct	816
Ala Asp Asn Asp Ala Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala	
260 265 270	
ccc ctg aac ttg att tca aat gtc aat gag aca tct gtg aac ttg gaa	864
Pro Leu Asn Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu	
275 280 285	
tgg agt agc cct cag aat aca ggt ggc cgc cag gac att tcc tat aat	912
Trp Ser Ser Pro Gln Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn	
290 295 300	
gtg gta tgc aag aaa tgt gga gct ggt gac ccc agc aag tgc cga ccc	960
Val Val Cys Lys Lys Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro	
305 310 315 320	
tgt gga agt ggg gtc cac tac acc cgg cag cag aat ggc ttg aag acc	1008
Cys Gly Ser Gly Val His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr	
325 330 335	
acc aaa gtc tcc atc act gac ctc cta gct cac acc aat tac acc ttt	1056
Thr Lys Val Ser Ile Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe	
340 345 350	
gaa atc tgg gct gtg aat gga gtg tcc aaa tat aac cct aac cca gac	1104
Glu Ile Trp Ala Val Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp	
355 360 365	
caa tca gtt tot gtc act gtg acc acc aac caa gca gca cca tca tcc	1152
Gln Ser Val Ser Val Thr Thr Asn Gln Ala Ala Pro Ser Ser	
370 375 380	
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Ile Ala Leu Val Gln Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu 385 390 395 400	
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tgc agt ggg cgt ctc aaa gtg cct ggc aag aga gag atc tgt gtg gct Cys Ser Gly Arg Leu Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala 580 585 590	1776
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tct ggg atg aag tat tta tct gat atg agc tat gtg cat cgt gat ctg Ser Gly Met Lys Tyr Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu 675 680 685	2064
gcc gca cgg aac atc ctg gtg aac agc aac ttg gtc tgc aaa gtg tct Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser 690 695 700	2112
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cta gag gct gtg gtg cac gtg aac cag gag gac ctg gca aga att ggt Leu Glu Ala Val Val His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly 885 890 895	2688
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<211> 927

<212> PRT

<213> Pan troglodytes

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 35 40 45
 Cys Asn Ser Leu Pro Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn
 50 55 60
 Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu
 65 70 75 80
 Asn Gln Phe Val Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr
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 Gln Val Asp Ile Gly Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg
 100 105 110
 Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp
 115 120 125
 Val Gly Ala Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys
 130 135 140
 Cys Pro Leu Thr Val Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr
 145 150 155 160
 Gly Ala Asp Thr Ser Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn
 165 170 175
 Asn Ser Glu Glu Lys Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly
 180 185 190

Glu Trp Leu Val Pro Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu
 195 200 205
 Glu Arg Ser Gly Glu Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala
 210 215 220
 Leu Ser Thr Asp Ala Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser
 225 230 235 240
 Val Trp Glu Gly Ala Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg
 245 250 255
 Ala Asp Asn Asp Ala Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala
 260 265 270
 Pro Leu Asn Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu
 275 280 285
 Trp Ser Ser Pro Gln Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn
 290 295 300
 Val Val Cys Lys Lys Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro
 305 310 315 320
 Cys Gly Ser Gly Val His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr
 325 330 335
 Thr Lys Val Ser Ile Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe
 340 345 350
 Glu Ile Trp Ala Val Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp
 355 360 365
 Gln Ser Val Ser Val Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser
 370 375 380
 Ile Ala Leu Val Gln Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu
 385 390 395 400
 Ala Trp Leu Glu Pro Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu
 405 410 415
 Val Lys Tyr Tyr Glu Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val
 420 425 430
 Arg Thr Ala Ala Arg Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr

435	440	445
Ser Tyr Val Phe His Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp 450 455 460		
Phe Ser Glu Pro Leu Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile 465 470 475 480		
Ile Gly Asp Gly Ala Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly 485 490 495		
Ser Val Val Leu Val Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg 500 505 510		
Arg Arg Ser Lys Tyr Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys 515 520 525		
His Leu Asn Gln Gly Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu 530 535 540		
Asp Pro Asn Gln Ala Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser 545 550 555 560		
Cys Ile Lys Ile Glu Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val 565 570 575		
Cys Ser Gly Arg Leu Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala 580 585 590		
Ile Lys Thr Leu Lys Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe 595 600 605		
Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile 610 615 620		
His Leu Glu Gly Val Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr 625 630 635 640		
Glu Tyr Met Glu Asn Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp 645 650 655		
Gly Arg Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly 660 665 670		
Ser Gly Met Lys Tyr Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu 675 680 685		

Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser
690 695 700

Asp Phe Gly Met Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr
705 710 715 720

Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala
725 730 735

Ile Ala Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly
740 745 750

Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp
755 760 765

Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu
770 775 780

Pro Pro Pro Met Asp Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp
785 790 795 800

Cys Trp Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val
805 810 815

Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr
820 825 830

Gly Thr Glu Ser Ser Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser
835 840 845

Pro Glu Phe Ser Ala Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile
850 855 860

Lys Met Asp Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr
865 870 875 880

Leu Glu Ala Val Val His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly
885 890 895

Ile Thr Ala Ile Thr His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala
900 905 910

Met Arg Thr Gln Met Gln Gln Met His Gly Arg Met Val Pro Val
915 920 925

<210> 37

<211> 2907

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)..(2904)

<400> 37

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

tcc ctg gtg gaa gtt cga ggc tcc tgt gtc aac aac tca gaa gag aag Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys 225 230 235 240	720
gat gtg cca aaa atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro 245 250 255	768
att ggc aac tgc cta tgc aac gct ggg cat gag gag cgg agc gga gaa Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu 260 265 270	816
tgc caa gct tgc aaa att gga tat tac aag gct ctg tcc ecg gat gcc Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala 275 280 285	864
acc tgt gcc aag tgc cca ccc cac agc tac tct gtc tgg gaa gga gcc Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala 290 295 300	912
acc tcg tgc acc tgt gac cga ggc ttt ttc aga gct gac aac gat gct Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala 305 310 315 320	960
gcc tct atg ccc tgc acc cgt cca ccg tct gct ccc ctg aac ttg att Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile 325 330 335	1008
tca aat gtc aat gag aca tct gtg aac ttg gaa tgg agt agc cct cag Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln 340 345 350	1056
aat aca ggt ggc cgc cag gac att tcc tat aat gtg gta tgc aag aaa Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys 355 360 365	1104
tgt gga gct ggt gac ccc agc aag tgc cga ccc tgt gga agt ggg gtc Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val 370 375 380	1152
cac tac acc ccg cag cag aat ggc ttg aag acc acc aaa gtc tcc atc His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile 385 390 395 400	1200
act gac ctg cta gct cac acc aat tac acc ttt gaa atc tgg gct gtg Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val 405 410 415	1248
aat gga gtg tcc aaa tat aac cct aac cca gac caa tca gtt tct gtc Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val 420 425 430	1296
act gtg acc acc aac caa gca qca cca tca tcc att gct ttg gtc cag Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln 435 440 445	1344
gct aaa gaa gtc aca aga tac agt gtg gca ctg gct tgg ctg gaa cca Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro 450 455 460	1392
gat cgg ccc aat ggg gta atc ctg gaa tat gaa gtc aag tat tat gag Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu 465 470 475 480	1440

465	470	475	480	
aag gat cag aat gag cga agc tat cgt ata gtt cgg aca gct gcc agg				1488
Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg				
	485	490	495	
aac aca gat atc aaa ggc ctg aac cct ctc act tcc tat gtt ttc cac				1536
Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His				
	500	505	510	
gtg cga gcc agg aca gca gct ggc tat gga gac ttc agt gag ccc ttg				1584
Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu				
	515	520	525	
gag gtc aca acc aac aca gtg cct tcc cgg atc att gga gat ggg gct				1632
Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala				
	530	535	540	
aac tcc aca gtc ctt ctg gtc tct gtc tca ggc agt gtg gtg ctg gtg				1680
Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val				
	545	550	555	560
gta att ctc att gca gct ttt gtc atc agc cgg aga cgg agt aaa tac				1728
Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr				
	565	570	575	
agt aaa gcc aaa caa gaa gcg gat gaa gag aaa cat ttg aat caa ggt				1776
Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly				
	580	585	590	
gta aga aca tat gtg gac ccc ttt acg tac gaa gat ccc aac caa gca				1824
Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala				
	595	600	605	
gtt cga gag ttt gcc aaa gaa att gac gca tcc tgc att aag att gaa				1872
Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu				
	610	615	620	
aaa gtt ata gga gtt ggt gaa ttt ggt gag gta tgc agt ggg cgt ctc				1920
Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu				
	625	630	635	640
aaa gtg cct ggc aag aga gag atc tgt gtg gct atc aag act ctg aaa				1968
Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys				
	645	650	655	
gct ggt tat aca gac aaa cag agg aga gac ttc ctg agt gag gcc agc				2016
Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser				
	660	665	670	
atc atg gga cag ttt gac cat ccg aac atc att cac ttg gaa ggc gtg				2064
Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val				
	675	680	685	
gtc act aaa tgt aaa cca gta atg atc ata aca gag tac atg gag aat				2112
Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn				
	690	695	700	
ggc tcc ttg gat gca ttc ctc agg aaa aat gat ggc aga ttt aca gtc				2160
Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val				
	705	710	715	720
att cag ctg gtg ggc atg ctt cgt ggc att ggg tct ggg atg aag tat				2208

Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr	
725 730 735	
tta tct gat atg agc tat gtg cat cgt gat ctg gcc gca cgg aac atc	2256
Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile	
740 745 750	
ctg gtg aac agc aac ttg gtc tgc aaa gtg tct gat ttt ggc atg tcc	2304
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser	
755 760 765	
cga gtg ctt gag gat gat cgg gaa gca gct tac acc acc agg ggt ggc	2352
Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly	
770 775 780	
aag att cct atc cgg tgg act gcg cca gaa gca att gcc tat cgt aaa	2400
Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys	
785 790 795 800	
ttc aca tca gca agt gat gta tgg agc tat gga atc gtt atg tgg gaa	2448
Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu	
805 810 815	
gtg atg tog tac ggg gag agg ccc tat tgg gat atg tcc aat caa gat	2496
Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp	
820 825 830	
gtg att aaa gcc att gag gaa ggc tat cgg tta ccc cct cca atg gac	2544
Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Met Asp	
835 840 845	
tgc ccc att gca ctc cac cag ctg atg cta gac tgc tgg cag aag gag	2592
Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu	
850 855 860	
agg agc gac agg cct aaa ttt ggg cag att gtc aac atg ttg gac aaa	2640
Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys	
865 870 875 880	
ctc atc cgc aac ccc aac agc ttg aag agg aca ggg acg gag agc tcc	2688
Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser	
885 890 895	
aga cct aac act gcc ttg ttg gat cca agc tcc cct gaa ttc tct gct	2736
Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala	
900 905 910	
gtg gta tca gtg ggc gat tgg ctc cag gcc att aaa atg gac cgg tat	2784
Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr	
915 920 925	
aag gat aac ttc aca gct gct ggt tat acc aca cta gag gct gtg gtg	2832
Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val	
930 935 940	
cac gtg aac cag gac agt gtc cag gca atg cga acc caa atg cag cag	2880
His Val Asn Gln Asp Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln	
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Met His Gly Arg Met Val Pro Val	
965	

<210> 38

<211> 968

<212> PRT

<213> Pan troglodytes

<400> 38

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

Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
 225 230 235 240
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
 260 265 270
 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
 275 280 285
 Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
 290 295 300
 Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
 305 310 315 320
 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
 325 330 335
 Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
 340 345 350
 Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
 355 360 365
 Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
 370 375 380
 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile
 385 390 395 400
 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
 405 410 415
 Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val
 420 425 430
 Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
 435 440 445
 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
 450 455 460
 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
 465 470 475 480

Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
 485 490 495
 Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
 500 505 510
 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
 515 520 525
 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
 530 535 540
 Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
 545 550 555 560
 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
 565 570 575
 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
 580 585 590
 Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
 595 600 605
 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
 610 615 620
 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
 625 630 635 640
 Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
 660 665 670
 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
 675 680 685
 Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
 690 695 700
 Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
 705 710 715 720
 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr

725 730 735
 Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 740 745 750
 Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser
 755 760 765
 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
 770 775 780
 Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
 785 790 795 800
 Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
 805 810 815
 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
 820 825 830
 Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
 835 840 845
 Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
 850 855 860
 Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
 865 870 875 880
 Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser
 885 890 895
 Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
 900 905 910
 Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
 915 920 925
 Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
 930 935 940
 His Val Asn Gln Asp Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln
 945 950 955 960
 Met His Gly Arg Met Val Pro Val
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<210> 39

<211> 3015

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)..(3012)

<400> 39

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tta ttg gat tcc aga tct gtt cag gga gaa ctt ggg tgg ata gca agc Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser 35 40 45	144
cct ctg gaa gga ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat Pro Leu Glu Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn 50 55 60	192
aca cca atc cga acc tac caa gtg tgc aat gtg atg gaa ccc agc cag Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln 65 70 75 80	240
aat aac tgg cta cga act gat tgg atc acc cga gaa ggg gct cag agg Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg 85 90 95	288
gtg tat att gag att aaa ttc acc ttg agg gac tgc aat agt ctt ccg Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro 100 105 110	336
ggc gtc atg ggg act tgc aag gag acg ttt aac ctg tac tac tat gaa Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Glu 115 120 125	384
tca gac aac gac aaa gag cgt ttc atc aga gag aac cag ttt gtc aaa Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys 130 135 140	432
att gac acc att gct gct gat gag agc ttc acc caa gtg gac att ggt Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly 145 150 155 160	480
gac aga atc atg aag ctg aac acc gag atc cgg gat gta ggg cca tta Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu 165 170 175	528
agc aaa aag ggg ttt tac ctg gct ttt cag gat gtg ggg gcc tgc atc Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile 180 185 190	576
gcc ctg gta tca gtc cgt gtg ttc tat aaa aag tgt cca ctc aca gtc Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val 195 200 205	624

cgc aat ctg gcc cag ttt cct gac acc atc aca ggg gct gat acg tct Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser 210 215 220	672
tcc ctg gtg gaa gtt cga gcc tcc tgt gtc aac aac tca gaa gag aag Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys 225 230 235 240	720
gat gtg cca aaa atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro 245 250 255	768
att gcc aac tgc cta tgc aac gct ggg cat gag gag cgg agc gga gaa Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu 260 265 270	816
tgc caa gct tgc aaa att gga tat tac aag gct ctc tcc acg gat gcc Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala 275 280 285	864
acc tgt gcc aag tgc cca ccc cac agc tac tct gtc tgg gaa gga gcc Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala 290 295 300	912
acc tcg tgc acc tgt gac cga gcc ttt ttc aga gct gac aac gat gct Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala 305 310 315 320	960
gcc tct atg ccc tgc acc cgt cca ccg tct gct ccc ctg aac ttg att Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile 325 330 335	1008
tca aat gtc aat gag aca tct gtg aac ttg gaa tgg agt agc cct cag Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln 340 345 350	1056
aat aca ggt ggc cgc cag gac att tcc tat aat gtg gta tgc aag aaa Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys 355 360 365	1104
tgt gga gct ggt gac ccc agc aag tgc cga ccc tgt gga agt ggg gtc Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val 370 375 380	1152
cac tac acc ccg cag cag aat ggc ttg aag acc acc aaa gtc tcc atc His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile 385 390 395 400	1200
act gac ctc cta gct cac acc aat tac acc ttt gaa atc tgg gct gtg Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val 405 410 415	1248
aat gga gtg tcc aaa tat aac cct aac cca gac caa tca gtt tct gtc Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val 420 425 430	1296
act gtg acc acc aac caa gca gca cca tca tcc att gct ttg gtc cag Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln 435 440 445	1344
gct aaa gaa gtc aca aga tac agt gtg gca ctg gct tgg ctg gaa cca Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro 450 455 460	1392

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aag gat cag aat gag cga agc tat cgt ata gtt cgg aca gct gcc agg Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg 485 490 495	1488
aac aca gat atc aaa ggc ctg aac cct ctc act tcc tat gtt ttc cac Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His 500 505 510	1536
gtg cga gcc agg aca gca gct ggc tat gga gac ttc agt gag ccc ttg Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu 515 520 525	1584
gag gtc aca acc aac aca ggt aac aag gac cac cca gac tca gtc act Glu Val Thr Thr Asn Thr Gly Asn Lys Asp His Pro Asp Ser Val Thr 530 535 540	1632
tct gag cta att ttt gta tgt tta gct gta gtc act ggg gtc tct gtt Ser Glu Leu Ile Phe Val Cys Leu Ala Val Val Thr Gly Val Ser Val 545 550 555 560	1680
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gcc aaa caa gaa gcg gat gaa gag aaa cat ttg aat caa gct ccg cct Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Ala Pro Pro 580 585 590	1776
ccc tgg ttc aca cca ttc tcc cac ctc agc ctc ctg agt gta aga aca Pro Trp Phe Thr Pro Phe Ser His Leu Ser Leu Leu Ser Val Arg Thr 595 600 605	1824
tat gtg gac ccc ttt acg tac gaa gat ccc aac caa gca gtt cga gag Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu 610 615 620	1872
ttt gcc aaa gaa att gac gca tcc tgc att aag att gaa aaa gtt ata Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile 625 630 635 640	1920
gga gtt ggt gaa ttt ggt gag gta tgc agt ggg cgt ctc aaa gtg cct Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro 645 650 655	1968
ggc aag aga gag atc tgt gtg gct atc aag act ctg aaa gct ggt tat Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr 660 665 670	2016
aca gac aaa cag agg aga gac ttc ctg agt gag gcc aqc atc atg gga Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly 675 680 685	2064
cag ttt gac cat ccg aac atc att cac ttg gaa ggc gtg gtc act aaa Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val Thr Lys 690 695 700	2112
tgt aaa cca gta atg atc ata aca gag tac atg gag aat ggc tcc ttg Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu	2160

705	710	715	720	
gat gca ttc ctc agg aaa aat gat ggc aga ttt aca gtc att cag ctg				2208
Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln Leu	725	730	735	
gtg ggc atg ctt cgt ggc att ggg tct ggg atg aag tat tta tct gat				2256
Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp	740	745	750	
atg agc tat gtg cat cgt gat ctg gcc gca cgg aac atc ctg gtg aac				2304
Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn	755	760	765	
agc aac ttg gtc tgc aaa gtg tct gat ttt ggc atg tcc cga gtg ctt				2352
Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu	770	775	780	
gag gat gat cgg gaa gca gct tac acc acc agg ggt ggc aag att cct				2400
Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro	785	790	795	800
atc cgg tgg act gcg cca gaa gca att gcc tat cgt aaa ttc aca tca				2448
Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser	805	810	815	
gca agt gat gta tgg agc tat gga atc gtt atg tgg gaa gtg atg tog				2496
Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser	820	825	830	
tac ggg gag agg ccc tat tgg gat atg tcc aat caa gat gtg att aaa				2544
Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys	835	840	845	
gcc att gag gaa ggc tat cgg tta ccc cct cca atg gac tgc ccc att				2592
Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile	850	855	860	
gca ctc cac cag ctg atg cta gac tgc tgg cag aag gag agg agc gac				2640
Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp	865	870	875	880
agg cct aaa ttt ggg cag att gtc aac atg ttg gac aaa ctc atc cgc				2688
Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg	885	890	895	
aac ccc aac agc ttg aag agg aca ggg acg gag agc tcc agg caa gtg				2736
Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Gln Val	900	905	910	
gtg act cac tta aat tcc tgc ctt ttc atc aga ggc cac ttc atg gct				2784
Val Thr His Leu Asn Ser Cys Leu Phe Ile Arg Gly His Phe Met Ala	915	920	925	
ctc tgc aac ctg ggt gtg ggc gat tgg ctc cag gcc att aaa atg gac				2832
Leu Cys Asn Leu Gly Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp	930	935	940	
cgg tat aag gat aac ttc aca gct gct ggt tat acc aca cta gag gct				2880
Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala	945	950	955	960
gtg gtg cac gtg aac cag gag gac ctg gca aga att ggt atc aca gcc				2928
Val Val His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala	965	970	975	
atc acg cac cag aat aag att ttg agc agt gtc cag gca atg cga acc				2976
Ile Thr His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr	980	985	990	
caa atg cag cag atg cac ggc aga atg gtt ccc gtc tga				3015
Gln Met Gln Gln Met His Gly Arg Met Val Pro Val	995	1000		

<210> 40

<211> 1004

<212> PRT

<213> Pan troglodytes

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

Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
 180 185 190
 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205
 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
 210 215 220
 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
 225 230 235 240
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
 260 265 270
 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
 275 280 285
 Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
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 Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
 305 310 315 320
 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
 325 330 335
 Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
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 Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
 355 360 365
 Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
 370 375 380
 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile
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 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
 405 410 415
 Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val
 420 425 430

Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
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 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
 465 470 475 480
 Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
 485 490 495
 Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
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 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
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 Glu Val Thr Thr Asn Thr Gly Asn Lys Asp His Pro Asp Ser Val Thr
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 Ser Glu Leu Ile Phe Val Cys Leu Ala Val Val Thr Gly Val Ser Val
 545 550 555 560
 Leu Leu Ser Trp Phe Leu Leu Cys Lys Gln Arg Ser Lys Tyr Ser Lys
 565 570 575
 Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Ala Pro Pro
 580 585 590
 Pro Trp Phe Thr Pro Phe Ser His Leu Ser Leu Leu Ser Val Arg Thr
 595 600 605
 Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu
 610 615 620
 Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile
 625 630 635 640
 Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro
 645 650 655
 Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr
 660 665 670
 Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly
 675 680 685

Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val Thr Lys
 690 695 700
 Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu
 705 710 715 720
 Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln Leu
 725 730 735
 Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp
 740 745 750
 Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn
 755 760 765
 Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu
 770 775 780
 Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro
 785 790 795 800
 Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser
 805 810 815
 Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser
 820 825 830
 Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys
 835 840 845
 Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile
 850 855 860
 Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp
 865 870 875 880
 Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg
 885 890 895
 Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Gln Val
 900 905 910
 Val Thr His Leu Asn Ser Cys Leu Phe Ile Arg Gly His Phe Met Ala
 915 920 925
 Leu Cys Asn Leu Gly Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp
 930 935 940
 Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala
 945 950 955 960
 Val Val His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala
 965 970 975
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<210> 41

<211> 2958

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)..(2955)

<400> 41

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tta ttg gat tcc aga tct gtt cag gga gaa ctt ggg tgg ata gca agc Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser 35 40 45	144
cct ctg gaa gga ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn 50 55 60	192
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aat aac tgg cta cga act gat tgg atc acc cga gaa ggg gct cag agg Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg 85 90 95	288
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Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys 130 135 140	
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gac aga atc atg aag ctg aac acc gag atc cgg gat gta ggg cca tta Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu 165 170 175	528
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gcc ctg gta tca gtc cgt gtg ttc tat aaa aag tgt cca ctc aca gtc Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val 195 200 205	624
cgc aat ctg gcc cag ttt cct gac acc atc aca ggg gct gat acg tct Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser 210 215 220	672
tcc ctg gtg gaa gtt cga ggc tcc tgt gtc aac aac tca gaa gag aag Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys 225 230 235 240	720
gat gtg cca aaa atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro 245 250 255	768
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gga cag ttt gac cat ccg aac atc att cac ttg gaa ggc gtg gtc act Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val Thr 675 680 685	2064
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cct aac act gac ttg ttg gat cca agc tcc cct gaa ttc tot gct gtg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala Val 900 905 910	2736
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<210> 42

<211> 985

<212> PRT

<213> Pan troglodytes

<400> 42

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35     40     45

Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
50     55     60

Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
65     70     75     80

Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
85     90     95

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
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Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
130    135    140

Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
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Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
165    170    175

Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
180    185    190

Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
195    200    205

Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
210    215    220

Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
225    230    235    240

Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
245    250    255

Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
260    265    270

Cys Gln Ala Arg Pro Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr
275    280    285

Asp Ala Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu
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Gly Ala Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn
305    310    315    320

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325    330    335

Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser
340    345    350

Pro Gln Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys
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 Gly Val His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val
 385 390 395 400
 Ser Ile Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp
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 Ala Val Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val
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 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
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 His Thr Gln Pro Ile Leu Leu Leu Thr Pro Val Val Cys Ser Val Ile
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 Ser Asp Tyr Lys Cys Leu Asn Gly Thr Arg Thr Gly Glu Gln Arg Gly
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 Asp Arg Tyr Ile Gln Pro Thr Tyr His Val Tyr His Ser Gly Val Arg
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 Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg
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 Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val
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Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val
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 Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly
 645 650 655
 Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met
 660 665 670
 Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val Thr
 675 680 685
 Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser
 690 695 700
 Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln
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 Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser
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 Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val
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 Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg
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 Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys Leu
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 Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr His
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tgc gac gct gtc acc ggt tcc agg gtg tac ccc gcg aat gaa gtt acc      96
Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
           20           25           30

tta ctg gat tcc aga tct gtt cag gga gaa ctt ggg tgg ata gca agc      144
Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
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cct ctg gaa gga ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat      192
Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
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aca cca atc cga acc tac caa gtg tgc aat gtg atg gaa ccc agc cag      240
Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
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gta tat att gag att aaa ttc acc ttg agg gac tgc aac agt ctt cgg      336
Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
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ggc gtc atg ggg act tgc aag gag acg ttt aac ctg tac tac tat gaa      384
Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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tca gac aac gac aaa gag cgt ttc atc aga gag aac cag ttt gtc aaa      432
Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
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att gac acc att gct gct gat gag agc ttc acc caa gtg gac att ggt      480
Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
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Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
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Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
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gcc ctg gta tca gtc cgt gtg ttc tat aaa aag tgt cca ctc aca gtc      624
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
           195           200           205

cgc aat ctg gcc cag ttt ccc gac acc atc aca ggg gct gat acg tot      672
Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
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tcc ctg gtg gaa gtt cga gcc tcc tgt gtc aac aac tca gaa gag aag      720
Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
           225           230           235           240

gat gtg cca aaa atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc      768
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att ggc aac tgt cta tgc aac gct ggg cat gag gag cgg agc gga gaa      816
Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
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tgc caa gct tgc aaa att gga tat tac aag gct ctc tcc acg gat gcc      864
Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
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acc tgt gcc aag tgc cca ccc cac agc tac tct gtc tgg gaa gga gcc      912
Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
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acc tgc tgc acc tgt gac cga gcc ttt ttc aga gct gac aat gat gct      960
Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
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gcc tcc atg ccc tgc acc cgt cca cca tct gct ccc ctg aac ttg att      1008
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
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tcg aat gtc aac gag aca tct gtg aac ttg gaa tgg agt ago cct cag      1056

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Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val	
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His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile	
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acc gac ctc cta gct cat acc aat tac acc ttt gaa atc tgg gct gtg	1248
Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val	
405 410 415	
aat gga gtg tcc aaa tat aac cct agc cca gac caa tca gtt tcc gtc	1296
Asn Gly Val Ser Lys Tyr Asn Pro Ser Pro Asp Gln Ser Val Ser Val	
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act gtg aca acc aac caa gca gca cca tca tcc att gct ttg gtc cag	1344
Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln	
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Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro	
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Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg	
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Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His	
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580 585 590	

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 Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
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<213> Macaca mulatta

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 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
 50 55 60
 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
 65 70 75 80

Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
 85 90 95
 Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
 100 105 110
 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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 Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
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 225 230 235 240
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 260 265 270
 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
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 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile

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Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
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His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile
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Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
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Asn Gly Val Ser Lys Tyr Asn Pro Ser Pro Asp Gln Ser Val Ser Val
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Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
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Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
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Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
515          520          525

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Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
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Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
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Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
915 920 925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
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His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
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tta ctg gat tcc aga tct gtt cag gga gaa ctt ggg tgg ata gca agc 144
Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
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gat cgg ccc aat ggt gta atc ctg gaa tac gaa gtc aag tat tat gag Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu 465 470 475 480			1440
aag gat cag aat gag cga agc tat cgt ata gtt cgg aca gct gcc agg Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg 485 490 495			1488
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Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val 545 550 555 560	
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ggt cga gaa ttt gcc aaa gaa att gac gca tcc tgc att aag att gaa Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu 610 615 620	1872
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tta tct gat atg agc tat gtg cat cgt gat ctg gcc gca cgg aac atc Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 740 745 750	2256
ctg gtg aac agc aac ttg gtc tgc aaa gtg tct gat ttt ggc atg tcc Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser 755 760 765	2304
cga gtg ctt gag gat gat ccg gaa gca gct tac act acc agg ggt ggc Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly 770 775 780	2352
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 820 825 830
 gtg att aaa gcc att gag gaa ggc tat cgg tta ccc cct cca atg gac 2544
 Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
 835 840 845
 tgc ccc att gca ctc cac cag ctg atg cta gac tgc tgg cag aag gag 2592
 Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
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 aga agc gac agg cct aaa ttt ggg cag att gtc aac atg ttg gac aaa 2640
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 865 870 875 880
 ctc atc cgc aac ccc aac agc ttg aag agg aca ggg acg gag agc tcc 2688
 Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser
 885 890 895
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 Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
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 Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
 930 935 940
 cac gtg aac cag gac agc gtc cag gca atg cga acc caa atg cag cag 2880
 His Val Asn Gln Asp Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln
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 Met His Gly Arg Met Val Pro Val
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<211> 968

<212> PRT

<213> Macaca mulatta

<400> 46

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 35 40 45

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

Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
 305 310 315 320
 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
 325 330 335
 Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
 340 345 350
 Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
 355 360 365
 Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
 370 375 380
 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile
 385 390 395 400
 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
 405 410 415
 Asn Gly Val Ser Lys Tyr Asn Pro Ser Pro Asp Gln Ser Val Ser Val
 420 425 430
 Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
 435 440 445
 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
 450 455 460
 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
 465 470 475 480
 Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
 485 490 495
 Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
 500 505 510
 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
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 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
 530 535 540
 Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val

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Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
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Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
580          585          590
Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
595          600          605
Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
610          615          620
Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
625          630          635
Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
645          650          655
Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
660          665          670
Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
675          680          685
Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
690          695          700
Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
705          710          715          720
Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
725          730          735
Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
740          745          750
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser
755          760          765
Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
770          775          780
Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
785          790          795          800

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Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
805 810 815

Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
820 825 830

Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
835 840 845

Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
850 855 860

Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
865 870 875 880

Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser
885 890 895

Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
900 905 910

Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
915 920 925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
930 935 940

His Val Asn Gln Asp Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln
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<211> 2925

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Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr	
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cct ctg gaa gga ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn 50 55 60	192
aca cca atc cga acc tac caa gtg tgc aat gtg atg gaa ccc agc cag Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln 65 70 75 80	240
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850 855 860

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945 950 955 960

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<212> PRT

<213> Macaca mulatta

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 Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
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 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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 Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
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 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
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 Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
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 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
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 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
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 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
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Pro Pro Met Asp Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys
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Trp Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn
      850              855              860
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cac tat acc cca cag cag aat ggc ttg aag acc acc aaa gtc tcc atc His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile 385 390 395 400	1200
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gct aaa gaa gtc aca aga tac agt gtg gca ctg gct tgg ttg gaa cca Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro 450 455 460	1392
gat cgg ccc aat ggt gta atc ctg gaa tac gaa gtc aag tat tat gag Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu 465 470 475 480	1440

465	470	475	480	
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Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg	485	490	495	
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Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His	500	505	510	
gtg cga gcc agg aca gca gct ggc tat gga gac ttc agt gag ccc ttg				1584
Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu	515	520	525	
gag gtc aca acc aac aca gtg cct tcc cgg atc att gga gat ggg gcc				1632
Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala	530	535	540	
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Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val	545	550	555	560
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Val Ile Leu Ile Ala Ala Phe Phe Ser Cys Cys His Ser Gly Asp Gln	565	570	575	
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Pro Leu Met Ser Leu Ala Val Val Thr Gly Val Ser Val Leu Leu Ser	580	585	590	
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Cys Lys Tyr Ser Lys Ala Lys Gln Glu Ala Asp Glu Lys His Leu	595	600	605	
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Asn Gln Gly His Val Tyr Tyr Leu Gly Val Arg Thr Tyr Val Asp Pro	610	615	620	
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Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu Phe Ala Lys Glu	625	630	635	640
att gac gca tcc tgc att aag att gaa aaa gtt ata gga gtt ggt gaa				1968
Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile Gly Val Gly Glu	645	650	655	
ttt ggt gag gta tgc agc ggg cgt ctc aaa gtg cct ggc aag aga gag				2016
Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro Gly Lys Arg Glu	660	665	670	
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Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Asp Lys Gln	675	680	685	
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Pro Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Cys Lys Pro Val	705	710	715	720
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740 745 750

cgt ggc att ggg tct ggg atg aag tat tta tct gat atg agc tat gtg 2304
Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp Met Ser Tyr Val
755 760 765

cat cgt gat ctg gcc gca cgg aac atc ctg gtg aac agc aac ttg gtc 2352
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785 790 795 800

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Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
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Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg
835 840 845

ccc tac tgg gat atg tcc aat caa gat gtg att aaa gcc att gag gaa 2592
Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu
850 855 860

ggc tat cgg tta ccc cct cca atg gac tgc ccc att gca ctc cac cag 2640
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865 870 875 880

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Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe
885 890 895

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Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser
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915 920 925

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Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val Gly Asp Trp
930 935 940

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945 950 955 960

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Gly Tyr Thr Thr Leu Glu Ala Val Val His Val Asn Gln Glu Asp Leu
965 970 975

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Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys Ile Leu Ser
980 985 990

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 Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
 35 40 45
 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
 50 55 60
 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
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 Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
 85 90 95
 Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
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 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
 115 120 125
 Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
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 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
 145 150 155 160
 Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
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Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
 180 185 190
 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205
 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
 210 215 220
 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
 225 230 235 240
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
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 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
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 Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
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 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
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 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
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 Asn Gly Val Ser Lys Tyr Asn Pro Ser Pro Asp Gln Ser Val Ser Val
 420 425 430

Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
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 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
 465 470 475 480
 Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
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 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
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 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
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 Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
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 Val Ile Leu Ile Ala Ala Phe Phe Ser Cys Cys His Ser Gly Asp Gln
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 Pro Leu Met Ser Leu Ala Val Val Thr Gly Val Ser Val Leu Leu Ser
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 Cys Lys Tyr Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu
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 Asn Gln Gly His Val Tyr Tyr Leu Gly Val Arg Thr Tyr Val Asp Pro
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 Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu Phe Ala Lys Glu
 625 630 635 640
 Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile Gly Val Gly Glu
 645 650 655
 Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro Gly Lys Arg Glu
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 Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Asp Lys Gln

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Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Ala Phe Leu 725 730 735		
Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln Leu Val Gly Met Leu 740 745 750		
Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp Met Ser Tyr Val 755 760 765		
His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val 770 775 780		
Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu Asp Asp Pro 785 790 795 800		
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Gly Tyr Thr Thr Leu Glu Ala Val Val His Val Asn Gln Glu Asp Leu 965 970 975		
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Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
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Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
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Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
50     55     60

Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
65     70     75     80

Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
85     90     95

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
100    105    110

Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
115    120    125

Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
130    135    140

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

Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
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Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
180    185    190

Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
195    200    205

Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
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Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
225    230    235    240

Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
245    250    255

Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
260    265    270

Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
275    280    285

Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
290    295    300

Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
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Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
325    330    335

Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
340    345    350

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Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
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Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
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His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile
 385 390 395 400

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

Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
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Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
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Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
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Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
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Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
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Glu Val Thr Thr Asn Thr Glu Ser Phe Lys Ser Asn Gly Ala Asn Ser
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Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val Val Ile
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Leu Ile Ala Ala Phe Val Ile Ser Arg Ser Cys Gln Tyr Arg Thr Thr
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His Ser Val Gln Ala Ser Ile Leu His Cys Pro Thr Tyr His Val Tyr
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Tyr Leu Gly Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro
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Asn Gln Ala Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile
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 Lys Ile Glu Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser
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 Gly Arg Leu Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys
 645 650 655
 Thr Leu Lys Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser
 660 665 670
 Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu
 675 680 685
 Glu Gly Val Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr
 690 695 700
 Met Glu Asn Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg
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 Met Lys Tyr Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala
 740 745 750
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 Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met
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 915 920 925
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 930 935 940
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 945 950 955 960
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 <213> Macaca mulatta

<220>
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 <222> (172)..(2955)

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cttggttgga tagcaagccc tctggaagga ggggtggagg aagtgagtat c atg gat      177
                                     Met Asp
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gaa aaa aat aca cca atc cga acc tac caa gtg tgc aat gtg atg gaa      225
Glu Lys Asn Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu
      5              10              15

ccc agc cag aat aac tgg cta cga act gat tgg atc acc cga gaa ggg      273
Pro Ser Gln Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly
      20              25              30

gct cag agg gta tat att gag att aaa ttc acc ttg agg gac tgc aac      321

Ala Gln Arg Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn
  35              40              45              50

agt ctt ccg ggc gtc atg ggg act tgc aag gag acg ttt aac ctg tac      369
Ser Leu Pro Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr
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tac tat gaa tca gac aac gac aaa gag cgt ttc atc aga gag aac cag      417
Tyr Tyr Glu Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln
      70              75              80

ttt gtc aaa att gac acc att gct gct gat gag agc ttc acc caa gtg      465
Phe Val Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val
      85              90              95

gac att ggt gac aga atc atg aag ctg aac acc gag atc cgg gat gta      513
Asp Ile Gly Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val
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ggg cca tta agc aaa aag ggg ttt tac ctg gct ttt cag gat gtg ggg      561
Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly
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gcc tgc atc gcc ctg gta tca gtc cgt gtg ttc tat aaa aag tgt cca      609
Ala Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro
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ctc aca gtc cgc aat ctg gcc cag ttt ccc gac acc atc aca ggg gct      657
Leu Thr Val Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala
      150             155             160

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

gaa gag aag gat gtg cca aaa atg tac tgt ggg gca gat ggt gaa tgg      753
Glu Glu Lys Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp
      180             185             190

ctg gta ccc att ggc aac tgt cta tgc aac gct ggg cat gag gag cgg      801
Leu Val Pro Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg
      195             200             205             210

agc gga gaa tgc caa gct tgc aaa att gga tat tac aag gct ctc tcc      849
Ser Gly Glu Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser
      215             220             225

acg gat gcc acc tgt gcc aag tgc cca ccc cac agc tac tot gtc tgg      897
Thr Asp Ala Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp
      230             235             240

gaa gga gcc acc tcg tgc acc tgt gac cga ggc ttt ttc aga gct gac      945
Glu Gly Ala Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp
      245             250             255

aat gat gct gcc tcc atg ccc tgc acc cgt cca cca tct gct ccc ctg      993
Asn Asp Ala Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu
      260             265             270

aac ttg att tcg aat gtc aac gag aca tct gtg aac ttg gaa tgg agt      1041
Asn Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser
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gct gtg gtg cac gtg aac cag gag gac ctg gca aga att ggt atc aca Ala Val Val His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr 885 890 895			2865
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<211> 927

<212> PRT

<213> Macaca mulatta

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 Cys Asn Ser Leu Pro Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn
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 Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu
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 115 120 125
 Val Gly Ala Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys
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 Cys Pro Leu Thr Val Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr
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 Gly Ala Asp Thr Ser Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn
 165 170 175
 Asn Ser Glu Glu Lys Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly
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 Glu Trp Leu Val Pro Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu
 195 200 205
 Glu Arg Ser Gly Glu Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala
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Leu Ser Thr Asp Ala Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser
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 Val Trp Glu Gly Ala Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg
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 Ala Asp Asn Asp Ala Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala
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 275 280 285
 Trp Ser Ser Pro Gln Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn
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 Gln Ser Val Ser Val Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser
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 Phe Ser Glu Pro Leu Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile
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 Cys Ser Gly Arg Leu Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala
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 Ile Lys Thr Leu Lys Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe
 595 600 605
 Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile
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 Pro Pro Pro Met Asp Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp
 785 790 795 800
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 Pro Glu Phe Ser Ala Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile
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Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser				
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ccg ctg gaa gga ggg tgg gag gaa gtg agc ata atg gat gag aag aac				192
Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn				
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Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro				
100		105	110	
ggc gtc atg gga act tgc aaa gag act ttc aac ctc tat tac tat gaa				384
Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Glu				
115		120	125	
tca aac aac gac aag gag cgt ttt att cga gag agc cag ttt gcc aag				432
Ser Asn Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Ala Lys				
130		135	140	
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Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly				
145		150	155	160
gac agg atc atg aag ctg aat aca gag gtg cgg gac gtg ggg cct ctc				528
Asp Arg Ile Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu				
165		170	175	
agc aag aaa ggg ttt tac ttg gct ttc cag gac gtc ggt gcc tgc att				576
Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile				
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gct ttg gtg tct gtt cgt gtc ttc tat aag aag tgc cca ctg aca gtt				624
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val				
195		200	205	
cga aac ctg gca cag ttt cca gac acc att act ggg gct gat aca tcc				672
Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser				
210		215	220	
tct ctg gtg gag gtt cgt ggc tcc tgt gtc aac aac tcg gaa gag aag				720
Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys				
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gac gtg cca aaa atg tac tgc ggg gca gat ggt gaa tgg ctg gta ccc				768
Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro				
245		250	255	
att ggc aac tgt ctg tgc aat gct ggc tat gaa gaa cgc aat ggt gaa				816

Ile Gly Asn Cys Leu Cys Asn Ala Gly Tyr Glu Glu Arg Asn Gly Glu	
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Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Val	
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gca tgt gcc aaa tgc cgc cct cac agc tac tcc atc tgg gaa gcc tct	912
Ala Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Ile Trp Glu Gly Ser	
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acc tcc tgc acc tgt gat cgg ggc ttc ttc cga gca gaa aat gat gct	960
Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Glu Asn Asp Ala	
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gca tcc atg ccc tgc act cgc cct cca tcc gca ccc cag aac ctg att	1008
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Gln Asn Leu Ile	
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Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ala Pro Gln	
340 345 350	
aac aag gga gga cgg gac gac atc tcc tac aac gtg gtg tgc aag cgc	1104
Asn Lys Gly Gly Arg Asp Asp Ile Ser Tyr Asn Val Val Cys Lys Arg	
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tgc ggg gca ggg gag ccc agc cac tgc cgg tcc tgt gcc agt ggt gta	1152
Cys Gly Ala Gly Glu Pro Ser His Cys Arg Ser Cys Gly Ser Gly Val	
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cat ttc agc ccc cag cag aac ggg ctg aaa acc acg aag gtt tcc atc	1200
His Phe Ser Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile	
385 390 395 400	
act gac ctc ctg gca cac acc aac tac acc ttt gag gtc tgg gca gtg	1248
Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Val Trp Ala Val	
405 410 415	
aat gga gtg tcc aag cac aac ccc agc cag gac caa gct gtg tca gtc	1296
Asn Gly Val Ser Lys His Asn Pro Ser Gln Asp Gln Ala Val Ser Val	
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Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Pro Ile Ala Leu Ile Gln	
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gct aaa gag ata acg agg cac agc gtt gcc ttg gcc tgg ctg gaa cct	1392
Ala Lys Glu Ile Thr Arg His Ser Val Ala Leu Ala Trp Leu Glu Pro	
450 455 460	
gac agg ccc aat gga gtc atc ctg gag tat gaa gtc aag tac tat gaa	1440
Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu	
465 470 475 480	
aag gac caa aac gag cgc agc tat cgc att gtg aag aca gcc tcc agg	1488
Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Lys Thr Ala Ser Arg	
485 490 495	
aat act gac atc aaa ggt ttg aac ccc ctg act tca tat gta ttt cat	1536
Asn Thr Asp Ile Lys Gly Leu Asn Asn Pro Leu Thr Ser Tyr Val Phe His	
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agt aaa gct aag caa gag gca gat gag gag aaa cat ttg aac caa ggt Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly 580 585 590	1776
gtc aga aca tat gtg gat cct ttt aca tat gag gat cca aat caa gct Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala 595 600 605	1824
gtg agg gaa ttt gcc aaa gaa att gat gcc tcc tgc ata aag att gag Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu 610 615 620	1872
aaa gtt att ggt gtg ggg gaa ttt ggt gaa gta tgc agt gga cgt ctc Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu 625 630 635 640	1920
aaa gtt cca gga aaa aga gaa atc tgt gtg gct atc aag act ctg aaa Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys 645 650 655	1968
gct ggt tac act gac aaa caa cgg aga gac ttc ctg agt gag gcc agc Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser 660 665 670	2016
atc atg gga caa ttt gac cac ccc aat atc atc cac ttg gaa ggc gtt Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val 675 680 685	2064
gtt act aaa tgt aaa cca gta atg atc ata act gag tac atg gag aat Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn 690 695 700	2112
ggc tcc ttg gat gcc ttc ctc cgg aag aat gat ggc aga ttt aca gta Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val 705 710 715 720	2160
atc cag ttg gtg ggg atg ctt cgt ggc atc ggc tca gga atg aag tat Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr 725 730 735	2208
ctg tct gac atg agc tat gtg cat cgg gat cta gct gct cga aac ata Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 740 745 750	2256
ctg gtc aac agc aac ttg gtc tgc aaa gtg tct gac ttc ggc atg tcc Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser 755 760 765	2304

cgt gtc ctg gaa gat gac cct gag gca gct tat acc aca cgg ggt ggc Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly 770 775 780	2352
aag atc cct atc cga tgg act gca cca gag gca att gcc tac cgt aaa Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys 785 790 795 800	2400
ttt aca tcg gct agt gac gtg tgg agc tat ggc atc gtc atg tgg gaa Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu 805 810 815	2448
gtg atg tcc tat gga gag aga cct tac tgg gat atg tcc aat caa gac Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp 820 825 830	2496
gtt att aaa gcc att gag gaa ggg tat cgg ttg cca ccc cca atg gac Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp 835 840 845	2544
tgc ccc att gct ctc cat cag ctg atg tta gac tgc tgg cag aag gaa Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu 850 855 860	2592
cgc agc gac aga cct aaa ttt gga cag att gtc aac atg ctg gac aaa Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys 865 870 875 880	2640
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aag gat aac ttc aca gct gct ggc tat acc acc cta gag gct gtg gtg Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val 930 935 940	2832
cat atg aac cag gac gac ctg gcc agg atc ggg atc act gcc atc aca His Met Asn Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr 945 950 955 960	2880
cac cag aac aag atc ttg agc agc gtt caa gcc atg cgc agc caa atg His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Ser Gln Met 965 970 975	2928
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<211> 986

<212> PRT

<213> Gallus gallus

<400> 58

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

245	250	255
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Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Val 275 280 285		
Ala Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Ile Trp Glu Gly Ser 290 295 300		
Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Glu Asn Asp Ala 305 310 315 320		
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Gln Asn Leu Ile 325 330 335		
Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ala Pro Gln 340 345 350		
Asn Lys Gly Gly Arg Asp Asp Ile Ser Tyr Asn Val Val Cys Lys Arg 355 360 365		
Cys Gly Ala Gly Glu Pro Ser His Cys Arg Ser Cys Gly Ser Gly Val 370 375 380		
His Phe Ser Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile 385 390 395 400		
Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Val Trp Ala Val 405 410 415		
Asn Gly Val Ser Lys His Asn Pro Ser Gln Asp Gln Ala Val Ser Val 420 425 430		
Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Pro Ile Ala Leu Ile Gln 435 440 445		
Ala Lys Glu Ile Thr Arg His Ser Val Ala Leu Ala Trp Leu Glu Pro 450 455 460		
Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu 465 470 475 480		
Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Lys Thr Ala Ser Arg 485 490 495		

Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
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 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Gly Pro Phe
 515 520 525
 Glu Phe Thr Thr Asn Thr Val Pro Ser Pro Ile Ile Gly Asp Gly Thr
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 Asn Pro Thr Val Leu Leu Val Ser Val Ala Gly Ser Val Val Leu Val
 545 550 555 560
 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
 565 570 575
 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
 580 585 590
 Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
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 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
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 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
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 Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
 660 665 670
 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
 675 680 685
 Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
 690 695 700
 Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
 705 710 715 720
 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
 725 730 735
 Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 740 745 750

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser
 755 760 765
 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
 770 775 780
 Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
 785 790 795 800
 Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
 805 810 815
 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
 820 825 830
 Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
 835 840 845
 Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
 850 855 860
 Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
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 Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Ser Glu Ser Ser
 885 890 895
 Arg Pro Ser Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
 900 905 910
 Val Val Ser Val Ser Asp Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr
 915 920 925
 Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
 930 935 940
 His Met Asn Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
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 Gln Gln Met His Gly Arg Met Val Pro Val
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<211> 2820

<212> DNA

<213> Gallus gallus

<400> 59

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<211> 849

<212> PRT

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<400> 60

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 Val Arg Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe
 35 40 45

 Gln Asp Val Gly Ala Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr
 50 55 60

 Lys Lys Cys Pro Leu Thr Val Arg Asn Leu Ala Gln Phe Pro Asp Thr
 65 70 75 80

 Ile Thr Gly Ala Asp Thr Ser Ser Leu Val Glu Val Arg Gly Ser Cys
 85 90 95

 Val Asn Asn Ser Glu Glu Lys Asp Val Pro Lys Met Tyr Cys Gly Ala
 100 105 110

 Asp Gly Glu Trp Leu Val Pro Ile Gly Asn Cys Leu Cys Asn Ala Gly
 115 120 125

 Tyr Glu Glu Arg Asn Gly Glu Cys Gln Ala Cys Lys Ile Gly Tyr Tyr
 130 135 140

 Lys Ala Leu Ser Thr Asp Val Ala Cys Ala Lys Cys Pro Pro His Ser
 145 150 155 160

 Tyr Ser Ile Trp Glu Gly Ser Thr Ser Cys Thr Cys Asp Arg Gly Phe
 165 170 175

 Phe Arg Ala Glu Asn Asp Ala Ala Ser Met Pro Cys Thr Arg Pro Pro
 180 185 190

 Ser Ala Pro Gln Asn Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn
 195 200 205

 Leu Glu Trp Ser Ala Pro Gln Asn Lys Gly Gly Arg Asp Asp Ile Ser
 210 215 220

 Tyr Asn Val Val Cys Lys Arg Cys Gly Ala Gly Glu Pro Ser His Cys
 225 230 235 240

 Arg Ser Cys Gly Ser Gly Val His Phe Ser Pro Gln Gln Asn Gly Leu
 245 250 255

 Lys Thr Thr Lys Val Ser Ile Thr Asp Leu Leu Ala His Thr Asn Tyr
 260 265 270

 Thr Phe Glu Val Trp Ala Val Asn Gly Val Ser Lys His Asn Pro Ser
 275 280 285

 Gln Asp Gln Ala Val Ser Val Thr Val Thr Thr Asn Gln Ala Ala Pro
 290 295 300

 Ser Pro Ile Ala Leu Ile Gln Ala Lys Glu Ile Thr Arg His Ser Val
 305 310 315 320

 Ala Leu Ala Trp Leu Glu Pro Asp Arg Pro Asn Gly Val Ile Leu Glu
 325 330 335

Tyr Glu Val Lys Tyr Tyr Glu Lys Asp Gln Asn Glu Arg Thr Tyr Arg
 340 345 350
 Ile Val Lys Thr Ala Ser Arg Asn Thr Asp Ile Lys Gly Leu Asn Pro
 355 360 365
 Leu Thr Ser Tyr Val Phe His Val Arg Ala Arg Thr Ala Ala Gly Tyr
 370 375 380
 Gly Asp Phe Ser Gly Pro Phe Glu Phe Thr Thr Asn Thr Val Pro Ser
 385 390 395 400
 Pro Ile Ile Gly Asp Gly Thr Asn Pro Thr Val Leu Leu Val Ser Val
 405 410 415
 Ala Gly Ser Val Val Leu Val Val Ile Leu Ile Ala Ala Phe Val Ile
 420 425 430
 Ser Arg Arg Arg Ser Lys Tyr Ser Lys Ala Lys Gln Glu Ala Asp Glu
 435 440 445
 Glu Lys His Leu Asn Gln Gly Val Arg Thr Tyr Val Asp Pro Phe Thr
 450 455 460
 Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu Phe Ala Lys Glu Ile Asp
 465 470 475 480
 Ala Ser Cys Ile Lys Ile Glu Lys Val Ile Gly Val Gly Glu Phe Gly
 485 490 495
 Glu Val Cys Ser Gly Arg Leu Lys Val Pro Gly Lys Arg Glu Ile Cys
 500 505 510
 Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Asp Lys Gln Arg Arg
 515 520 525
 Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn
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 Ile Ile His Leu Glu Gly Val Val Thr Lys Cys Lys Pro Val Met Ile
 545 550 555 560
 Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Ala Phe Leu Arg Lys
 565 570 575
 Asn Asp Gly Arg Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly
 580 585 590

Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp Met Ser Tyr Val His Arg
595 600 605

Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys
610 615 620

Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu Asp Asp Pro Glu Ala
625 630 635 640

Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro
645 650 655

Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser
660 665 670

Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr
675 680 685

Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu Gly Tyr
690 695 700

Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala Leu His Gln Leu Met
705 710 715 720

Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe Gly Gln
725 730 735

Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser Leu Lys
740 745 750

Arg Thr Gly Ser Glu Ser Ser Arg Pro Ser Thr Ala Leu Leu Asp Pro
755 760 765

Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val Ser Asp Trp Leu Gln
770 775 780

Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr
785 790 795 800

Thr Thr Leu Glu Ala Val Val His Met Asn Gln Asp Asp Leu Ala Arg
805 810 815

Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys Ile Leu Ser Ser Val
820 825 830

Gln Ala Met Arg Ser Gln Met Gln Gln Met His Gly Arg Met Val Pro
835 840 845

Val

<210> 61

<211> 2961

<212> DNA

<213> Xenopus laevis

<220>

<221> CDS

<222> (1)..(2958)

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

Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile	
180 185 190	
gcc ctt gtg tct gtc cga gtg ttc tac aag aag tgt cca ttg act gta	624
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val	
195 200 205	
aga aac ttg gca cag ttc cct gac acc att aca ggt tca gac acc tct	672
Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ser Asp Thr Ser	
210 215 220	
tct ttg gtg gaa gtt cga ggc tct tgt gta gac aac tca gaa gag aaa	720
Ser Leu Val Glu Val Arg Gly Ser Cys Val Asp Asn Ser Glu Glu Lys	
225 230 235 240	
gat gtg cct aag atg tac tgt ggt gct gat gga gag tgg ctg gtg ccc	768
Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro	
245 250 255	
att gga aac tgc tta tgt aac gct ggg ttt gag gag cac aat gga gga	816
Ile Gly Asn Cys Leu Cys Asn Ala Gly Phe Glu Glu His Asn Gly Gly	
260 265 270	
tgc caa gcc tgc aaa gtt gga tac tac aaa gcc ctc tca aca gat gca	864
Cys Gln Ala Cys Lys Val Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala	
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gct tgc tcc aag tgt ccc cca cac agt tat gct ctc cgg gaa gcc tca	912
Ala Cys Ser Lys Cys Pro Pro His Ser Tyr Ala Leu Arg Glu Gly Ser	
290 295 300	
acc tcc tgc acc tgt gac cgt ggc tat ttt cga gct gac act gac cgg	960
Thr Ser Cys Thr Cys Asp Arg Gly Tyr Phe Arg Ala Asp Thr Asp Pro	
305 310 315 320	
gct tct atg ccc tgc act aga ccc cca tct gct cct cag aac cta atc	1008
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Gln Asn Leu Ile	
325 330 335	
tca aac gtc aat gag aca tct gtg aat ttg gag tgg agt cgg cca caa	1056
Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Pro Pro Gln	
340 345 350	
aat tct ggt gga agg cct gat gtc tcc tac aat ttg gtc tgt aaa agg	1104
Asn Ser Gly Gly Arg Pro Asp Val Ser Tyr Asn Leu Val Cys Lys Arg	
355 360 365	
tgc ggc tct gac ctg act cgc tgt cgg cct tgt ggc agt gga gtg cac	1152
Cys Gly Ser Asp Leu Thr Arg Cys Arg Pro Cys Gly Ser Gly Val His	
370 375 380	
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Tyr Ser Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile Asn	
385 390 395 400	
gac ctg caa gcc cat act aac tac acc ttt gag gtc tgg gcc att aat	1248
Asp Leu Gln Ala His Thr Asn Tyr Thr Phe Glu Val Trp Ala Ile Asn	
405 410 415	
ggg gtc tcc aag cag aac cct gaa caa gat cag gct gtg tca gtt act	1296
Gly Val Ser Lys Gln Asn Pro Glu Gln Asp Gln Ala Val Ser Val Thr	
420 425 430	

gtg acc acc aac caa gct gct cct tca act gta acc cag ata cag cca Val Thr Thr Asn Gln Ala Ala Pro Ser Thr Val Thr Gln Ile Gln Pro 435 440 445	1344
aaa gag atc acc agg cac agt gtg tct ttg act tgg cca gag cct gag Lys Glu Ile Thr Arg His Ser Val Ser Leu Thr Trp Pro Glu Pro Glu 450 455 460	1392
cga gcc aat ggg gtc atc ctg gaa tac gaa gtc aag tat tat gag aag Arg Ala Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys 465 470 475 480	1440
gac cag aat gag cgt agt tat cga att gtt aag acg gcc tcg cga agt Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Lys Thr Ala Ser Arg Ser 485 490 495	1488
gca gac atc aaa ggt ctc aac ccc ctt act ggt tat gtg ttc cat gtt Ala Asp Ile Lys Gly Leu Asn Pro Leu Thr Gly Tyr Val Phe His Val 500 505 510	1536
cgt gct cgg aca gct gca gga tat ggg gag ttc agt gga ccc ttt gag Arg Ala Arg Thr Ala Ala Gly Tyr Gly Glu Phe Ser Gly Pro Phe Glu 515 520 525	1584
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ccc act gtg ctt ttg gtg tcc gtg gct gga agc att gtc ctt gtg gtc Pro Thr Val Leu Leu Val Ser Val Ala Gly Ser Ile Val Leu Val Val 545 550 555 560	1680
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aaa gcc aag cag gaa gca gac gag gaa aaa cat tta aac caa gga gta Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly Val 580 585 590	1776
aag act tat gtg gac cca ttt aca tat gaa gat cct aac cag gct gtc Lys Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val 595 600 605	1824
cgc gaa ttt gca aag gaa atc gat gcc tct tgt att aag atc gaa aaa Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys 610 615 620	1872
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gtc cct gga aag aga gag att tat gtt gca att aag acc ctg aaa gct Val Pro Gly Lys Arg Glu Ile Tyr Val Ala Ile Lys Thr Leu Lys Ala 645 650 655	1968
ggt tac acc gat aag cag agg aga gac ttt ctc agt gag gcc agc atc Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile 660 665 670	2016
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acc aaa tgc aag cca gtg atg ata atc acc gag tac atg gag aac gga Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly 690 695 700	2112
tcc ttg gat gca ttc ctt cgg aag aat gat ggt cgg ttt aca gta ata Ser Leu Asp Ala Phe Met Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile 705 710 715 720	2160
cag ctt gtg gga atg ctg cgt ggc att ggg tct gga atg aaa tac ctt Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu 725 730 735	2208
tcg gac atg agt tat gtg cac cgg gac cta gct gct cgt aat atc ctt Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu 740 745 750	2256
gtg aac agc aac cta gtc tgt aag gtc tct gac ttt ggc atg tct cgg Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg 755 760 765	2304
gtg ctg gaa gat gac cct gaa gca gcc tac aca acc agg ggt ggc aag Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys 770 775 780	2352
atc cca atc cga tgg act gca cca gaa gct att gca tac agg aaa ttc Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe 785 790 795 800	2400
act tct gct agt gat gtc tgg agc tat ggc att gtc atg tgg gaa gtc Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val 805 810 815	2448
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cct att gca ctg cat cag ctc atg ttg gac tgc tgg cag aag gat cgt Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg 850 855 860	2592
agt gac cga cca aaa ttt ggg cag ata gtc agc atg ctg gat aaa ctc Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Ser Met Leu Asp Lys Leu 865 870 875 880	2640
atc agg aac cca aac agt ttg aaa agg act ggg ctg gag aat tca agc Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Leu Glu Asn Ser Ser 885 890 895	2688
aga aca aat acg gct ctg ctg gac ccc agt tcg cct gaa tgg tcc cag Arg Thr Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Trp Ser Gln 900 905 910	2736
gtg gct tct gtg ctt gat tgg ctg cag gcc atc aaa atg gaa aga tac Val Ala Ser Val Leu Asp Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr 915 920 925	2784
aaa gat aac ttc aca gca gcc gga tac acc agc ttg gaa gca gtc gtg Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Ser Leu Glu Ala Val Val 930 935 940	2832
cat gtg aat caa gat gac ttg acc agg att ggc att agt tcc cct toa His Val Asn Gln Asp Asp Leu Thr Arg Ile Gly Ile Ser Ser Pro Ser 945 950 955 960	2880
cac cag aac aag atc ctg agc agc gtc caa gga atg agg acc cag ttg His Gln Asn Lys Ile Leu Ser Ser Val Gln Gly Met Arg Thr Gln Leu 965 970 975	2928
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<212> PRT

<213> Xenopus laevis

<400> 62

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

165	170	175
Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile 180 185 190		
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val 195 200 205		
Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ser Asp Thr Ser 210 215 220		
Ser Leu Val Glu Val Arg Gly Ser Cys Val Asp Asn Ser Glu Glu Lys 225 230 235 240		
Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro 245 250 255		
Ile Gly Asn Cys Leu Cys Asn Ala Gly Phe Glu Glu His Asn Gly Gly 260 265 270		
Cys Gln Ala Cys Lys Val Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala 275 280 285		
Ala Cys Ser Lys Cys Pro Pro His Ser Tyr Ala Leu Arg Glu Gly Ser 290 295 300		
Thr Ser Cys Thr Cys Asp Arg Gly Tyr Phe Arg Ala Asp Thr Asp Pro 305 310 315 320		
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Gln Asn Leu Ile 325 330 335		
Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Pro Pro Gln 340 345 350		
Asn Ser Gly Gly Arg Pro Asp Val Ser Tyr Asn Leu Val Cys Lys Arg 355 360 365		
Cys Gly Ser Asp Leu Thr Arg Cys Arg Pro Cys Gly Ser Gly Val His 370 375 380		
Tyr Ser Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile Asn 385 390 395 400		
Asp Leu Gln Ala His Thr Asn Tyr Thr Phe Glu Val Trp Ala Ile Asn 405 410 415		

Gly Val Ser Lys Gln Asn Pro Glu Gln Asp Gln Ala Val Ser Val Thr
 420 425 430
 Val Thr Thr Asn Gln Ala Ala Pro Ser Thr Val Thr Gln Ile Gln Pro
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 Lys Glu Ile Thr Arg His Ser Val Ser Leu Thr Trp Pro Glu Pro Glu
 450 455 460
 Arg Ala Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys
 465 470 475 480
 Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Lys Thr Ala Ser Arg Ser
 485 490 495
 Ala Asp Ile Lys Gly Leu Asn Pro Leu Thr Gly Tyr Val Phe His Val
 500 505 510
 Arg Ala Arg Thr Ala Ala Gly Tyr Gly Glu Phe Ser Gly Pro Phe Glu
 515 520 525
 Phe Thr Thr Asn Thr Val Pro Ser Pro Met Ile Gly Glu Gly Thr Ser
 530 535 540
 Pro Thr Val Leu Leu Val Ser Val Ala Gly Ser Ile Val Leu Val Val
 545 550 555 560
 Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr Ser
 565 570 575
 Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly Val
 580 585 590
 Lys Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val
 595 600 605
 Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys
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 Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys
 625 630 635 640
 Val Pro Gly Lys Arg Glu Ile Tyr Val Ala Ile Lys Thr Leu Lys Ala
 645 650 655
 Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile
 660 665 670

Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val
675 680 685

Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly
690 695 700

Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile
705 710 715 720

Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu
725 730 735

Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu
740 745 750

Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg
755 760 765

Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys
770 775 780

Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe
785 790 795 800

Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val
805 810 815

Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val
820 825 830

Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys
835 840 845

Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg
850 855 860

Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Ser Met Leu Asp Lys Leu
865 870 875 880

Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Leu Glu Asn Ser Ser
885 890 895

Arg Thr Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Trp Ser Gln
900 905 910

Val Ala Ser Val Leu Asp Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr
915 920 925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Ser Leu Glu Ala Val Val
930 935 940

His Val Asn Gln Asp Asp Leu Thr Arg Ile Gly Ile Ser Ser Pro Ser
945 950 955 960

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<210> 63

<211> 2958

<212> DNA

<213> *Xenopus laevis*

<220>

<221> CDS

<222> (1)..(2955)

<400> 63

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ctg ctg gat tcc agg tca gtg caa gga gag ctt ggc tgg ata gca agt Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser 35 40 45	144
cct ttg gaa gga ggg tgg gaa gaa gtg agt atc atg gat gaa aag aat Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn 50 55 60	192
aca cct ata cga act tac caa gtc tgc aat gtc atg gaa tgc agc caa Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ser Ser Gln 65 70 75 80	240
aac aac tgg tta cgg act gac tgg att ccc cga agt gga gct cag aga Asn Asn Trp Leu Arg Thr Asp Trp Ile Pro Arg Ser Gly Ala Gln Arg 85 90 95	288
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tct ttg gtg gaa gtt cga ggc tct tgt gta gac aac tca gaa gag aaa Ser Leu Val Glu Val Arg Gly Ser Cys Val Asp Asn Ser Glu Glu Lys 225 230 235 240	720
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aat tct ggt gga agg cct gat gtc tcc tac aat ttg gtc tgt aaa agg Asn Ser Gly Gly Arg Pro Asp Val Ser Tyr Asn Leu Val Cys Lys Arg 355 360 365	1104
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gac ctg caa gcc cat act aac tac acc ttt gag gtc tgg gcc att aat Asp Leu Gln Ala His Thr Asn Tyr Thr Phe Glu Val Trp Ala Ile Asn 405 410 415	1248
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aaa gag atc acc agg cac agt gtg tct ttg act tgg cca gag cct gag Lys Glu Ile Thr Arg His Ser Val Ser Leu Thr Trp Pro Glu Pro Glu 450 455 460	1392
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cgt gct cgg aca gct gca gga tat ggg gag ttc agt gga ccc ttt gag Arg Ala Arg Thr Ala Ala Gly Tyr Gly Glu Phe Ser Gly Pro Phe Glu 515 520 525	1584
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cgc gaa ttt gca aag gaa atc gat gcc tct tgt att aag atc gaa aaa Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys 610 615 620	1872
gta att gga gta ggt gaa ttt ggt gaa gtg tgc agt ggg cgt ctg aag Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys 625 630 635 640	1920

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Val Pro Gly Lys Arg Glu Ile Tyr Val Ala Ile Lys Thr Leu Lys Ala
645 650 655

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Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile
660 665 670

atg ggt cag ttt gac cat cct aac atc atc cac ctt gaa ggt gtt gtc 2064
Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Gly Val Val
675 680 685

acc aaa tgc aag cca gtg atg ata atc acc gag tac atg gag aac gga 2112
Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly
690 695 700

tcc ttg gat gca ttc ctt cgg aag aat gat ggt cgg ttt aca gta ata 2160
Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile
705 710 715 720

cag ctt gtg gga atg ctg cgt ggc att ggg tct gga atg aaa tac ctt 2208
Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu
725 730 735

tcg gac atg agt tat gtg cac cgg gac cta gct gct cgt aat atc ctt 2256
Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu
740 745 750

gtg aac agc aac cta gtc tgt aag gtc tct gac ttt ggc atg tct cgg 2304
Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg
755 760 765

gtg ctg gaa gat gac cct gaa gca gcc tac aca aca agg ggt ggc aag 2352
Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys
770 775 780

atc cca atc cga tgg act gca cca gaa gct att gca tac agg aaa ttc 2400
Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe
785 790 795 800

act tct gct agt gat gtc tgg agc tat ggc att gtc atg tgg gaa gtc 2448
Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val
805 810 815

atg tct tat gga gag agg cct tac tgg gat atg tcc aat caa gat gta 2496
Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val
820 825 830

att aaa gca atc gag gaa gga tac agg ctg ccc cgg cct atg gac tgc 2544
Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys
835 840 845

oct att gca cta cat cag ctg atg ttg gac tgc tgg cag aag gat cgt 2592
Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg
850 855 860

agt gac cga cca aaa ttt ggg cag ata gtc agc atg ctg gat aaa ctg 2640
Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Ser Met Leu Asp Lys Leu
865 870 875 880

atc agg aac cca aac agt ttg aaa agg act ggg ctg gag aat tca aga 2688
Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Leu Glu Asn Ser Arg
885 890 895

aca aac acg gct ctg ctg gac ccc agt tgg cct gaa tgg tcc cag gtg 2736
Thr Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Trp Ser Gln Val
900 905 910

gct tct gtg ctt gat tgg ctg cag gca tca aaa tgg aaa aga tac aaa 2784
Ala Ser Val Leu Asp Trp Leu Gln Ala Ser Lys Trp Lys Arg Tyr Lys
915 920 925

gat aac ttc aca gcg gcc gga tac acc agc ttg gaa gca gtc gtg cat 2832
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930 935 940

gtg aat caa gat gac ttg acc agg att ggc att agt tcc cct tca cac 2880
Val Asn Gln Asp Asp Leu Thr Arg Ile Gly Ile Ser Ser Pro Ser His
945 950 955 960

cag aac aag atc ctg agc agc gtc caa gga atg agg acc cag ttg cag 2928
Gln Asn Lys Ile Leu Ser Ser Val Gln Gly Met Arg Thr Gln Leu Gln
965 970 975

caa atg caa ggc aga atg gtt cct gtt tga 2958
Gln Met Gln Gly Arg Met Val Pro Val
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<210> 64

<211> 985

<212> PRT

<213> Xenopus laevis

<400> 64

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

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Asp Leu Gln Ala His Thr Asn Tyr Thr Phe Glu Val Trp Ala Ile Asn 405 410 415		
Gly Val Ser Lys Gln Asn Pro Glu Gln Asp Gln Ala Val Ser Val Thr 420 425 430		
Val Thr Thr Asn Gln Ala Ala Pro Ser Thr Val Thr Gln Ile Gln Pro 435 440 445		
Lys Glu Ile Thr Arg His Ser Val Ser Leu Thr Trp Pro Glu Pro Glu 450 455 460		
Arg Ala Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys 465 470 475 480		
Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Lys Thr Ala Ser Arg Ser 485 490 495		
Ala Asp Ile Lys Gly Leu Asn Pro Leu Thr Gly Tyr Val Phe His Val 500 505 510		
Arg Ala Arg Thr Ala Ala Gly Tyr Gly Glu Phe Ser Gly Pro Phe Glu 515 520 525		
Phe Thr Thr Asn Thr Val Pro Ser Pro Met Ile Gly Glu Gly Thr Ser 530 535 540		
Pro Thr Val Leu Leu Val Ser Val Ala Gly Ser Ile Val Leu Val Val 545 550 555 560		
Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr Ser 565 570 575		
Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly Val 580 585 590		
Lys Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val 595 600 605		
Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys 610 615 620		

Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys
 625 630 635 640
 Val Pro Gly Lys Arg Glu Ile Tyr Val Ala Ile Lys Thr Leu Lys Ala
 645 650 655
 Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile
 660 665 670
 Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val
 675 680 685
 Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly
 690 695 700
 Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile
 705 710 715 720
 Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu
 725 730 735
 Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu
 740 745 750
 Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg
 755 760 765
 Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys
 770 775 780
 Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe
 785 790 795 800
 Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val
 805 810 815
 Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val
 820 825 830
 Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys
 835 840 845
 Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg
 850 855 860
 Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Ser Met Leu Asp Lys Leu
 865 870 875 880
 Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Leu Glu Asn Ser Arg
 885 890 895
 Thr Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Trp Ser Gln Val
 900 905 910
 Ala Ser Val Leu Asp Trp Leu Gln Ala Ser Lys Trp Lys Arg Tyr Lys
 915 920 925
 Asp Asn Phe Thr Ala Ala Gly Tyr Thr Ser Leu Glu Ala Val Val His
 930 935 940
 Val Asn Gln Asp Asp Leu Thr Arg Ile Gly Ile Ser Ser Pro Ser His
 945 950 955 960
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<210> 65

<211> 2961

<212> DNA

<213> *Xenopus laevis*

<220>

<221> CDS

<222> (1)..(2958)

<400> 65

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ctg ctg gat tcc agg tca gtg caa gga gag ctt ggc tgg ata gca agt Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser 35 40 45	144
cct ttg gaa gga ggg tgg gaa gaa gtg agt atc atg gat gaa aag aat Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn 50 55 60	192
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gta tat gtt gaa att aaa ttt aca tta agg gac tgc aac agc ttg cct Val Tyr Val Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro 100 105 110	336
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tct ttg gtg gaa gtt cga ggc tct tgt gta gac aac tca gaa gag aaa Ser Leu Val Glu Val Arg Gly Ser Cys Val Asp Asn Ser Glu Glu Lys 225 230 235 240	720
gat gtg cct aag atg tac tgt ggt gct gat gga gag tgg ctg gtg ccc Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro 245 250 255	768
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Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys	
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Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val	
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 865 870 875 880
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 885 890 895
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 Arg Thr Asn Thr Thr Leu Leu Asp Pro Ser Ser Pro Glu Trp Ser Gln
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 930 935 940
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 His Val Asn Gln Asp Asp Leu Thr Arg Ile Gly Ile Ser Ser Pro Ser
 945 950 955 960
 cac cag aac aag att ctg agc agt gtt cag gga atg agg acc cag atg 2928
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 Gln Gln Ile Gln Gly Arg Met Val Pro Val
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<210> 66

<211> 986

<212> PRT

<213> Xenopus laevis

<400> 66

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 35 40 45
 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
 50 55 60
 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ser Ser Gln
 65 70 75 80

Asn Asn Trp Leu Arg Thr Asp Trp Ile Pro Arg Ser Gly Ala Gln Arg
 85 90 95
 Val Tyr Val Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
 100 105 110
 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
 145 150 155 160
 Asp Arg Ile Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu
 165 170 175
 Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
 180 185 190
 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205
 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ser Asp Thr Ser
 210 215 220
 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asp Asn Ser Glu Glu Lys
 225 230 235 240
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly Phe Glu Glu His Asn Gly Gly
 260 265 270
 Cys Gln Ala Cys Lys Val Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
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 Ala Cys Ser Lys Cys Pro Pro His Ser Tyr Ala Leu Arg Glu Gly Ser
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 Thr Ser Cys Thr Cys Asp Arg Gly Tyr Phe Arg Ala Asp Thr Asp Pro
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 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Gln Asn Leu Ile
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 Asn Ser Gly Gly Arg Pro Asp Val Ser Tyr Asn Leu Val Cys Lys Arg
 355 360 365
 Cys Gly Ser Asp Leu Thr Arg Cys Arg Pro Cys Gly Ser Gly Val His
 370 375 380
 Tyr Ser Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile Thr
 385 390 395 400
 Asp Leu Gln Ala His Thr Asn Tyr Thr Phe Glu Val Trp Ser Ile Asn
 405 410 415
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 420 425 430
 Val Thr Thr Asn Gln Ala Ala Pro Ser Thr Val Thr Gln Ile Gln Pro
 435 440 445
 Lys Asp Ile Thr Arg His Ser Val Ser Leu Thr Trp Pro Glu Pro Glu
 450 455 460
 Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys
 465 470 475 480
 Asp Gln Asn Glu Arg Thr Tyr Arg Ile Val Lys Thr Thr Ser Arg Ser
 485 490 495
 Ala Asp Ile Lys Gly Leu Asn Pro Leu Thr Ala Tyr Val Phe His Val
 500 505 510
 Arg Ala Arg Thr Ala Ala Gly Tyr Gly Glu Phe Ser Gly Pro Phe Glu
 515 520 525
 Phe Thr Thr Asn Thr Val Pro Ser Pro Met Ile Gly Glu Gly Ala Ser
 530 535 540
 Pro Thr Val Leu Leu Val Ser Val Ala Gly Ser Ile Val Leu Val Val
 545 550 555 560
 Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr Ser
 565 570 575
 Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly Val

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Lys	Thr	Tyr	Val	Asp	Pro	Phe	Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val		
595						600						605					
Arg	Glu	Phe	Ala	Lys	Glu	Ile	Asp	Ala	Ser	Cys	Ile	Lys	Ile	Glu	Lys		
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Val	Ile	Gly	Val	Gly	Glu	Phe	Gly	Glu	Val	Cys	Ser	Gly	Arg	Leu	Lys		
625						630						635					
Val	Pro	Gly	Lys	Arg	Glu	Ile	Tyr	Val	Ala	Ile	Lys	Thr	Leu	Lys	Ala		
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Gly	Tyr	Thr	Asp	Lys	Gln	Arg	Arg	Asp	Phe	Leu	Ser	Glu	Ala	Ser	Ile		
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Met	Gly	Gln	Phe	Asp	His	Pro	Asn	Ile	Ile	His	Leu	Glu	Gly	Val	Val		
675						680						685					
Thr	Lys	Cys	Lys	Pro	Val	Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	Gly		
690						695						700					
Ser	Leu	Asp	Ala	Phe	Leu	Arg	Lys	Asn	Asp	Gly	Arg	Phe	Thr	Val	Ile		
705						710						715					
Gln	Leu	Val	Gly	Ile	Leu	Arg	Gly	Ile	Gly	Ser	Gly	Met	Lys	Tyr	Leu		
725						730						735					
Ser	Asp	Met	Ser	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu		
740						745						750					
Val	Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Met	Ser	Arg		
755						760						765					
Val	Leu	Glu	Asp	Asp	Pro	Glu	Ala	Ala	Tyr	Thr	Thr	Arg	Gly	Gly	Lys		
770						775						780					
Ile	Pro	Ile	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ala	Tyr	Arg	Lys	Phe		
785						790						795					
Thr	Ser	Ala	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Val	Met	Trp	Glu	Val		
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Met	Ser	Tyr	Gly	Glu	Arg	Pro	Tyr	Trp	Asp	Met	Ser	Asn	Gln	Asp	Val		
820						825						830					

Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys
835 840 845

Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg
850 855 860

Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Ser Met Leu Asp Lys Leu
865 870 875 880

Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Leu Asp Asn Ser Ser
885 890 895

Arg Thr Asn Thr Thr Leu Leu Asp Pro Ser Ser Pro Glu Trp Ser Gln
900 905 910

Val Ala Ser Val Leu Asp Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr
915 920 925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Ser Leu Glu Ala Val Val
930 935 940

His Val Asn Gln Asp Asp Leu Thr Arg Ile Gly Ile Ser Ser Pro Ser
945 950 955 960

His Gln Asn Lys Ile Leu Ser Ser Val Gln Gly Met Arg Thr Gln Met
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Gln Gln Ile Gln Gly Arg Met Val Pro Val
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<210> 67

<211> 3278

<212> DNA

<213> *Xenopus laevis*

<220>

<221> CDS

<222> (73)..(3033)

<400> 67

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gctgcagcca cc atg gct ggg att gta cat ggc atc ttg ttt tgt ggc ctc 111
Met Ala Gly Ile Val His Gly Ile Leu Phe Cys Gly Leu
1 5 10

ttt gga ctt tgt tgg gca gtg acg gga tct agg att tac cca gcc agt 159
Phe Gly Leu Cys Trp Ala Val Thr Gly Ser Arg Ile Tyr Pro Ala Ser
15 20 25

gaa gtt acc ctg ctg gat tcc agg tca gtg caa gga gag ctt ggc tgg 207
Glu Val Thr Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp

30	35	40	45	
ata gca agt cct ttg gaa gga ggg tgg gaa gaa gtg agt atc atg gat				255
Ile Ala Ser Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp	50	55	60	
gaa aag aat aca cct ata cga act tac caa gtc tgc aat gtc atg gaa				303
Glu Lys Asn Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu	65	70	75	
tcg agc caa aac aac tgg tta cgg act gac tgg att ccc cga agt gga				351
Ser Ser Gln Asn Asn Trp Leu Arg Thr Asp Trp Ile Pro Arg Ser Gly	80	85	90	
gct cag aga gta tat gtt gaa att aaa ttt aca tta agg gac tgc aac				399
Ala Gln Arg Val Tyr Val Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn	95	100	105	
agc ttg cct ggg gta atg ggt acc tgc aaa gag acc ttt aat ctg tat				447
Ser Leu Pro Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr	110	115	120	125
tat tat gag tcc aac aat gac aaa gag cgt ttc att cgt gaa acc cag				495
Tyr Tyr Glu Ser Asn Asn Asp Lys Glu Arg Phe Ile Arg Glu Thr Gln	130	135	140	
tat gtg aaa atc gat acc att gca gcc gat gag agc ttc acc cag gtt				543
Tyr Val Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val	145	150	155	
gat att ggg gac cgt att atg aag ctg aac act gag gtt aga gat gtt				591
Asp Ile Gly Asp Arg Ile Met Lys Leu Asn Thr Glu Val Arg Asp Val	160	165	170	
ggt cca ctc agt aag aag gcc ttc tac ttg gcc ttc cag gat gtg gga				639
Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly	175	180	185	
gca tgc att gcc ctt gtg tct gtc cga gtg ttc tac aag aag tgt cca				687
Ala Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro	190	195	200	205
ttg act gta aga aac ttg gca cag ttc cct gac acc att aca ggt tca				735
Leu Thr Val Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ser	210	215	220	
gac acc tct tct ttg gtg gaa gtt cga ggc tot tgt gta gac aac tca				783
Asp Thr Ser Ser Leu Val Glu Val Arg Gly Ser Cys Val Asp Asn Ser	225	230	235	
gaa gag aaa gat gtg cct aag atg tac tgt ggt gct gat gga gag tgg				831
Glu Glu Lys Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp	240	245	250	
ctg gtg ccc att gga aac tgc tta tgt aac gct ggg ttt gag gag cac				879
Leu Val Pro Ile Gly Asn Cys Leu Cys Asn Ala Gly Phe Glu Glu His	255	260	265	
aat gga gga tgc caa gcc tgc aaa gtt gga tac tac aaa gcc ctc tca				927
Asn Gly Gly Cys Gln Ala Cys Lys Val Gly Tyr Tyr Lys Ala Leu Ser	270	275	280	285
aca gat gca gct tgc tcc aag tgt ccc cca cac agt tat gct ctc cgg				975

Thr Asp Ala Ala Cys Ser Lys Cys Pro Pro His Ser Tyr Ala Leu Arg	
290 295 300	
gaa ggc tca acc tcc tgc acc tgt gac cgt ggc tat ttt cga gct gac	1023
Glu Gly Ser Thr Ser Cys Thr Cys Asp Arg Gly Tyr Phe Arg Ala Asp	
305 310 315	
act gac ccg gct tct atg ccc tgc act aga ccc cca tct gct cct cag	1071
Thr Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Gln	
320 325 330	
aac cta atc tca aac gtc aat gag aca tct gtg aat ttg gag tgg agt	1119
Asn Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser	
335 340 345	
ccg cca caa aat tct ggt gga agg cct gat gtc tcc tac aat ttg gtc	1167
Pro Pro Gln Asn Ser Gly Gly Arg Pro Asp Val Ser Tyr Asn Leu Val	
350 355 360 365	
tgt aaa agg tgc ggc tct gac ctg act cgc tgt cgg cct tgt ggc agt	1215
Cys Lys Arg Cys Gly Ser Asp Leu Thr Arg Cys Arg Pro Cys Gly Ser	
370 375 380	
gga gtg cac tat agc ccc cag caa aat ggc ctg aag act aoc aaa gtg	1263
Gly Val His Tyr Ser Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val	
385 390 395	
tcc att aat gac ctg caa gcc cat act aac tac acc ttt cag gtc tgg	1311
Ser Ile Asn Asp Leu Gln Ala His Thr Asn Tyr Thr Phe Glu Val Trp	
400 405 410	
gcc att aat ggt gtc tcc aag cag aac cct gaa caa gat cag gct gtg	1359
Ala Ile Asn Gly Val Ser Lys Gln Asn Pro Glu Gln Asp Gln Ala Val	
415 420 425	
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Ser Val Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Thr Val Thr Gln	
430 435 440 445	
ata cag cca aaa gag atc acc agg cac agt gtg tct ttg act tgg cca	1455
Ile Gln Pro Lys Glu Ile Thr Arg His Ser Val Ser Leu Thr Trp Pro	
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gag cct gag cga gcc aat ggg gtc atc ctg gaa tac gaa gtc aag tat	1503
Glu Pro Glu Arg Ala Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr	
465 470 475	
tat gag aag gac cag aat gag cgt agt tat cga att gtt aag acg gcc	1551
Tyr Glu Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Lys Thr Ala	
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tcg cga agt gca gac atc aaa ggt ctc aac ccc ctt act cgt tat gtg	1599
Ser Arg Ser Ala Asp Ile Lys Gly Leu Asn Pro Leu Thr Gly Tyr Val	
495 500 505	
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Phe His Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Glu Phe Ser Gly	
510 515 520 525	
ccc ttt gag ttc acc acg aat aca gtg cca tcc ccg atg att ggc gaa	1695
Pro Phe Glu Phe Thr Thr Asn Thr Val Pro Ser Pro Met Ile Gly Glu	
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caa gga gta aag act tat gtg gac cca ttt aca tat gaa gat cct aac Gln Gly Val Lys Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn 590 595 600 605	1887
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atc gaa aaa gta att gga gta ggt gaa ttt ggt gaa gtg tgc agt ggg Ile Glu Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly 625 630 635	1983
cgt ctg aag gtc cct gga aag aga gag att tat gtt gca att aag acc Arg Leu Lys Val Pro Gly Lys Arg Glu Ile Tyr Val Ala Ile Lys Thr 640 645 650	2031
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gcc agc atc atg ggt cag ttt gac cat cct aac atc atc cac ctt gaa Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu 670 675 680 685	2127
ggt gtt gtc acc aaa tgc aag cca gtg atg ata atc acc gag tac atg Gly Val Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met 690 695 700	2175
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aaa tac ctt tcg gac atg agt tat gtg cac cgg gac cta gct gct cgt Lys Tyr Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg 735 740 745	2319
aat atc ctt gtg aac agc aac cta gtc tgt aag gtc tct gac ttt gcc Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly 750 755 760 765	2367
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Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met
      800                      805                      810

tgg gaa gtc atg tct tat gga gag agg cct tac tgg gat atg tcc aat      2559
Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn
      815                      820                      825

caa gat gta att aaa gca atc gag gaa gga tac agg ctg ccc ccg cct      2607
Gln Asp Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro
      830                      835                      840                      845

atg gac tgc cct att gca ctg cat cag ctc atg ttg gac tgc tgg cag      2655
Met Asp Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln
      850                      855                      860

aag gat cgt agt gac cga cca aaa ttt ggg cag ata gtc agc atg ctg      2703
Lys Asp Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Ser Met Leu
      865                      870                      875

gat aaa ctc atc agg aac cca aac agt ttg aaa agg act ggg ctg gag      2751
Asp Lys Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Leu Glu
      880                      885                      890

aat tca agc aga aca aat acg gct ctg ctg gac ccc agt tgg cct gaa      2799
Asn Ser Ser Arg Thr Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu
      895                      900                      905

tgg tcc cag gtg gct tct gtg ctt gat tgg ctg cag gcc atc aaa atg      2847
Trp Ser Gln Val Ala Ser Val Leu Asp Trp Leu Gln Ala Ile Lys Met
      910                      915                      920                      925

gaa aga tac aaa gat aac ttc aca gca gcc gga tac acc agc ttg gaa      2895
Glu Arg Tyr Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Ser Leu Glu
      930                      935                      940

gca gtc gtg cat gtg aat caa gat gac ttg acc agg att ggc att agt      2943
Ala Val Val His Val Asn Gln Asp Asp Leu Thr Arg Ile Gly Ile Ser
      945                      950                      955

tcc cct tca cac cag aac aag atc ctg agc agc gtc caa gga atg agg      2991
Ser Pro Ser His Gln Asn Lys Ile Leu Ser Ser Val Gln Gly Met Arg
      960                      965                      970

acc cag ttg cag caa atg caa ggc agg atg gtt cct gtt tga      3033
Thr Gln Leu Gln Gln Met Gln Gly Arg Met Val Pro Val
      975                      980                      985

agctgcagga cgtaaagg ggggcaattt ctcaagaactc ttgaaagaaa aattagtta      3093

cctcatccat gcactttaat tgaagaactg cacttttttt acattatcct caccocgtgg      3153

gacaaggact ctgcagaagt atttggggat aagctgaaac tcatttaaca tggagcattt      3213

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aaaaa
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<210> 68
<211> 986
<212> PRT
<213> Xenopus laevis

<400> 68

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 Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
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 Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Ser Ser Gln
 65 70 75 80
 Asn Asn Trp Leu Arg Thr Asp Trp Ile Pro Arg Ser Gly Ala Gln Arg
 85 90 95
 Val Tyr Val Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
 100 105 110
 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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 Ser Asn Asn Asp Lys Glu Arg Phe Ile Arg Glu Thr Gln Tyr Val Lys
 130 135 140
 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
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 Asp Arg Ile Met Lys Leu Asn Thr Glu Val Arg Asp Val Gly Pro Leu
 165 170 175
 Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
 180 185 190
 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205
 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ser Asp Thr Ser
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 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asp Asn Ser Glu Glu Lys
 225 230 235 240

Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly Phe Glu Glu His Asn Gly Gly
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 Thr Ser Cys Thr Cys Asp Arg Gly Tyr Phe Arg Ala Asp Thr Asp Pro
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 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Gln Asn Leu Ile
 325 330 335
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 Asn Ser Gly Gly Arg Pro Asp Val Ser Tyr Asn Leu Val Cys Lys Arg
 355 360 365
 Cys Gly Ser Asp Leu Thr Arg Cys Arg Pro Cys Gly Ser Gly Val His
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 Tyr Ser Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile Asn
 385 390 395 400
 Asp Leu Gln Ala His Thr Asn Tyr Thr Phe Glu Val Trp Ala Ile Asn
 405 410 415
 Gly Val Ser Lys Gln Asn Pro Glu Gln Asp Gln Ala Val Ser Val Thr
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 Lys Glu Ile Thr Arg His Ser Val Ser Leu Thr Trp Pro Glu Pro Glu
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 Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Lys Thr Ala Ser Arg Ser
 485 490 495

Ala Asp Ile Lys Gly Leu Asn Pro Leu Thr Gly Tyr Val Phe His Val
500 505 510

Arg Ala Arg Thr Ala Ala Gly Tyr Gly Glu Phe Ser Gly Pro Phe Glu
515 520 525

Phe Thr Thr Asn Thr Val Pro Ser Pro Met Ile Gly Glu Gly Thr Ser
530 535 540

Pro Thr Val Leu Leu Val Ser Val Ala Gly Ser Ile Val Leu Val Val
545 550 555 560

Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr Ser
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Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly Val
580 585 590

Lys Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val
595 600 605

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610 615 620

Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys
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Val Pro Gly Lys Arg Glu Ile Tyr Val Ala Ile Lys Thr Leu Lys Ala
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Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile
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Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val
675 680 685

Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly
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Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile
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Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu
725 730 735

Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu

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Val	Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Met	Ser	Arg		
755					760					765							
Val	Leu	Glu	Asp	Asp	Pro	Glu	Ala	Ala	Tyr	Thr	Thr	Arg	Gly	Gly	Lys		
770					775					780							
Ile	Pro	Ile	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Ala	Tyr	Arg	Lys	Phe		
785					790					795					800		
Thr	Ser	Ala	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Val	Met	Trp	Glu	Val		
805					810					815							
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Ile	Arg	Asn	Pro	Asn	Ser	Leu	Lys	Arg	Thr	Gly	Leu	Glu	Asn	Ser	Ser		
885					890					895							
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900					905					910							
Val	Ala	Ser	Val	Leu	Asp	Trp	Leu	Gln	Ala	Ile	Lys	Met	Glu	Arg	Tyr		
915					920					925							
Lys	Asp	Asn	Phe	Thr	Ala	Ala	Gly	Tyr	Thr	Ser	Leu	Glu	Ala	Val	Val		
930					935					940							
His	Val	Asn	Gln	Asp	Asp	Leu	Thr	Arg	Ile	Gly	Ile	Ser	Ser	Pro	Ser		
945					950					955					960		
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<210> 69

<211> 2961

<212> DNA

<213> Danio rerio

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<221> CDS

<222> (1)..(2958)

<220>

<221> misc_feature

$\langle 222 \rangle$ (1269)..(1269)

<223> The 'w' at location 1269 stands for a or t.

<400> 69

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ccg act ttc gta tta acc gca cgg gtc tac cct cct aat gaa gtg aca Pro Thr Phe Val Leu Thr Ala Arg Val Tyr Pro Pro Asn Glu Val Thr 20 25 30	96
ctg ctg gac tcg aga act gtg caa gga gaa ttg aaa tgg gtt gca agt Leu Leu Asp Ser Arg Thr Val Gln Gly Glu Leu Lys Trp Val Ala Ser 35 40 45	144
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gca tct atg ccc tgc aca cag ccc cca tct gct cct cag cac ctc att Ala Ser Met Pro Cys Thr Gln Pro Pro Ser Ala Pro Gln His Leu Ile 325 330 335	1008
tcc aat gtg aac gag act tcg gta aat ctg gag tgg acg gct cca gca Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Thr Ala Pro Ala 340 345 350	1056
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ttt tcc cct cag cag ctg ggt cta cgc act acc cgg gtg tcc ata aat Phe Ser Pro Gln Gln Leu Gly Leu Arg Thr Thr Arg Val Ser Ile Asn 385 390 395 400	1200
gac ctg cag gct cac acc aac tac acc ttc gag atc tgg gca gtc aac Asp Leu Gln Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val Asn 405 410 415	1248
ggg gtc tcc aaa cag agt ccw gga ccc gaa caa gca gtc tct gtg act Gly Val Ser Lys Gln Ser Xaa Gly Pro Glu Gln Ala Val Ser Val Thr 420 425 430	1296
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435	440	445	
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aga ccc aat gga gtc att ctt gag tac gag gtc aaa tac tat gag aag Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys 465 470 475 480			1440
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gct gag atc aaa ggc ctg agc cca ctc acc tcc tac gtg ttt cat gtg Ala Glu Ile Lys Gly Leu Ser Pro Leu Thr Ser Tyr Val Phe His Val 500 505 510			1536
cgt gcc cgc acc gct gct ggc tac gga gaa ttc agt gcc cct ttt gag Arg Ala Arg Thr Ala Ala Gly Tyr Gly Glu Phe Ser Ala Pro Phe Glu 515 520 525			1584
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aaa gcc aag cag gat tct gat gag gag agg cat tta cac cca gga gtc Lys Ala Lys Gln Asp Ser Asp Glu Glu Arg His Leu His Pro Gly Val 580 585 590			1776
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cgt gaa ttc gct aaa gaa atc gac gcc tcc tgc atc aag atc gaa aag Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys 610 615 620			1872
gtc atc ggc att gga gaa ttc gga gag gtg tgc agt ggc cgt ctc aag Val Ile Gly Ile Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys 625 630 635 640			1920
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Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly	
690 695 700	
tca ctg gat gct ttt ctt agg aag aat gat gga cgg ttt aca gtg att	2160
Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile	
705 710 715 720	
cag ctg gtg ggc atc ctg cga ggc att gct tca gga atg aaa tat ctc	2208
Gln Leu Val Gly Ile Leu Arg Gly Ile Ala Ser Gly Met Lys Tyr Leu	
725 730 735	
tcc gat atg agc tat gtc cat cgt gac ttg gcg gct cgc aac att ctg	2256
Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu	
740 745 750	
gtc aac agc aac ctg gtg tgc aaa gtg tcc gac ttt ggc atg tct cga	2304
Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg	
755 760 765	
gtt ttg gag gaa gac cca gat gct gct tat acc acc aga gga ggc aag	2352
Val Leu Glu Glu Asp Pro Asp Ala Ala Tyr Thr Thr Arg Gly Gly Lys	
770 775 780	
ata ccc att cgc tgg acg gct cct gaa gcc att act tac agg aag ttc	2400
Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Thr Tyr Arg Lys Phe	
785 790 795 800	
acc tcc gca tct gac gtc tgg agc tat ggc atc gtc atg tgg gaa gtg	2448
Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val	
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atg tca tat gga gag cgg cca tat tgg gac atg agc aac cag gat gtg	2496
Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val	
820 825 830	
ata aag gcc att gag gaa ggc tac agg ctg cct cct ccc atg gac tgt	2544
Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys	
835 840 845	
cca gtt tct ttg cac cag ttg atg ttg gat tgc tgg cag aaa gag cgc	2592
Pro Val Ser Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg	
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Ala Glu Arg Pro Lys Phe Ser Gln Ile Val Asn Met Leu Asp Lys Leu	
865 870 875 880	
atc cgc aac cct aac agc ctg aaa agg aca gga gga gaa ata gcc aga	2688
Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Gly Glu Ile Ala Arg	
885 890 895	
ccc aac acc acc ctc ctg gag cct agc agc cca gaa ttc acg tct acc	2736
Pro Asn Thr Thr Leu Leu Glu Pro Ser Ser Pro Glu Phe Thr Ser Thr	
900 905 910	
ctg gga tca gtt gcc gac tgg ctg cag gcc atc aac atg gaa cgt tac	2784
Leu Gly Ser Val Ala Asp Trp Leu Gln Ala Ile Asn Met Glu Arg Tyr	
915 920 925	
aga gac aac ttc acc gct gct ggc tat acc act cca gaa gct gtg gtc	2832
Arg Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Pro Glu Ala Val Val	
930 935 940	
cat atg aca caa gag gac atg acg agg ata ggg atc tcc acc gcc gca	2880
His Met Thr Gln Glu Asp Met Thr Arg Ile Gly Ile Ser Thr Ala Ala	
945 950 955 960	
cac cag gat aag atc ctc aac agc gcg cag gga atg ttg tcc cag atg	2928
His Gln Asp Lys Ile Leu Asn Ser Ala Gln Gly Met Leu Ser Gln Met	
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cag caa atg cag gac agg atg gtt oct gtc tga	2961
Gln Gln Met Gln Asp Arg Met Val Pro Val	
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<211> 986

<212> PRT

<213> Danio rerio

<220>

<221> misc_feature

<222> (423)..(423)

<223> The 'Xaa' at location 423 stands for Pro.

<400> 70

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Leu Leu Asp Ser Arg Thr Val Gln Gly Glu Leu Lys Trp Val Ala Ser
35      40      45

Pro Thr Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
50      55      60

Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
65      70      75      80

Asn Asn Trp Leu Arg Thr Asp Trp Ile Pro Arg Gly Gly Ala Gln Arg
85      90      95

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
100     105     110

Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
115     120     125

Ser Asn Asn Asp Lys Glu Arg Tyr Ile Arg Glu Asn Gln Phe Thr Lys
130     135     140

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

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

405	410	415
Gly Val Ser Lys Gln Ser Xaa Gly Pro Glu Gln Ala Val Ser Val Thr 420 425 430		
Val Thr Thr Asn Gln Ala Ala Pro Ser Pro Val Thr Thr Ile Gln Ala 435 440 445		
Lys Asp Ile Thr Arg His Ala Val Ser Leu Ala Trp Gln Gln Pro Glu 450 455 460		
Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys 465 470 475 480		
Asp Gln Asn Glu Arg Ser Tyr Arg Ile Met Lys Thr Ser Ser Arg Ser 485 490 495		
Ala Glu Ile Lys Gly Leu Ser Pro Leu Thr Ser Tyr Val Phe His Val 500 505 510		
Arg Ala Arg Thr Ala Ala Gly Tyr Gly Glu Phe Ser Ala Pro Phe Glu 515 520 525		
Phe Met Thr Asn Ser Val Pro Ser Pro Ile Ile Gly Asp Gly Ala Asn 530 535 540		
Ser Thr Val Leu Leu Val Ser Val Ile Gly Ser Val Ile Leu Leu Leu 545 550 555 560		
Ile Phe Ile Gly Val Phe Ile Ile Ser Arg Arg Arg Ser Lys Tyr Ser 565 570 575		
Lys Ala Lys Gln Asp Ser Asp Glu Glu Arg His Leu His Pro Gly Val 580 585 590		
Arg Ile Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val 595 600 605		
Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys 610 615 620		
Val Ile Gly Ile Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys 625 630 635 640		
Met Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys Ala 645 650 655		

Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile
 660 665 670
 Met Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val
 675 680 685
 Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly
 690 695 700
 Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile
 705 710 715 720
 Gln Leu Val Gly Ile Leu Arg Gly Ile Ala Ser Gly Met Lys Tyr Leu
 725 730 735
 Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu
 740 745 750
 Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg
 755 760 765
 Val Leu Glu Glu Asp Pro Asp Ala Ala Tyr Thr Thr Arg Gly Gly Lys
 770 775 780
 Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Thr Tyr Arg Lys Phe
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 Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val
 805 810 815
 Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val
 820 825 830
 Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys
 835 840 845
 Pro Val Ser Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg
 850 855 860
 Ala Glu Arg Pro Lys Phe Ser Gln Ile Val Asn Met Leu Asp Lys Leu
 865 870 875 880
 Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Gly Glu Ile Ala Arg
 885 890 895
 Pro Asn Thr Thr Leu Leu Glu Pro Ser Ser Pro Glu Phe Thr Ser Thr
 900 905 910
 Leu Gly Ser Val Ala Asp Trp Leu Gln Ala Ile Asn Met Glu Arg Tyr
 915 920 925
 Arg Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Pro Glu Ala Val Val
 930 935 940
 His Met Thr Gln Glu Asp Met Thr Arg Ile Gly Ile Ser Thr Ala Ala
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aga gct cta gcc aca gac ggc agc tgc tct aag tgt ccc ctg cac agc Arg Ala Leu Ala Thr Asp Gly Ser Cys Ser Lys Cys Pro Leu His Ser 35 40 45	144
tac tct gtg aga gag gga tct act tcc tgt gcc tgt gat aaa ggc ttc Tyr Ser Val Arg Glu Gly Ser Thr Ser Cys Ala Cys Asp Lys Gly Phe 50 55 60	192
ttc agg tct gag acg gac cct gca tct atg ccc tgc aca cag ccc cca Phe Arg Ser Glu Thr Asp Pro Ala Ser Met Pro Cys Thr Gln Pro Pro 65 70 75 80	240
tct gct cct cag cac ctc att tcc aat gtg aac gag act tcg gta aat Ser Ala Pro Gln His Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn 85 90 95	288
ctg gag tgg acg gct cca gca tcc tct ggt ggc aga cag gac ctt gcc Leu Glu Trp Thr Ala Pro Ala Ser Ser Gly Gly Arg Gln Asp Leu Ala 100 105 110	336
tat aac gtt ata tgc aag cgg tgc agc tcg gac ggt caa cgc tgt cag Tyr Asn Val Ile Cys Lys Arg Cys Ser Ser Asp Gly Gln Arg Cys Gln 115 120 125	384
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gag gac ccc aac caa gca gtc cgt gaa ttc gct aaa gaa atc gac gcc Glu Asp Pro Asn Gln Ala Val Arg Glu Phe Ala Lys Glu Ile Asp Ala 355 360 365	1104
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ctg cct cct ccc atg gac tgt cca gtt tct ttg cac cag ttg atg ttg Leu Pro Pro Pro Met Asp Cys Pro Val Ser Leu His Gln Leu Met Leu 595 600 605			1824
gat tgc tgg cag aaa gag cgc gca gaa agg cca aag ttc agt caa att Asp Cys Trp Gln Lys Glu Arg Ala Glu Arg Pro Lys Phe Ser Gln Ile 610 615 620			1872
gtc aac atg ctg gac aaa ctc atc cgc aac cct aac agc ctg aaa agg Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg 625 630 635 640			1920
aca gga gga gaa ata gcc aga ccc aac acc acc ctc ctg gag cct agc Thr Gly Gly Glu Ile Ala Arg Pro Asn Thr Thr Leu Leu Glu Pro Ser 645 650 655			1968
agc cca gaa ttc acg tct acc ctg gga tca gtt gcc gac tgg ctg cag Ser Pro Glu Phe Thr Ser Thr Leu Gly Ser Val Ala Asp Trp Leu Gln 660 665 670			2016
gcc atc aac atg gaa cgt tac aga gac aac ttc acc gct gct gcc tat Ala Ile Asn Met Glu Arg Tyr Arg Asp Asn Phe Thr Ala Ala Gly Tyr 675 680 685			2064
acc act cca gaa gct gtg gtc cat atg aca caa gag gac atg acg agg Thr Thr Pro Glu Ala Val Val His Met Thr Gln Glu Asp Met Thr Arg 690 695 700			2112
ata ggg atc tcc acc gct gca cac cag gat aag atc ctc aac agc gcg Ile Gly Ile Ser Thr Ala Ala His Gln Asp Lys Ile Leu Asn Ser Ala 705 710 715 720			2160
cag gga atg ttg tcc cag atg cag caa atg cag gac agg atg gtt cct Gln Gly Met Leu Ser Gln Met Gln Gln Met Gln Asp Arg Met Val Pro 725 730 735			2208
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<211> 737

<212> PRT

<213> Danio rerio

<400> 72

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35      40      45

Tyr Ser Val Arg Glu Gly Ser Thr Ser Cys Ala Cys Asp Lys Gly Phe
50      55      60

Phe Arg Ser Glu Thr Asp Pro Ala Ser Met Pro Cys Thr Gln Pro Pro
65      70      75      80

Ser Ala Pro Gln His Leu Ile Ser Asn Val Asn Glu Thr Ser Val Asn
85      90      95

Leu Glu Trp Thr Ala Pro Ala Ser Ser Gly Gly Arg Gln Asp Leu Ala
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Tyr Asn Val Ile Cys Lys Arg Cys Ser Ser Asp Gly Gln Arg Cys Gln
115     120     125

Pro Cys Gly Asn Gly Ile His Phe Ser Pro Gln Gln Leu Gly Leu Arg
130     135     140

Thr Thr Arg Val Ser Ile Asn Asp Leu Gln Ala His Thr Asn Tyr Thr
145     150     155     160

Phe Glu Ile Trp Ala Val Asn Gly Val Ser Lys Gln Ser Pro Gly Pro
165     170     175

Glu Gln Ala Val Ser Val Thr Val Thr Thr Asn Gln Ala Ala Pro Ser
180     185     190

Pro Val Thr Thr Ile Gln Ala Lys Asp Ile Thr Arg His Ala Val Ser
195     200     205

Leu Ala Trp Gln Gln Pro Glu Arg Pro Asn Gly Val Ile Leu Glu Tyr
210     215     220

Glu Val Lys Tyr Tyr Glu Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile
225     230     235     240

Met Lys Thr Ser Ser Arg Ser Ala Glu Ile Lys Gly Leu Ser Pro Leu
245     250     255

Thr Ser Tyr Val Phe His Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly
260     265     270

Glu Phe Ser Ala Pro Phe Glu Phe Met Thr Asn Ser Val Pro Ser Pro
275     280     285

Ile Ile Gly Asp Gly Ala Asn Ser Thr Val Leu Leu Val Ser Val Ile
290     295     300

Gly Ser Val Ile Leu Leu Leu Ile Phe Ile Gly Val Phe Ile Ile Ser
305     310     315     320

Arg Arg Arg Ser Lys Tyr Ser Lys Ala Lys Gln Asp Ser Asp Glu Glu
325     330     335

Arg His Leu His Pro Gly Val Arg Ile Tyr Val Asp Pro Phe Thr Tyr
340     345     350

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Glu Asp Pro Asn Gln Ala Val Arg Glu Phe Ala Lys Glu Ile Asp Ala
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 Ser Cys Ile Lys Ile Glu Lys Val Ile Gly Ile Gly Glu Phe Gly Glu
 370 375 380
 Val Cys Ser Gly Arg Leu Lys Met Pro Gly Lys Arg Glu Ile Cys Val
 385 390 395 400
 Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp
 405 410 415
 Phe Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile
 420 425 430
 Ile Arg Leu Glu Gly Val Val Thr Lys Cys Lys Pro Val Met Ile Ile
 435 440 445
 Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn
 450 455 460
 Asp Gly Arg Phe Thr Val Ile Gln Leu Val Gly Ile Leu Arg Gly Ile
 465 470 475 480
 Ala Ser Gly Met Lys Tyr Leu Ser Asp Met Ser Tyr Val His Arg Asp
 485 490 495
 Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val
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 Ser Asp Phe Gly Met Ser Arg Val Leu Glu Glu Asp Pro Asp Ala Ala
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 Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu
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 Ala Ile Thr Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr
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 Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp
 565 570 575
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 580 585 590
 Leu Pro Pro Pro Met Asp Cys Pro Val Ser Leu His Gln Leu Met Leu
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 Asp Cys Trp Gln Lys Glu Arg Ala Glu Arg Pro Lys Phe Ser Gln Ile
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 Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg
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 Ser Pro Glu Phe Thr Ser Thr Leu Gly Ser Val Ala Asp Trp Leu Gln
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 690 695 700
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<220>

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      20              25              30

ttg gat tcc aga tcc gtt cag gga gaa ctt ggg tgg att gca agc cct      203
Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro

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cca atc cga acc tac caa gtg tgc aac gtg atg gaa ccc agc cag aat      299
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85              90              95

tac att gag att aag ttc acc ttg agg gac tgc aat agt ctt ccg ggc      395
tyr ile glu ile lys phe thr leu arg asp cys asn ser leu pro gly
100              105              110

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val met gly thr cys lys glu thr phe asn leu tyr tyr tyr glu ser
115              120              125

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130              135              140              145

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arg ile met lys leu asn thr glu ile arg asp val gly pro leu ser
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180              185              190

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leu val ser val arg val phe tyr lys lys cys pro leu thr val arg
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aat ctg gcc cag ttt cca gac acc atc aca ggg gcc gat acg tct tcc      731
asn leu ala gln phe pro asp thr ile thr gly ala asp thr ser ser
210              215              220              225

ctg gtg gaa gtc cga ggc tcc tgt gtc aac aac tca gaa gag aag gat      779
leu val glu val arg gly ser cys val asn asn ser glu glu lys asp
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gtg cca aaa atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc att      827
val pro lys met tyr cys gly ala asp gly glu trp leu val pro ile
245              250              255

ggc aac tgc ctg tgc aat gct ggg cat gaa gag cgg aat gga gaa tgc      875
gly asn cys leu cys asn ala gly his glu glu arg asn gly glu cys
260              265              270

caa gcc tgc aaa att gga tat tac aag gct ctc tcc acg gat gcc acc      923
gln ala cys lys ile gly tyr tyr lys ala leu ser thr asp ala thr
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tgt gcc aag tgc cca ccc cac agc tac tcc gtc tgg gaa gga gcc aca      971

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<212> PRT

<213> Equus caballus

<400> 74

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 Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
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 Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Ser Gln Phe Ala Lys
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 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
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 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
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 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Asn Gly Glu

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Cys Gly Ala Gly Asp Ser Ser Lys Cys Arg Pro Cys Gly Ser Gly Val 370 375 380		
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 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
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 755 760 765

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 Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
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agc aaa aag ggg ttc tat ctg gcg ttt cag gat gtg gga gcc tgc atc Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile 180 185 190	576
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Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Asn Gly Glu				
260	265	270		
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Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala				
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325	330	335		
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Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu				
465	470	475	480	
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Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg 485 490 495	
aac acg gat atc aaa ggc ctg aac cct ctg acg tcc tat gtt ttc cat Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His 500 505 510	1536
gtc cga ggc agg aca gca gct ggc tat gga gac ttc agc gag ccc ctg Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu 515 520 525	1584
gag gtc aca act aac aca gtg cct tcc cgg atc att gga gat ggg gcc Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala 530 535 540	1632
aac tcc acc gtc ctg ctg gtc tcc gtc tca ggc agc gtt gtg ctg gtg Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val 545 550 555 560	1680
gtc att ctc atc gcc gcc ttt gtc atc agc agg aga cga agt aaa tac Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr 565 570 575	1728
agt aaa gca aag caa gaa gca gat gaa gag aaa cat ttg aat caa ggt Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly 580 585 590	1776
gtt aga act tac gtg gac ccc ttt acc tac gaa gat ccc aat caa gca Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala 595 600 605	1824
gtt cga gaa ttt gcc aaa gaa atc gac gca tcc tgc att aag atc gaa Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu 610 615 620	1872
aaa gtc atc gga gtt ggt gaa ttt ggt gaa gta tgc agt ggg cgt ctc Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu 625 630 635 640	1920
aaa gtg cct ggc aaa aga gaa att tat gtg gct atc aag acg ctg aaa Lys Val Pro Gly Lys Arg Glu Ile Tyr Val Ala Ile Lys Thr Leu Lys 645 650 655	1968
gct ggt tat aca gac aaa cag agg agg gac ttc ctg agt gag gcc agc Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser 660 665 670	2016
atc atg gga cag ttc gac cac ccc aat atc att cac ttg gaa ggc gtc Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val 675 680 685	2064
gtc acc aaa tgt aaa cca gta atg atc ata aca gag tac atg gag aac Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn 690 695 700	2112
ggc tcc ttg gac gca ttc ctc agg aag aat gat ggc agg ttt acg gtc Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val 705 710 715 720	2160
att cag ctg gtg ggc atg ctt cgt ggc att ggg tcc ggg atg aag tat Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr 725 730 735	2208

tta tcg gat atg agc tac gtg cat cga gac ctg gct gca cgg aac att Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 740 745 750	2256
cta gtc aat agc aac ttg gtc tgc aaa gtg tct gat ttc ggc atg tcc Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser 755 760 765	2304
cgg gtg ctg gag gat gat cca gaa gcc gct tat act acc agg ggt ggc Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Arg Gly Gly 770 775 780	2352
aag att cct atc cgg tgg act gcg cca gaa gca att gcc tat cgt aaa Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys 785 790 795 800	2400
ttc aca tca gca agt gat gta tgg agc tac ggg atc gtt atg tgg gaa Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu 805 810 815	2448
gtg atg tcg tat gga gag aga ccc tac tgg gac atg tcc aat caa gat Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp 820 825 830	2496
gtg att aaa gcc atc gag gaa ggc tat cgg ctg ccc cct cca atg gac Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp 835 840 845	2544
tgc ccc att gca ctc cac cag ctg atg ctg gac tgc tgg cag aag gag Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu 850 855 860	2592
aga agc gac agg ccg aaa ttt ggg cag att gtc aac atg ttg gac aaa Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys 865 870 875 880	2640
ctc atc cgc aac ccc aac agc ttg aag agg acg ggg acc gag agc tcc Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser 885 890 895	2688
aga cct aac act gcc ttg ttg gat cca agc tcc cct gag ttc tct gcc Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala 900 905 910	2736
gtg gta tcg gtg ggt gat tgg ctc cag gcc att aaa atg gac cga tat Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr 915 920 925	2784
aag gat aac ttc act gct gct ggt tat acc aca cta gag gct gta gtg Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val 930 935 940	2832
cac atg aac cag gat gac ctg gcc aga att ggc atc acg gct gtc aca His Met Asn Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Val Thr 945 950 955 960	2880
cac cag aat aag att ttg aac agc atc cag gcg atg aga acc caa atg His Gln Asn Lys Ile Leu Asn Ser Ile Gln Ala Met Arg Thr Gln Met 965 970 975	2928
caa cag ata cac ggc aga atg gtt ccc gtc tga Gln Gln Ile His Gly Arg Met Val Pro Val 980 985	2961

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<211> 986

<212> PRT

<213> Sus scrofa

<400> 76

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

Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Lys Lys
 225 230 235 240
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Asn Gly Glu
 260 265 270
 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
 275 280 285
 Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
 290 295 300
 Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
 305 310 315 320
 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
 325 330 335
 Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
 340 345 350
 Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
 355 360 365
 Cys Gly Ala Gly Asp Ser Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
 370 375 380
 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile
 385 390 395 400
 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
 405 410 415
 Asn Gly Val Ser Lys Tyr Asn Pro Ser Pro Asp Gln Ser Val Ser Val
 420 425 430
 Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
 435 440 445
 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
 450 455 460
 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu

465	470	475	480
Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg	485	490	495
Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His	500	505	510
Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu	515	520	525
Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala	530	535	540
Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val	545	550	555
Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr	565	570	575
Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly	580	585	590
Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala	595	600	605
Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu	610	615	620
Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu	625	630	635
Lys Val Pro Gly Lys Arg Glu Ile Tyr Val Ala Ile Lys Thr Leu Lys	645	650	655
Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser	660	665	670
Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val	675	680	685
Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn	690	695	700
Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val	705	710	715
			720

Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
 725 730 735
 Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 740 745 750
 Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser
 755 760 765
 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
 770 775 780
 Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
 785 790 795 800
 Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
 805 810 815
 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
 820 825 830
 Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
 835 840 845
 Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
 850 855 860
 Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
 865 870 875 880
 Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser
 885 890 895
 Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
 900 905 910
 Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
 915 920 925
 Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
 930 935 940
 His Met Asn Gln Asp Asp Leu Ala Arg Ile Gly Ile Thr Ala Val Thr
 945 950 955 960
 His Gln Asn Lys Ile Leu Asn Ser Ile Gln Ala Met Arg Thr Gln Met
 965 970 975
 Gln Gln Ile His Gly Arg Met Val Pro Val
 980 985

<210> 77

<211> 2961

<212> DNA

<213> Ornithorhynchus anatinus

<220>

<221> CDS

<222> (1)..(2958)

<400> 77

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

gcc ctg gta tcc gtg cgg gtg ttc tac aag aag tgc cca ctg aca gtt Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val 195 200 205	624
cgc aac ctg gct cag ttt ccc gac acc gtc acc ggg gct gac aca tcc Arg Asn Leu Ala Gln Phe Pro Asp Thr Val Thr Gly Ala Asp Thr Ser 210 215 220	672
tcc cta gtg gag gtc cga ggc tcc tgt gtt aat aac tca gaa gag aag Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys 225 230 235 240	720
gat gtt cca aag atg tat tgt ggg gca gat ggt gaa tgg ttg gtg cct Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro 245 250 255	768
att ggc aac tgt gtg tgc aat gct ggg cac gaa gag cgc aat gga gaa Ile Gly Asn Cys Val Cys Asn Ala Gly His Glu Glu Arg Asn Gly Glu 260 265 270	816
tgt caa gcc tgt aaa att gga tac tac aag gcc ctg tcc acc gac gct Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala 275 280 285	864
tcc tgt gcc aaa tgt cct cct cat agc tat tcc gtc tgg gaa gga gcc Ser Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala 290 295 300	912
acc tct tgc acc tgt gac aga gga ttt ttc cga gca gac aac gat gcc Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala 305 310 315 320	960
gcc tct atg ccc tgc act cgt cct ccc tcg gct ccc ctg aac ctg att Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile 325 330 335	1008
tcc aaa gtc aat gag aca tcg gtg aat ttg gag tgg agc agc cct cag Ser Lys Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln 340 345 350	1056
aac acg ggt ggt cga cag gat att tcc tat aat gtg gta tgc aag aaa Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys 355 360 365	1104
tgt ggc acc ggt gat ctc agc cga tgt cgg tcc tgt ggg agt gga gta Cys Gly Thr Gly Asp Leu Ser Arg Cys Arg Ser Cys Gly Ser Gly Val 370 375 380	1152
cac tac acc ccc caa cag aat ggt ctg aag agc acc aaa gtc tct atc His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Ser Thr Lys Val Ser Ile 385 390 395 400	1200
act gac ctc ttg gca cac acg aac tac acc ttt gaa atc tgg gcc gtg Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val 405 410 415	1248
aac gga gta tcc aaa cac aac ccc agc cat gac caa tca gtc tct gtc Asn Gly Val Ser Lys His Asn Pro Ser His Asp Gln Ser Val Ser Val 420 425 430	1296
aca gtt acg acc aat caa gca gct cct tct tca att gct ttg atc cag Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Ile Gln	1344

435	440	445	
gct aaa gaa ata aca aga tac agt gtt gcg tta gct tgg tta gag cct Ala Lys Glu Ile Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro 450 455 460			1392
gat agg cca aat gga gtc atc ttg gag tat gaa gtc aaa tat tat gag Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu 465 470 475 480			1440
aag gat cag aat gaa cgc agc tac cga att gtt agg aca gca tcc aga Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ser Arg 485 490 495			1488
aac act gat atc aaa ggc ctg aat cct ttg act tcc tat gta ttt cat Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His 500 505 510			1536
gtg cgg gcc cgg acc gca gcc gga tat gga gat ttc agc gaa ccg ttt Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Phe 515 520 525			1584
gaa ttc aca acc aac aca gtc cct tca cga atc att gga gat ggt acc Glu Phe Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Thr 530 535 540			1632
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gtc att ctc att gct gca ttt gtc atc agc aga aga cgc agt aaa tac Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr 565 570 575			1728
agc aag gct aag caa gaa gcg gat gaa gag aaa cat ttg aat caa ggg Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly 580 585 590			1776
gtg aga acc tat gtg gat cct ttt acc tat gaa gat cct aac caa gct Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala 595 600 605			1824
gtc cga gaa ttt gcc aag gaa ata gat gcc tct tgc atc aag att gaa Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu 610 615 620			1872
aaa gtc att gga gtt ggt gag ttt ggc gaa gta tgc agt ggg cgt ctc Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu 625 630 635 640			1920
aaa gtg cct ggc aag cgg gag atc tgt gtg gca att aag act ctc aaa Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys 645 650 655			1968
gca ggg tat acg gac aaa caa agg agg gac ttc ttg agt gag gcc agc Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser 660 665 670			2016
atc atg ggg cag ttt gac cac cct aat atc atc cac tta gaa ggc gtc Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val 675 680 685			2064
gtc acc aaa tgt aag cca gta atg atc ata acc gag tac atg gaa aat			2112

Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn	
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gga tcc ttg gat gca ttc ctg agg aag aat gat ggc cga ttt aca gtc	2160
Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val	
705 710 715 720	
ata cag ttg gtg ggg atg ctt cgt ggc att ggc tgg gga atg aag tat	2208
Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr	
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ctg tcc gat atg agt tac gtg cat agg gat cta gct gcc cga aac atc	2256
Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile	
740 745 750	
ctg gta aat agt aac ctg gtc tgc aaa gtg tcc gat ttt ggc atg tct	2304
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser	
755 760 765	
cga gta ctt gag gat gat ccc gaa gct gct tat acg aca egg ggc ggc	2352
Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly	
770 775 780	
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Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys	
785 790 795 800	
ttc aca tca gca agt gat gtg tgg agc tat gga att gta atg tgg gaa	2448
Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu	
805 810 815	
gtg atg tca tat ggg gag aga cgg tac tgg gac atg tcc aat caa gac	2496
Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp	
820 825 830	
gta att aaa gcc atc gaa gaa gga tat aga cta cct ccc cct atg gac	2544
Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp	
835 840 845	
tgt ccc att gca ctc cat cag ctg atg ctt gac tgt tgg cag aag gag	2592
Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu	
850 855 860	
aga agt gac agg cct aaa ttt gga cag att gtc aat atg ttg gac aaa	2640
Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys	
865 870 875 880	
ctc atc cgc aac ccc aac agc ttg aag agg acg ggc acg gag agc tcc	2688
Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser	
885 890 895	
aga cct aat act gcc ttg ttg gac cca agt tct cct gaa ttc tct gct	2736
Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala	
900 905 910	
gtg gtg tca gtg act gac tgg ctc cag gcc att aaa atg gag cgg tac	2784
Val Val Ser Val Thr Asp Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr	
915 920 925	
aag gat aac ttc aca gct gct ggc tac acc acc cta gag gct gtg gtg	2832
Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val	
930 935 940	
cac atg aac cag gac gac ctg aca aga att ggc atc acc gcc atc aca	2880
His Met Asn Gln Asp Asp Leu Thr Arg Ile Gly Ile Thr Ala Ile Thr	
945 950 955 960	
cat cag aac aag att ttg ggc agc gtc cag tca atg cgg acc caa atg	2928
His Gln Asn Lys Ile Leu Gly Ser Val Gln Ser Met Arg Thr Gln Met	
965 970 975	
caa cag atg cac ggc aga atg gtt occ gtc tga	2961
Gln Gln Met His Gly Arg Met Val Pro Val	
980 985	

<210> 78

<211> 986

<212> PRT

<213> Ornithorhynchus anatinus

<400> 78

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

Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
 180 185 190
 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
 195 200 205
 Arg Asn Leu Ala Gln Phe Pro Asp Thr Val Thr Gly Ala Asp Thr Ser
 210 215 220
 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
 225 230 235 240
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
 245 250 255
 Ile Gly Asn Cys Val Cys Asn Ala Gly His Glu Glu Arg Asn Gly Glu
 260 265 270
 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
 275 280 285
 Ser Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
 290 295 300
 Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
 305 310 315 320
 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile
 325 330 335
 Ser Lys Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
 340 345 350
 Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
 355 360 365
 Cys Gly Thr Gly Asp Leu Ser Arg Cys Arg Ser Cys Gly Ser Gly Val
 370 375 380
 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Ser Thr Lys Val Ser Ile
 385 390 395 400
 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
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 Asn Gly Val Ser Lys His Asn Pro Ser His Asp Gln Ser Val Ser Val
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Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Ile Gln
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 Ala Lys Glu Ile Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
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 Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ser Arg
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 Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
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 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Phe
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 Glu Phe Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Thr
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 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
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 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
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 Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys
 645 650 655
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
 660 665 670
 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val

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Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn 690 695 700		
Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val 705 710 715 720		
Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr 725 730 735		
Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 740 745 750		
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser 755 760 765		
Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly 770 775 780		
Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys 785 790 795 800		
Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu 805 810 815		
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Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp 835 840 845		
Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu 850 855 860		
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Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser 885 890 895		
Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala 900 905 910		
Val Val Ser Val Thr Asp Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr 915 920 925		
Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val 930 935 940		
His Met Asn Gln Asp Asp Leu Thr Arg Ile Gly Ile Thr Ala Ile Thr 945 950 955 960		
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tgcttaccta gcac atg caa tac ctg aac acc ttc tat ggc tgc ccc aag	350
Met Gln Tyr Leu Asn Thr Phe Tyr Gly Cys Pro Lys	
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Glu Ser Cys Asn Leu Phe Val Leu Lys Asp Thr Leu Lys Lys Met Gln	
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Lys Phe Phe Gly Leu Pro Gln Thr Gly Asp Leu Asp Gln Asn Thr Ile	
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Glu Thr Met Arg Lys Pro Arg Cys Gly Asn Pro Asp Val Ala Asn Tyr	
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Asn Phe Phe Pro Arg Lys Pro Lys Trp Asp Lys Asn Gln Ile Thr Tyr	
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Arg Ile Ile Gly Tyr Thr Pro Asp Leu Asp Pro Glu Thr Val Asp Asp	
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<213> Homo sapiens

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Leu Pro Gln Thr Gly Asp Leu Asp Gln Asn Thr Ile Glu Thr Met Arg

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Glu Tyr Asn Ser Cys Thr Asp Thr Gly Arg Ser Asp Gly Phe Leu Trp 195 200 205		
Cys Ser Thr Thr Tyr Asn Phe Glu Lys Asp Gly Lys Tyr Gly Phe Cys 210 215 220		
Pro His Glu Ala Leu Phe Thr Met Gly Gly Asn Ala Glu Gly Gln Pro 225 230 235 240		
Cys Lys Phe Pro Phe Arg Phe Gln Gly Thr Ser Tyr Asp Ser Cys Thr 245 250 255		
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tcc cgg agt gag ttg aac cag gtg gac caa gtg ggc tac gtg acc tat Ser Arg Ser Glu Leu Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr 685 690 695			2116
gac atc ctg cag tgc cct gag gac tag ggctcccgtc ctgctttggc Asp Ile Leu Gln Cys Pro Glu Asp 700 705			2163
agtgccatgt aaatccccac tgggaccaac cctggggaag gagccagttt gccggataca			2223
aactggtatt ctgttctgga ggaaggag gagtgaggt gggctgggcc ctctcttctc			2283
acctttgtttt tttgttgag tgtttctaataa aaacttgat tctctaacct ttaaaaaaaa			2343
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa			2387

<210> 82

<211> 707

<212> PRT

<213> Homo sapiens

<400> 82

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

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

Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
 35          40          45

Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser
 50          55          60

Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu
 65          70          75          80

Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
 85          90          95

Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
100          105          110

Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
115          120          125

Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala
130          135          140

Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
145          150          155          160

Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
165          170          175

Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
180          185          190

Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
195          200          205

Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
210          215          220

Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
225          230          235          240

Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
245          250          255

Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro
260          265          270

Ser Glu Arg Leu Tyr Thr Gln Asp Gly Asn Ala Asp Gly Lys Pro Cys
275          280          285

Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr
290          295          300

Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr
305          310          315          320

Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr
325          330          335

Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr
340          345          350

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Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp
 355 360 365
 Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys
 370 375 380
 Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala
 385 390 395 400
 His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu
 405 410 415
 Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His
 420 425 430
 Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu
 435 440 445
 Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro
 450 455 460
 Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg
 465 470 475 480
 Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro
 485 490 495
 Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val
 500 505 510
 Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly
 515 520 525
 Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu
 530 535 540
 Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp
 545 550 555 560
 Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Arg Leu Ser
 565 570 575
 Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly
 580 585 590
 Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala
 595 600 605
 Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met
 610 615 620
 Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
 625 630 635 640
 Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly
 645 650 655
 Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr
 660 665 670
 Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu
 675 680 685
 Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys
 690 695 700
 Pro Glu Asp
 705
 <210> 83
 <211> 1404
 <212> DNA
 <213> Mus musculus

<220>

<221> CDS

<222> (1)..(1401)

<400> 83

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atg aca gag ata cct gca cct ttg tcc tac ttc cag aat gcc cag atg      48
Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1      5      10      15

tct gag gac agc cac tcc agc agc gcc atc cgg agc cag aat gac agc      96
Ser Glu Asp Ser His Ser Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser
20     25     30

caa gaa cgg cag cag cag cat gac agg cag aga ctt gac aac cct gag      144
Gln Glu Arg Gln Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu
35     40     45

cca ata tct aat ggg cgg ccc cag agt aac tca aga cag gtg gtg gaa      192
Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu
50     55     60

caa gat gag gag gaa gac gaa gag ctg aca ttg aaa tat gga gcc aag      240
Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65     70     75     80

cat gtc atc atg ctc ttt gtc ccc gtg acc ctc tgc atg gtc gtc gtc      288
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val

                        85                        90                        95

gtg gcc acc atc aaa tca gtc agc ttc tat acc cgg aag gac ggt cag      336
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100    105    110

cta atc tac acc cca ttc aca gaa gac act gag act gta ggc caa aga      384
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115    120    125

gcc ctg cac tcg atc ctg aat gcg gcc atc atg atc agt gtc att gtc      432
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130    135    140

att atg acc atc ctc ctg gtg gtc ctg tat aaa tac agg tgc tac aag      480
Ile Met Thr Ile Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145    150    155    160

gtc atc cac gcc tgg ctt att att tca tct ctg ttg ttg ctg ttc ttt      528
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
165    170    175

ttt tcg ttc att tac tta ggg gaa gta ttt aag acc tac aat gtc gcc      576
Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180    185    190

gtg gac tac gtt aca gta gca ctc cta atc tgg aat ttt ggt gtg gtc      624
Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
195    200    205

ggg atg att gcc atc cac tgg aaa gcc ccc ctt cga ctg cag cag gcg      672
Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210    215    220

tat ctc att atg atc agt gcc ctc atg gcc ctg gta ttt atc aag tac      720
Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225    230    235    240

ctc ccc gaa tgg acc gca tgg ctc atc ttg gct gtg att tca gta tat      768
Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245    250    255

gat ttg gtg gct gtt tta tgt ccc aaa ggc cca ctt cgt atg ctg gtt      816
Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
260    265    270

gaa aca gct cag gaa aga aat gag act ctc ttt cca gct ctt atc tat      864
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275    280    285

tcc tca aca atg gtg tgg ttg gtg aat atg gct gaa gga gac cca gaa      912
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290    295    300

gcc caa agg agg gta ccc aag aac ccc aag tat aac sca caa aga gcg      960
Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala
305    310    315    320

gag aga gag aca cag gac agt ggt tct ggg aac gat gat ggt ggc ttc      1008
Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe
325    330    335

agt gag gag tgg gag gcc caa aga gac agt cac ctg ggg cct cat cgc      1056

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Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

tcc act ccc gag tca aga gct gct gtc cag gaa ctt tct ggg agc att 1104
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile
355 360 365

cta acg agt gaa gac ccg gag gaa aga gga gta aaa ctt gga ctg gga 1152
Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

gat ttc att ttc tac agt gtt ctg gtt ggt aag gcc tca gca acc gcc 1200
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

agt gga gac tgg aac aca acc ata gcc tgc ttt gta gcc ata ctg atc 1248
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

ggc ctg tgc ctt aca tta ctc ctg ctc gcc att ttc aag aaa gcg ttg 1296
Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

cca gcc ctc ccc atc tcc atc acc ttc ggg ctc gtg ttc tac ttc gcc 1344
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

acg gat tac ctt gtg cag ccc ttc atg gac caa ctt gca ttc cat cag 1392
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

ttt tat atc tag 1404
Phe Tyr Ile
465

<210> 84

<211> 467

<212> PRT

<213> Mus musculus

<400> 84

Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15

Ser Glu Asp Ser His Ser Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser
20 25 30

Gln Glu Arg Gln Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu
35 40 45

Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu
50 55 60

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

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
 85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
 100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
 115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
 130 135 140

Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
 145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
 165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
 180 185 190

Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
 195 200 205

Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
 210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300

Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala
 305 310 315 320

Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe
 325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile
 355 360 365

Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 450 455 460

Phe Tyr Ile
 465

<210> 85

<211> 1407

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(1404)

<400> 85

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atg aca gag ata cct gca cct ttg tcc tac ttc cag aat gca cag atg      48
Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1          5          10          15

tct gag gac agc cac tcc agc agc gtc cgt agc cag aat gac aat caa      96
Ser Glu Asp Ser His Ser Ser Ser Val Arg Ser Gln Asn Asp Asn Gln
          20          25          30

gaa cgg cag cag cat cat gac aga cag aga ctt gac aac cct gag tcg     144
Glu Arg Gln Gln His His Asp Arg Gln Arg Leu Asp Asn Pro Glu Ser
          35          40          45

ata tct aat ggc cga ccc cag agt aac ttt acc agg cag gtg ata gag     192
Ile Ser Asn Gly Arg Pro Gln Ser Asn Phe Thr Arg Gln Val Ile Glu
          50          55          60

caa gat gag gag gaa gac gaa gag ctg aca ttg aaa tat gga gcc aag     240
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65          70          75          80

cac gtc atc atg ctc ttt gtt cct gtg acc ctc tgc atg gtc gtt gtg     288
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
          85          90          95

gtg gcc act atc aag tca gtc agc ttc tac acc cgg aag gat ggg cag     336
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
          100          105          110

cta atc tat acc cca ttc aca gaa gac acc gag act gta ggc cag aga     384
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
          115          120          125

gcc ctg cac tcg atc ttg aat gcc gcc atc atg atc agt gtc atc gtc     432
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
          130          135          140

gtt atg acc atc ctc ctg gtg gtc ctg tat aag tac agg tgc tac aag     480
Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145          150          155          160

gtc atc cat gcc tgg ctt att gtt tca tct ctg ttg ttg ctg ttc ttt     528
Val Ile His Ala Trp Leu Ile Val Ser Ser Leu Leu Leu Leu Phe
          165          170          175

ttt tca ttc att tac tta ggg gaa gta ttc aag acc tac aat gtc gcc     576
Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
          180          185          190

gtg gac tat att acg gtt gca ctc ctg atc tgg aat ttt ggt gtg gtc     624
Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
          195          200          205

ggg atg att gcc att cac tgg aaa ggc cca ctc cga ctg cag cag gcg     672
Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
          210          215          220

tat ctc att atg atc agt gcc ctc atg tcc ctg gta ttt atc aag tac     720
Tyr Leu Ile Met Ile Ser Ala Leu Met Ser Leu Val Phe Ile Lys Tyr
225          230          235          240

ctc cct gaa tgg acc gca tgg ctc atc ttg gct gtg att tca gta tat     768
Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
          245          250          255

gat ttg gtg gct gtt ctg tgc ccc aaa ggt cca ctt cgt atg ctg gtc     816
Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
          260          265          270

gaa aca gct cag gaa aga aat gag act ctc ttt cca gct ctt atc tat     864
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
          275          280          285

tcc tca acc atg gtg tgg ttg gtg aat atg gct gaa gga gac cca gaa     912
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
          290          295          300

gcc caa agg agg gta ccc aaa aac ccc aag tat agc aca caa gga aca     960
Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Ser Thr Gln Gly Thr

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305	310	315	320	
gag agg gaa gag aca cag gac act ggc act ggg agc gat gat ggt ggc				1008
Glu Arg Glu Glu Thr Gln Asp Thr Gly Thr Gly Ser Asp Asp Gly Gly	325	330	335	
ttc agt gag gag tgg gag gcc caa aga gac agt cac ctg ggg cct cat				1056
Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His	340	345	350	
cgc tcc act cct gag tca aga gct gct gtc cag gaa ctt tct ggg agc				1104
Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser	355	360	365	
atc ctc act agt gaa gac ccg gag gaa aga gga gta agg ctt ggg ctg				1152
Ile Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Arg Leu Gly Leu	370	375	380	
gga gat ttc att ttc tac agt gtt ctg gtt ggt aag gcc tca gcg acc				1200
Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr	385	390	395	400
gcc agt ggg gac tgg aac aca acc ata gcc tgc ttt gta gcc ata ttg				1248
Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu	405	410	415	
atc ggc ctg tgc ctt acg tta ctc ctg ctc gcc att ttc aag aaa gcg				1296
Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala	420	425	430	
ttg ccg gcc ctt ccc atc tcc atc acc ttc ggg ctc att ttc tac ttt				1344
Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe	435	440	445	
gcc acg gat tat ctc gtg cag ccc ttc atg gac caa ctt gca ttc cat				1392
Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His	450	455	460	
caa ttt tat atc tag				1407
Gln Phe Tyr Ile				
465				

<210> 86

<211> 468

<212> PRT

<213> Rattus norvegicus

<400> 86

Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met			
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Ser Glu Asp Ser His Ser Ser Ser Val Arg Ser Gln Asn Asp Asn Gln			
20	25	30	
Glu Arg Gln Gln His His Asp Arg Gln Arg Leu Asp Asn Pro Glu Ser			
35	40	45	
Ile Ser Asn Gly Arg Pro Gln Ser Asn Phe Thr Arg Gln Val Ile Glu			

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

Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Ser Thr Gln Gly Thr
305 310 315 320

Glu Arg Glu Glu Thr Gln Asp Thr Gly Thr Gly Ser Asp Asp Gly Gly
325 330 335

Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His
340 345 350

Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser
355 360 365

Ile Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Arg Leu Gly Leu
370 375 380

Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr
385 390 395 400

Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu
405 410 415

Ile Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala
420 425 430

Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe
435 440 445

Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His
450 455 460

Gln Phe Tyr Ile
465

<210> 87

<211> 1404

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1401)

<400> 87

atg aca gag tta cct gca cgg ttg tcc tac ttc cag aat gca cag atg 48
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15

tct gag gac aac cac ctg agc aat act gta cgt agc cag aat gac aat 96
Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20 25 30

aga gaa cgg cag gag cac aac gac aga cgg agc ctt ggc cac cct gag Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu 35 40 45	144
cca tta tct aat gga cga ccc cag ggt aac tcc cgg cag gtg gtg gag Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu 50 55 60	192
caa gat gag gaa gaa gat gag gag ctg aca ttg aaa tat ggc gcc aag Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys 65 70 75 80	240
cat gtg atc atg ctc ttt gtc cct gtg act ctc tgc atg gtg gtg gtc His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val 85 90 95	288
gtg gct acc att aag tca gtc agc ttt tat acc cgg aag gat ggg cag Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln 100 105 110	336
cta atc tat acc cca ttc aca gaa gat acc gag act gtg ggc cag aga Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg 115 120 125	384
gcc ctg cac tca att ctg aat gct gcc atc atg atc agt gtc att gtt Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val 130 135 140	432
gtc atg act atc ctc ctg gtg gtt ctg tat aaa tac agg tgc tat aag Val Met Thr Ile Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys 145 150 155 160	480
gtc atc cat gcc tgg ctt att ata tca tct cta ttg ttg ctg ttc ttt Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe 165 170 175	528
ttt tca ttc att tac ttg ggg gaa gtg ttt aaa acc tat aac gtt gct Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala 180 185 190	576
gtg gac tac att act gtt gca ctc ctg atc tgg aat ttt ggt gtg gtg Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val 195 200 205	624
gga atg att tcc att cac tgg aaa ggt cca ctt cga ctc cag cag gca Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala 210 215 220	672
tat ctc att atg att agt gcc ctc atg gcc ctg gtg ttt atc aag tac Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr 225 230 235 240	720
ctc cct gaa tgg act gcg tgg ctc atc ttg gct gtg att tca gta tat Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr 245 250 255	768
gat tta gtg gct gtt ttg tgt ccg aaa ggt cca ctt cgt atg ctg gtt Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val 260 265 270	816
gaa aca gct cag gag aga aat gaa acg ctt ttt cca gct ctc att tac Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr 275 280 285	864

tcc tca aca atg gtg tgg ttg gtg aat atg gca gaa gga gac ccg gaa 912
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300
 gct caa agg aga gta tcc aaa aat tcc aag tat aat gca gaa agc aca 960
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
 305 310 315 320
 gaa agg gag tca caa gac act gtt gca gag aat gat gat ggc ggg ttc 1008
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
 325 330 335
 agt gag gaa tgg gaa gcc cag agg gac agt cat cta ggg cct cat cgc 1056
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350
 tct aca cct gag tca cga gct gct gtc cag gaa ctt tcc agc agt atc 1104
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
 355 360 365
 ctc gct ggt gaa gac cca gag gaa agg gga gta aaa ctt gga ttg gga 1152
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380
 gat ttc att ttc tac agt gtt ctg gtt ggt aaa gcc tca gca aca gcc 1200
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400
 agt gga gac tgg aac aca acc ata gcc tgt ttc gta gcc ata tta att 1248
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415
 ggt ttg tgc ctt aca tta tta ctc ctt gcc att ttc aag aaa gca ttg 1296
 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430
 cca gct ctt cca atc tcc atc acc ttt ggg ctt gtt ttc tac ttt gcc 1344
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 435 440 445
 aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc cat caa 1392
 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
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 Phe Tyr Ile
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<210> 88

<211> 467

<212> PRT

<213> Homo sapiens

<400> 88

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

275 280 285
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
 305 310 315 320
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
 325 330 335
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
 355 360 365
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415
 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
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 Phe Tyr Ile
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 <211> 1347
 <212> DNA
 <213> Mus musculus
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 <221> CDS
 <222> (1)..(1344)
 <400> 89
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Arg	Thr	Ser	Leu	Met	Ser	Ala	Glu	Ser	Pro	Thr	Ser	Arg	Ser	Cys	Gln
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gaa	ggc	agg	cca	ggc	ccg	gag	gat	gga	gag	agc	act	gcc	cag	tgg	agg
Glu	Gly	Arg	Pro	Gly	Pro	Glu	Asp	Gly	Glu	Ser	Thr	Ala	Gln	Trp	Arg
		35				40					45				
act	cag	gag	agc	gaa	gaa	gac	tgt	gaa	gag	gac	ccg	gac	cgc	tac	gca
Thr	Gln	Glu	Ser	Glu	Glu	Asp	Cys	Glu	Glu	Asp	Pro	Asp	Arg	Tyr	Ala
	50					55				60					
tgc	agt	ggg	gct	cct	ggg	cga	ccg	tcg	ggc	ctg	gag	gaa	gag	ctg	acc
Cys	Ser	Gly	Ala	Pro	Gly	Arg	Pro	Ser	Gly	Leu	Glu	Glu	Glu	Leu	Thr
65				70				75					80		
ctc	aag	tat	ggg	gcg	aaa	cgt	gtg	atc	atg	cta	ttc	gtg	cct	gtc	acg
Leu	Lys	Tyr	Gly	Ala	Lys	Arg	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr
			85					90					95		
ctg	tgt	atg	atc	gtg	gtg	gtg	gcc	act	atc	aag	tct	gtg	cgt	ttc	tac
Leu	Cys	Met	Ile	Val	Val	Val	Ala	Thr	Ile	Lys	Ser	Val	Arg	Phe	Tyr
			100					105					110		
act	gag	aag	aac	ggg	cag	ctc	atc	tac	acg	ccc	ttc	acg	gag	gac	acg
Thr	Glu	Lys	Asn	Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr
		115				120					125				
ccc	tcg	gtg	ggc	cag	cgg	ctc	ctc	aac	tcc	gtg	ctt	aac	acc	ctc	atc
Pro	Ser	Val	Gly	Gln	Arg	Leu	Leu	Asn	Ser	Val	Leu	Asn	Thr	Leu	Ile
		130				135					140				
atg	atc	agc	gtc	atc	gta	gtc	atg	acc	atc	ttc	ctc	gtg	gta	ctc	tac
Met	Ile	Ser	Val	Ile	Val	Val	Met	Thr	Ile	Phe	Leu	Val	Val	Leu	Tyr
145				150						155				160	
aag	tat	cga	tgc	tac	aag	ttc	atc	cat	ggc	tgg	ctg	atc	atg	tcc	tcc
Lys	Tyr	Arg	Cys	Tyr	Lys	Phe	Ile	His	Gly	Trp	Leu	Ile	Met	Ser	Ser
			165					170					175		
ctg	atg	ctc	ctc	ttc	ttg	ttc	acc	tac	atc	tac	ctc	ggg	gaa	gtg	ctc
Leu	Met	Leu	Leu	Phe	Leu	Phe	Thr	Tyr	Ile	Tyr	Leu	Gly	Glu	Val	Leu
			180					185					190		
aag	acc	tac	aat	gtg	gcc	atg	gac	tat	ccc	aca	ctc	ttc	ctg	gct	gtc
Lys	Thr	Tyr	Asn	Val	Ala	Met	Asp	Tyr	Pro	Thr	Leu	Phe	Leu	Ala	Val
		195				200					205				
tgg	aac	ttc	ggg	gca	gtg	ggc	atg	gtg	tgc	atc	cac	tgg	aag	ggg	cct
Trp	Asn	Phe	Gly	Ala	Val	Gly	Met	Val	Cys	Ile	His	Trp	Lys	Gly	Pro
	210					215					220				
cta	gcg	ctg	cag	cag	gct	tac	ctt	att	gtg	atc	agc	gca	ctc	atg	gcc
Leu	Ala	Leu	Gln	Gln	Ala	Tyr	Leu	Ile	Val	Ile	Ser	Ala	Leu	Met	Ala
225				230					235					240	
ctg	gtg	ttc	atc	aag	tac	ctg	ccg	gag	tgg	tct	gcc	tgg	gtc	atc	ttg
Leu	Val	Phe	Ile	Lys	Tyr	Leu	Pro	Glu	Trp	Ser	Ala	Trp	Val	Ile	Leu
			245					250					255		

ggt gcc atc tct gtg tac gat ctc gtg gcc gtg ctg tgc ccc aaa ggg 816
 Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
 260 265 270
 cca ctg agg atg ctg gtg gaa act gcc cag gag aga aat gag ccc ata 864
 Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
 275 280 285
 ttt cct gcc ctg ata tac tca tct gcc atg gtg tgg acg gtg ggc atg 912
 Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
 290 295 300
 gca aag ctg gac ccc tcc tct caa gga gcg ctg cag ctc ccc tat gac 960
 Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
 305 310 315 320
 cca gag atg gaa gaa gac tcc tac gac agt ttt gga gaa ccc tca tac 1008
 Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
 325 330 335
 cct gaa gcc ttc gaa gcc ccc ctg cct gcc tac cca ggg gag gag ctg 1056
 Pro Glu Ala Phe Glu Ala Pro Leu Pro Gly Tyr Pro Gly Glu Glu Leu
 340 345 350
 gag gag gag gag gaa agg gcc gtg aag ctc gcc ctg gga gac ttc atc 1104
 Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
 355 360 365
 ttc tac agc gtc ctg gtg gcc aag gct gca gcc act gcc aac gga gac 1152
 Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Asn Gly Asp
 370 375 380
 tgg aac act acg ctg gcc tgt ttt atc gcc atc ctc att gcc ttg tgt 1200
 Trp Asn Thr Thr Leu Ala Cys Phe Ile Ala Ile Leu Ile Gly Leu Cys
 385 390 395 400
 ctc acc ctc ctg ctg ctt gct gtg ttc aag aag gct ctg ccc gcc ctc 1248
 Leu Thr Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
 405 410 415
 ccc atc tcc atc acc ttt gga ctc atc ttc tac ttc tcc aca gac aac 1296
 Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
 420 425 430
 ctg gtg cgc cct ttc atg gac act ctg gcc tcc cac cag ctc tac atc 1344
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 tga 1347
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 <211> 448
 <212> PRT
 <213> Mus musculus
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 Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Ser Arg Ser Cys Gln

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

Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
 275 280 285

Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
 290 295 300

Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
 305 310 315 320

Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
 325 330 335

Pro Glu Ala Phe Glu Ala Pro Leu Pro Gly Tyr Pro Gly Glu Glu Leu
 340 345 350

Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
 355 360 365

Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Asn Gly Asp
 370 375 380

Trp Asn Thr Thr Leu Ala Cys Phe Ile Ala Ile Leu Ile Gly Leu Cys
 385 390 395 400

Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
 405 410 415

Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
 420 425 430

Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile
 435 440 445

<210> 91

<211> 1347

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(1344)

<400> 91

atg ctc aca ttc atg gcc tct gat agc gag gaa gag gtg tgc gat gag	48
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1 5 10 15	
cgg acg tcc ttg atg tca gcc gag agc cct aca tca cgt tcc tgc cag	96
Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Ser Arg Ser Cys Gln	
20 25 30	

gac agc agg cca ggc cca gag gat gga gag aac act gcc cag tgg agg Asp Ser Arg Pro Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg 35 40 45	144
agc cag gag aac gag gac gac tgt gag gag gac ccg gac cac tat gcc Ser Gln Glu Asn Glu Asp Asp Cys Glu Glu Asp Pro Asp His Tyr Ala 50 55 60	192
tgc agt ggg gtt cct ggg cga cca tog ggc ctg gag gag gag ctg acc Cys Ser Gly Val Pro Gly Arg Pro Ser Gly Leu Glu Glu Glu Leu Thr 65 70 75 80	240
ctc aag tat ggg gcg aag cac gtg atc atg ctg ttc gtg cct gtc acg Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr 85 90 95	288
ctg tgc atg att gtg gtg gtg gcc acc atc aag tcc gtg cgt ttc tac Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr 100 105 110	336
acg gag aag aac ggg cag ctc atc tac acg ccc ttc acc gag gac aca Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr 115 120 125	384
ccc tct gtg ggc cag cgg ctc ctc aac tcc gtg ctg aac act ctg atc Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile 130 135 140	432
atg atc agc gtc att gtg gtc atg act atc ttc cta gtg gta ctc tac Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr 145 150 155 160	480
aaa tat cgc tgt tac aag ttc atc cat ggc tgg ctg atc atg tcc tcc Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser 165 170 175	528
ctg atg ctc ctc ttc ttg ttc acc tac atc tac ctc ggg gaa gtg ttc Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Phe 180 185 190	576
aag acc tac aat gtg gcc atg gac tac ccc aca ctg ttc ctg gct gtc Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Phe Leu Ala Val 195 200 205	624
tgg aac ttc ggg gca gtg ggc atg gtg tgc atc cac tgg aag ggt ccc Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro 210 215 220	672
ctg gtg ctc cag cag gct tac ctc att gtg atc agc gca ctc atg gcc Leu Val Leu Gln Gln Ala Tyr Leu Ile Val Ile Ser Ala Leu Met Ala 225 230 235 240	720
ctg gtg ttc atc aag tac ctg ccg gag tgg tcc gct tgg gtc atc ttg Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu 245 250 255	768
ggc gcc atc tct gtg tac gat ctc gtg gct gtg ctg tgc ccc aaa ggg Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly 260 265 270	816
cca ctg agg atg ctg gtg gaa act gcc cag gaa aga aac gag ccc ata Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile 275 280 285	864

ttt cct gcc ctc ata tac tca tct gcc atg gtg tgg acg gta ggc atg 912
 Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
 290 295 300
 gcg aag ctg gac ccc tcc tct cag gga gca ctg cag ctc cct tac gat 960
 Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
 305 310 315 320
 cca gag atg gaa gaa gac tcc tat gac agt ttt ggg gaa ccc tca tac 1008
 Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
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 cct gaa gcc ttc gaa gct ccc cag cct ggc tac cca ggg gaa gag ccg 1056
 Pro Glu Ala Phe Glu Ala Pro Gln Pro Gly Tyr Pro Gly Glu Glu Pro
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 gag gag gag gag gaa agg ggt gta aag ctt ggt ctg gga gac ttc atc 1104
 Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
 355 360 365
 ttc tac agc gtt ctg gtg ggc aag gca gca gcc aca ggc aac gga gac 1152
 Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Asn Gly Asp
 370 375 380
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 Trp Ser Thr Thr Leu Ala Cys Phe Ile Ala Ile Leu Ile Gly Leu Cys
 385 390 395 400
 ctc acc ctc ctg ctg ctc gcc gtg ttc aag aag gcc ctg ccc gcc ctc 1248
 Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
 405 410 415
 ccc atc tcc atc acc ttc ggg ctc atc ttt tac ttc tcc aca gac aac 1296
 Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
 420 425 430
 ctg gtg cgt cct ttc atg gac acg ttg gcc tcc cac cag ctc tac atc 1344
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 435 440 445
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<210> 92

<211> 448

<212> PRT

<213> Rattus norvegicus

<400> 92

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 Asp Ser Arg Pro Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg
 35 40 45

Ser Gln Glu Asn Glu Asp Asp Cys Glu Glu Asp Pro Asp His Tyr Ala
 50 55 60
 Cys Ser Gly Val Pro Gly Arg Pro Ser Gly Leu Glu Glu Glu Leu Thr
 65 70 75 80
 Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
 85 90 95
 Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
 100 105 110
 Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr
 115 120 125
 Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
 130 135 140
 Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr
 145 150 155 160
 Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser
 165 170 175
 Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Phe
 180 185 190
 Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Phe Leu Ala Val
 195 200 205
 Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro
 210 215 220
 Leu Val Leu Gln Gln Ala Tyr Leu Ile Val Ile Ser Ala Leu Met Ala
 225 230 235 240
 Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
 245 250 255
 Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
 260 265 270
 Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
 275 280 285
 Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
 290 295 300
 Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
 305 310 315 320
 Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
 325 330 335
 Pro Glu Ala Phe Glu Ala Pro Gln Pro Gly Tyr Pro Gly Glu Glu Pro
 340 345 350
 Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
 355 360 365
 Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Asn Gly Asp
 370 375 380
 Trp Ser Thr Thr Leu Ala Cys Phe Ile Ala Ile Leu Ile Gly Leu Cys
 385 390 395 400
 Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
 405 410 415
 Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
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 Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile
 435 440 445

<210> 93
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<220>
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<400> 93
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 Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln
 20 25 30
 gag gcc agg cag gcc cca gag gat gga gag aac act gcc cag tgg aga 144
 Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg
 35 40 45
 agc cag gag aac gag gag gac ggt gag gag gac cct gac cgc tat gtc 192
 Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val
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 tgt agt ggg gtt ccc ggg cgg ccg cca gcc ctg gag gaa gag ctg acc 240
 Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr
 65 70 75 80
 ctc aaa tac gga gcg aag cac gtg atc atg ctg ttt gtg cct gtc act 288
 Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
 85 90 95
 ctg tgc atg atc gtg gtg gta gcc acc atc aag tct gtg cgc ttc tac 336
 Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
 100 105 110
 aca gag aag aat gga cag ctc atc tac acg cca ttc act gag gac aca 384
 Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr
 115 120 125
 ccc tgg gtg gcc cag cgc ctc ctc aac tcc gtg ctg aac acc ctc atc 432
 Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
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 145 150 155 160
 aag tac cgc tgc tac aag ttc atc cat gcc tgg ttg atc atg tct tca 528
 Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser
 165 170 175
 ctg atg ctg ctg ttc ctc ttc acc tat atc tac ctt ggg gaa gtg ctc 576
 Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu
 180 185 190
 aag acc tac aat gtg gcc atg gac tac ccc acc ctc ttg ctg act gtc 624
 Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val
 195 200 205
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 210 215 220
 ctg gtg ctg cag cag gcc tac ctc atc atg atc agt gcg ctc atg gcc 720
 Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala
 225 230 235 240
 cta gtg ttc atc aag tac ctc cca gag tgg tcc gcg tgg gtc atc ctg 768
 Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
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 gcc gcc atc tct gtg tat gat ctc gtg gct gtg ctg tgt ccc aaa ggg 816
 Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
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 cct ctg aga atg ctg gta gaa act gcc cag gag aga aat gag ccc ata 864
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 Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp

305	310	315	320	
ccg gag atg gaa gaa gac tcc tat gac agt ttt ggg gag cct tca tac				1008
Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr	325	330	335	
ccc gaa gtc ttt gag cct ccc ttg act ggc tac cca ggg gag gag ctg				1056
Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu	340	345	350	
gag gaa gag gag gaa agg ggc gtg aag ctt ggc ctc ggg gac ttc atc				1104
Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile	355	360	365	
ttc tac agt gtg ctg gtg ggc aag gcg gct gcc acg ggc agc ggg gac				1152
Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp	370	375	380	
tgg aat acc acg ctg gcc tgc ttc gtg gcc atc ctc att ggc ttg tgt				1200
Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys	385	390	395	400
ctg acc ctc ctg ctg ctt gct gtg ttc aag aag gcg ctg ccc gcc ctc				1248
Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu	405	410	415	
ccc atc tcc atc acg ttc ggg ctc atc ttt tac ttc tcc acg gac aac				1296
Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn	420	425	430	
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Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile	435	440	445	
tga				1347
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Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg				
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Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val				
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Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr				
65	70	75	80	

Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
 85 90 95
 Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
 100 105 110
 Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr
 115 120 125
 Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
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 Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr
 145 150 155 160
 Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser
 165 170 175
 Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu
 180 185 190
 Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val
 195 200 205
 Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro
 210 215 220
 Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala
 225 230 235 240
 Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
 245 250 255
 Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
 260 265 270
 Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
 275 280 285
 Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
 290 295 300
 Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
 305 310 315 320
 Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
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 Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu
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 Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
 355 360 365
 Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp
 370 375 380
 Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys
 385 390 395 400
 Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
 405 410 415
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<211> 2127

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<213> Mus musculus

<220>

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<222> (1)..(2124)

<400> 95

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ctt ctt ctt ctg tct ttt tcc gtg gta ctg gca gga ttg tgt ggg gga      96
Leu Leu Leu Leu Ser Phe Ser Val Val Leu Ala Gly Leu Cys Gly Gly
      20      25      30

aac tca gtg gag agg aaa atc tac att ccc tta aat aaa aca gct cct      144
Asn Ser Val Glu Arg Lys Ile Tyr Ile Pro Leu Asn Lys Thr Ala Pro
      35      40      45

tgt gtc cgc ctg ctg aac gcc act cat cag att ggc tgc cag tct tca      192
Cys Val Arg Leu Leu Asn Ala Thr His Gln Ile Gly Cys Gln Ser Ser
      50      55      60

att agt ggg gat aca ggg gtt atc cac gta gtg gag aaa gaa gaa gac      240
Ile Ser Gly Asp Thr Gly Val Ile His Val Val Glu Lys Glu Glu Asp
      65      70      75      80

ctg aag tgg gtg ttg acc gat ggc ccc aac ccc cct tac atg gtt ctg      288
Leu Lys Trp Val Leu Thr Asp Gly Pro Asn Pro Pro Tyr Met Val Leu
      85      90      95

ctg gag ggc aag ctg ttc acc aga gat gta atg gag aag ctg aag gga      336
Leu Glu Gly Lys Leu Phe Thr Arg Asp Val Met Glu Lys Leu Lys Gly
      100      105      110

aca acc agt aga atc gct ggt ctt gcc gtg act cta gcc aag ccc aac      384
Thr Thr Ser Arg Ile Ala Gly Leu Ala Val Thr Leu Ala Lys Pro Asn
      115      120      125

tca act tca agc ttc tct cct agt gtg cag tgc cca aat gat ggg ttt      432
Ser Thr Ser Ser Phe Ser Pro Ser Val Gln Cys Pro Asn Asp Gly Phe
      130      135      140

ggg att tac tcc aac tcc tac ggg cca gag ttt gct cac tgc aag aaa      480
Gly Ile Tyr Ser Asn Ser Tyr Gly Pro Glu Phe Ala His Cys Lys Lys
      145      150      155      160

aca ctg tgg aat gaa ctg ggc aac gcc ttg gct tat gaa gac ttt agt      528
Thr Leu Trp Asn Glu Leu Gly Asn Gly Leu Ala Tyr Glu Asp Phe Ser
      165      170      175

ttc ccc atc ttt ctt ctt gaa gat gag aac gaa acc aag gtc atc aag      576
Phe Pro Ile Phe Leu Leu Glu Asp Glu Asn Glu Thr Lys Val Ile Lys
      180      185      190

cag tgc tat caa gat cac aac ctg ggt cag aat ggc tct gca cca agc      624
Gln Cys Tyr Gln Asp His Asn Leu Gly Gln Asn Gly Ser Ala Pro Ser
      195      200      205

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      210      215      220

agc act gcc acc tgc atg cgg cgc agc ttc atc cag agc acc ttc agc      720
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      225      230      235      240

atc aac cca gaa atc gtc tgt gac ccc tta tct gac tac aac gta tgg      768
Ile Asn Pro Glu Ile Val Cys Asp Pro Leu Ser Asp Tyr Asn Val Trp
      245      250      255

agc atg ctt aag cct ata aat aca tct gtg gga cta gaa cct gac gtc      816
Ser Met Leu Lys Pro Ile Asn Thr Ser Val Gly Leu Glu Pro Asp Val
      260      265      270

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Arg Val Val Val Ala Ala Thr Arg Leu Asp Ser Arg Ser Phe Phe Trp
      275      280      285

aat gtg gcc cca ggg gct gaa agt gct gta gcc tcc ttt gtc act cag      912
Asn Val Ala Pro Gly Ala Glu Ser Ala Val Ala Ser Phe Val Thr Gln
      290      295      300

ctg gct gca gct gaa gct ttg cac aag gca cct gat gtg acc act cta      960
Leu Ala Ala Ala Glu Ala Leu His Lys Ala Pro Asp Val Thr Thr Leu
      305      310      315      320

tcc cga aat gtg atg ttt gtc ttc ttc cag ggg gaa act ttt gac tac      1008
Ser Arg Asn Val Met Phe Val Phe Phe Gln Gly Glu Thr Phe Asp Tyr
      325      330      335

att ggc agc tca cgg atg gto tat gat atg gag aac ggc aag ttt ccc      1056

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Ile Gly Ser Ser Arg Met Val Tyr Asp Met Glu Asn Gly Lys Phe Pro	
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Val Arg Leu Glu Asn Ile Asp Ser Phe Val Glu Leu Gly Gln Val Ala	
355 360 365	
cta aga act tca cta gat ctc tgg atg cac aca gat ccc atg tct cag	1152
Leu Arg Thr Ser Leu Asp Ile Trp Met His Thr Asp Pro Met Ser Gln	
370 375 380	
aaa aat gag tct gtg aaa aac cag gtg gag gat ctt ctg gcc act ctg	1200
Lys Asn Glu Ser Val Lys Asn Gln Val Glu Asp Leu Leu Ala Thr Leu	
385 390 395 400	
gag aag agc ggt gct ggt gtc cct gaa gtt gtc ctg agg aga ctg gcc	1248
Glu Lys Ser Gly Ala Gly Val Pro Glu Val Val Leu Arg Arg Leu Ala	
405 410 415	
cag tcc cag gcc ctt cca cct tca tct cta caa cga ttt ctt cgg gct	1296
Gln Ser Gln Ala Leu Pro Pro Ser Ser Leu Gln Arg Phe Leu Arg Ala	
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Arg Asn Ile Ser Gly Val Val Leu Ala Asp His Ser Gly Ser Phe His	
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Asn Arg Tyr Tyr Gln Ser Ile Tyr Asp Thr Ala Glu Asn Ile Asn Val	
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Thr Tyr Pro Glu Trp Gln Ser Pro Glu Glu Asp Leu Asn Phe Val Thr	
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Asp Thr Ala Lys Ala Leu Ala Asn Val Ala Thr Val Leu Ala Arg Ala	
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ctg tat gag ctt gca gga gga acc aac ttc agc agc tcc atc cag gct	1536
Leu Tyr Glu Leu Ala Gly Gly Thr Asn Phe Ser Ser Ser Ile Gln Ala	
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Asp Pro Gln Thr Val Thr Arg Leu Leu Tyr Gly Phe Leu Val Lys Ala	
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Leu Asp Asp Arg Pro Leu Gln His Tyr Ile Ala Val Ser Ser Pro Thr	
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aac acg act tac gtt gtg cag tac gcc ttg gca aac ctg act ggc aag	1728
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Ala Thr Asn Leu Thr Arg Glu Gln Cys Gln Asp Pro Ser Lys Val Pro	
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aat gag agc aag gat tta tat gaa tac tcg tgg gta caa ggc cct tgg	1824
Asn Glu Ser Lys Asp Leu Tyr Glu Tyr Ser Trp Val Gln Gly Pro Trp	
595 600 605	
aat tcc aac agg aca gag agg ctc cca cag tgt gtg cgc tcc aca gtg	1872
Asn Ser Asn Arg Thr Glu Arg Leu Pro Gln Cys Val Arg Ser Thr Val	
610 615 620	
cga ctg gcc agg gcc ttg tcc cct gcc ttt gaa ctg agt cag tgg agc	1920
Arg Leu Ala Arg Ala Leu Ser Pro Ala Phe Glu Leu Ser Gln Trp Ser	
625 630 635 640	
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Ser Thr Glu Tyr Ser Thr Trp Ala Glu Ser Arg Trp Lys Asp Ile Gln	
645 650 655	
gct cgg ata ttc cta att gcc agc aaa gag ctt gag ttc atc acg ctg	2016
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<211> 708

<212> PRT

<213> Mus musculus

<400> 96

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35      40      45

Cys Val Arg Leu Leu Asn Ala Thr His Gln Ile Gly Cys Gln Ser Ser
50      55      60

Ile Ser Gly Asp Thr Gly Val Ile His Val Val Glu Lys Glu Glu Asp
65      70      75      80

Leu Lys Trp Val Leu Thr Asp Gly Pro Asn Pro Pro Tyr Met Val Leu
85      90      95

Leu Glu Gly Lys Leu Phe Thr Arg Asp Val Met Glu Lys Leu Lys Gly
100     105     110

Thr Thr Ser Arg Ile Ala Gly Leu Ala Val Thr Leu Ala Lys Pro Asn
115     120     125

Ser Thr Ser Ser Phe Ser Pro Ser Val Gln Cys Pro Asn Asp Gly Phe
130     135     140

Gly Ile Tyr Ser Asn Ser Tyr Gly Pro Glu Phe Ala His Cys Lys Lys
145     150     155     160

Thr Leu Trp Asn Glu Leu Gly Asn Gly Leu Ala Tyr Glu Asp Phe Ser
165     170     175

Phe Pro Ile Phe Leu Leu Glu Asp Glu Asn Glu Thr Lys Val Ile Lys
180     185     190

Gln Cys Tyr Gln Asp His Asn Leu Gly Gln Asn Gly Ser Ala Pro Ser
195     200     205

Phe Pro Leu Cys Ala Met Gln Leu Phe Ser His Met His Ala Val Ile
210     215     220

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305     310     315     320

Ser Arg Asn Val Met Phe Val Phe Phe Gln Gly Glu Thr Phe Asp Tyr
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Ile Gly Ser Ser Arg Met Val Tyr Asp Met Glu Asn Gly Lys Phe Pro
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 Glu Lys Ser Gly Ala Gly Val Pro Glu Val Val Leu Arg Arg Leu Ala
 405 410 415
 Gln Ser Gln Ala Leu Pro Pro Ser Ser Leu Gln Arg Phe Leu Arg Ala
 420 425 430
 Arg Asn Ile Ser Gly Val Val Leu Ala Asp His Ser Gly Ser Phe His
 435 440 445
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 450 455 460
 Thr Tyr Pro Glu Trp Gln Ser Pro Glu Glu Asp Leu Asn Phe Val Thr
 465 470 475 480
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 485 490 495
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 500 505 510
 Asp Pro Gln Thr Val Thr Arg Leu Leu Tyr Gly Phe Leu Val Lys Ala
 515 520 525
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 Leu Asp Asp Arg Pro Leu Gln His Tyr Ile Ala Val Ser Ser Pro Thr
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 565 570 575
 Ala Thr Asn Leu Thr Arg Glu Gln Cys Gln Asp Pro Ser Lys Val Pro
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 595 600 605
 Asn Ser Asn Arg Thr Glu Arg Leu Pro Gln Cys Val Arg Ser Thr Val
 610 615 620
 Arg Leu Ala Arg Ala Leu Ser Pro Ala Phe Glu Leu Ser Gln Trp Ser
 625 630 635 640
 Ser Thr Glu Tyr Ser Thr Trp Ala Glu Ser Arg Trp Lys Asp Ile Gln
 645 650 655
 Ala Arg Ile Phe Leu Ile Ala Ser Lys Glu Leu Glu Phe Ile Thr Leu
 660 665 670
 Ile Val Gly Phe Ser Ile Leu Ile Phe Ser Leu Ile Val Thr Tyr Cys
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<212> DNA

<213> Rattus norvegicus

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<222> (1)..(2124)

<400> 97

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1      5      10      15

ctc ctt ctt ctg tct ttt tcc gtg gta cta gca gga ttg tgt ggg gga      96
Leu Leu Leu Leu Ser Phe Ser Val Val Leu Ala Gly Leu Cys Gly Gly
20     25     30

aac tca gtg gag agg aag atc tac att ccc tta aat aaa aca gct cct      144
Asn Ser Val Glu Arg Lys Ile Tyr Ile Pro Leu Asn Lys Thr Ala Pro
35     40     45

tgt gtc cgc ctg ctc aat gcc act cat cag att ggc tgc cag tct tca      192
Cys Val Arg Leu Leu Asn Ala Thr His Gln Ile Gly Cys Gln Ser Ser
50     55     60

att agt ggg gat aca ggg gtt atc cac gta gtg gag aaa gaa gac gac      240
Ile Ser Gly Asp Thr Gly Val Ile His Val Val Glu Lys Glu Asp Asp
65     70     75     80

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Leu Lys Trp Val Leu Thr Asp Gly Pro Asn Pro Pro Tyr Met Val Leu
85     90     95

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100    105    110

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

tca acg tca agc ttc tct cct agc gtg cag tgc cca aat gat ggg ttt      432
Ser Thr Ser Ser Phe Ser Pro Ser Val Gln Cys Pro Asn Asp Gly Phe
130    135    140

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Gly Ile Tyr Ser Asn Ser Tyr Gly Pro Glu Phe Ala His Cys Lys Lys
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Thr Leu Trp Asn Glu Leu Gly Asn Gly Leu Ala Tyr Asp Asp Phe Ser
165    170    175

ttc ccc atc ttt ctt ctt gaa gat gag aac gaa acc aag gtc atc aag      576
Phe Pro Ile Phe Leu Leu Glu Asp Glu Asn Glu Thr Lys Val Ile Lys
180    185    190

cag tgc tat caa gat cac aac ctg ggt cag aat ggc tct gca ccg agc      624
Gln Cys Tyr Gln Asp His Asn Leu Gly Gln Asn Gly Ser Ala Pro Ser
195    200    205

ttc cca ctg tgt gct atg cag ctc ttc tca cac atg cac gcc gtc atc      672
Phe Pro Leu Cys Ala Met Gln Leu Phe Ser His Met His Ala Val Ile
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225    230    235    240

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Ile Asn Pro Glu Ile Val Cys Asp Pro Leu Ser Asp Tyr Asn Val Trp
245    250    255

agc atg ctt aag cct ata aat acg tot ggg gga tta gaa cct gat gtc      816
Ser Met Leu Lys Pro Ile Asn Thr Ser Gly Gly Leu Glu Pro Asp Val
260    265    270

agg gtt gtg gtt gca gcc aca cgg ctg gat agc cgg tcc ttc ttc tgg      864
Arg Val Val Val Ala Ala Thr Arg Leu Asp Ser Arg Ser Phe Phe Trp
275    280    285

aat gtg gcc cca ggg gca gaa agt gcc gtt gcc tcc ttt gtc act cag      912
Asn Val Ala Pro Gly Ala Glu Ser Ala Val Ala Ser Phe Val Thr Gln
290    295    300

ctg gcc gca gct gaa gct ttg cac aag gca cct gat gtg acc acc cta      960
Leu Ala Ala Ala Glu Ala Leu His Lys Ala Pro Asp Val Thr Thr Leu
305    310    315    320

ccc cga aat gtg atg ttt gtc ttc ttc cag ggg gaa act ttt gac tac      1008
Pro Arg Asn Val Met Phe Val Phe Phe Gln Gly Glu Thr Phe Asp Tyr
325    330    335

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att ggc agc tca agg atg gtc tat gac atg gag aac ggc aag ttt cct 1056
 Ile Gly Ser Ser Arg Met Val Tyr Asp Met Glu Asn Gly Lys Phe Pro
 340 345 350
 gtg cgg cta gag aac att gac tcc ttt gtg gag ctg ggg cag gtg gcc 1104
 Val Arg Leu Glu Asn Ile Asp Ser Phe Val Glu Leu Gly Gln Val Ala
 355 360 365
 cta agg acg tca cta gaa ctg tgg atg cac aca gat cct atg tct cag 1152
 Leu Arg Thr Ser Leu Glu Leu Trp Met His Thr Asp Pro Met Ser Gln
 370 375 380
 aaa aat gaa tct gtg aag aac cag gtg gag gat ctt ctg gtc act ctg 1200
 Lys Asn Glu Ser Val Lys Asn Gln Val Glu Asp Leu Leu Val Thr Leu
 385 390 395 400
 gag cag agt ggt gct gat acc cct caa gtt gtc ctg agc aga cta gtc 1248
 Glu Gln Ser Gly Ala Asp Thr Pro Gln Val Val Leu Ser Arg Leu Val
 405 410 415
 cag tcc cag gcc ctt cca cca tca tct cta caa cga ttt ctt cgg gct 1296
 Gln Ser Gln Ala Leu Pro Pro Ser Ser Leu Gln Arg Phe Leu Arg Ala
 420 425 430
 cga aac atc tct ggt gtg gtc ttg gct gac cac tct ggt tcc ttc cac 1344
 Arg Asn Ile Ser Gly Val Val Leu Ala Asp His Ser Gly Ser Phe His
 435 440 445
 aat cgg tat tac cag agc att tat gac act gct gag aac att aac gtg 1392
 Asn Arg Tyr Tyr Gln Ser Ile Tyr Asp Thr Ala Glu Asn Ile Asn Val
 450 455 460
 acc tat cct gag tcg cag agc cca gaa gag gac ctg aac ttt gta aca 1440
 Thr Tyr Pro Glu Ser Gln Ser Pro Glu Glu Asp Leu Asn Phe Val Thr
 465 470 475 480
 gac act gcc aag gca ctg gca gat gtt gcc aca gtg ctg gca cga gct 1488
 Asp Thr Ala Lys Ala Leu Ala Asp Val Ala Thr Val Leu Ala Arg Ala
 485 490 495
 ttg tac aag ctt gca gga gga acc aac ttc aac aac tcc att cag gct 1536
 Leu Tyr Lys Leu Ala Gly Gly Thr Asn Phe Asn Asn Ser Ile Gln Ala
 500 505 510
 gat ccc cag aca gtt aca cgt ctg ctg tat ggg ttc ctg gtc aga gct 1584
 Asp Pro Gln Thr Val Thr Arg Leu Leu Tyr Gly Phe Leu Val Arg Ala
 515 520 525
 aac aac tca tgg ttt cag tct atc ctg aga cat gat ctg agg tcc tat 1632
 Asn Asn Ser Trp Phe Gln Ser Ile Leu Arg His Asp Leu Arg Ser Tyr
 530 535 540
 ttg gat gat ggg cct ctt caa cac tac atc gct gtc tcc agc cct acc 1680
 Leu Asp Asp Gly Pro Leu Gln His Tyr Ile Ala Val Ser Ser Pro Thr
 545 550 555 560
 aac acg act tac gtt gtg cag tat gcc ttg gca aac ctg act ggc aag 1728
 Asn Thr Thr Tyr Val Val Gln Tyr Ala Leu Ala Asn Leu Thr Gly Lys
 565 570 575
 gtg acc aac ctg acc caa gag cag tgc cag gat cca agt aaa gtc cca 1776
 Val Thr Asn Leu Thr Gln Glu Gln Cys Gln Asp Pro Ser Lys Val Pro
 580 585 590
 aat gaa agc aag gat ttg tat gaa tac tcg tgg gta caa ggc cct tgg 1824
 Asn Glu Ser Lys Asp Leu Tyr Glu Tyr Ser Trp Val Gln Gly Pro Trp
 595 600 605
 aat tcc aac aag aca gag cgg ctg cca cgg tgt gtg cgc tcc aca gta 1872
 Asn Ser Asn Lys Thr Glu Arg Leu Pro Arg Cys Val Arg Ser Thr Val
 610 615 620
 cga ctg gct agg gcc ttg tcc ccc gcc ttt gag ctg agt cag tgg agc 1920
 Arg Leu Ala Arg Ala Leu Ser Pro Ala Phe Glu Leu Ser Gln Trp Ser
 625 630 635 640
 tcc aca gaa tac tct acg tgg gcc gag agc cgc tgg aaa gat atc caa 1968
 Ser Thr Glu Tyr Ser Thr Trp Ala Glu Ser Arg Trp Lys Asp Ile Gln
 645 650 655
 gct cgg ata ttc ctg att gcc agc aaa gaa ctt gag ttc atc acg ctg 2016
 Ala Arg Ile Phe Leu Ile Ala Ser Lys Glu Leu Glu Phe Ile Thr Leu
 660 665 670
 atc gtg ggc ttc agc atc ctg gtc ttt tct ctg atc gtc act tat tgt 2064
 Ile Val Gly Phe Ser Ile Leu Val Phe Ser Leu Ile Val Thr Tyr Cys
 675 680 685
 atc aac gcc aag gcc gat gtc ctt ttc gtt gct ccc cga gag cca gga 2112
 Ile Asn Ala Lys Ala Asp Val Leu Phe Val Ala Pro Arg Glu Pro Gly
 690 695 700
 gct gtg tct tac tga 2127
 Ala Val Ser Tyr
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<210> 98

<211> 708

<212> PRT

<213> Rattus norvegicus

<400> 98

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Met Ala Thr Ala Arg Gly Gly Ser Gly Pro Asp Pro Gly Ser Arg Gly
1      5      10      15

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20      25      30

Asn Ser Val Glu Arg Lys Ile Tyr Ile Pro Leu Asn Lys Thr Ala Pro
35      40      45

Cys Val Arg Leu Leu Asn Ala Thr His Gln Ile Gly Cys Gln Ser Ser
50      55      60

Ile Ser Gly Asp Thr Gly Val Ile His Val Val Glu Lys Glu Asp Asp
65      70      75      80

Leu Lys Trp Val Leu Thr Asp Gly Pro Asn Pro Pro Tyr Met Val Leu
85      90      95

Leu Glu Gly Lys Leu Phe Thr Arg Asp Ile Met Glu Lys Leu Lys Gly
100     105     110

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

Ser Thr Ser Ser Phe Ser Pro Ser Val Gln Cys Pro Asn Asp Gly Phe
130     135     140

Gly Ile Tyr Ser Asn Ser Tyr Gly Pro Glu Phe Ala His Cys Lys Lys
145     150     155     160

Thr Leu Trp Asn Glu Leu Gly Asn Gly Leu Ala Tyr Asp Asp Phe Ser
165     170     175

Phe Pro Ile Phe Leu Leu Glu Asp Glu Asn Glu Thr Lys Val Ile Lys
180     185     190

Gln Cys Tyr Gln Asp His Asn Leu Gly Gln Asn Gly Ser Ala Pro Ser
195     200     205

Phe Pro Leu Cys Ala Met Gln Leu Phe Ser His Met His Ala Val Ile
210     215     220

Ser Thr Ala Thr Cys Met Arg Arg Ser Phe Ile Gln Ser Thr Phe Ser
225     230     235     240

Ile Asn Pro Glu Ile Val Cys Asp Pro Leu Ser Asp Tyr Asn Val Trp
245     250     255

Ser Met Leu Lys Pro Ile Asn Thr Ser Gly Gly Leu Glu Pro Asp Val
260     265     270

Arg Val Val Val Ala Ala Thr Arg Leu Asp Ser Arg Ser Phe Phe Trp
275     280     285

Asn Val Ala Pro Gly Ala Glu Ser Ala Val Ala Ser Phe Val Thr Gln
290     295     300

Leu Ala Ala Ala Glu Ala Leu His Lys Ala Pro Asp Val Thr Thr Leu
305     310     315     320

Pro Arg Asn Val Met Phe Val Phe Phe Gln Gly Glu Thr Phe Asp Tyr
325     330     335

Ile Gly Ser Ser Arg Met Val Tyr Asp Met Glu Asn Gly Lys Phe Pro

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<210> 99
<211> 2130

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2127)

<400> 99

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1      5      10      15

ctc ctt cgc ctt ctg tct ttc tgc gtc cta cta gca ggt ttg tgc agg      96
Leu Leu Arg Leu Leu Ser Phe Cys Val Leu Leu Ala Gly Leu Cys Arg
20     25     30

gga aac tca gtg gag agg aag ata tat atc ccc tta aat aaa aca gct      144
Gly Asn Ser Val Glu Arg Lys Ile Tyr Ile Pro Leu Asn Lys Thr Ala
35     40     45

ccc tgt gtt cgc ctg ctc aac gcc act cat cag att ggc tgc cag tct      192
Pro Cys Val Arg Leu Leu Asn Ala Thr His Gln Ile Gly Cys Gln Ser
50     55     60

tca att agt gga gac aca ggg gtt atc cac gta gta gag aaa gag gag      240
Ser Ile Ser Gly Asp Thr Gly Val Ile His Val Val Glu Lys Glu Glu
65     70     75     80

gac cta cag tgg gta ttg act gat ggc ccc aac ccc cct tac atg gtt      288
Asp Leu Gln Trp Val Leu Thr Asp Gly Pro Asn Pro Pro Tyr Met Val
85     90     95

ctg ctg gag agc aag cat ttt acc agg gat tta atg gag aag ctg aaa      336
Leu Leu Glu Ser Lys His Phe Thr Arg Asp Leu Met Glu Lys Leu Lys
100    105    110

ggg aga acc agc cga att gct ggt ctt gca gtg tcc ttg acc aag ccc      384
Gly Arg Thr Ser Arg Ile Ala Gly Leu Ala Val Ser Leu Thr Lys Pro
115    120    125

agt cct gcc tca ggc ttc tct cct agt gta cag tgc cca aat gat ggg      432
Ser Pro Ala Ser Gly Phe Ser Pro Ser Val Gln Cys Pro Asn Asp Gly
130    135    140

ttt ggt gtt tac tcc aat tcc tat ggg cca gag ttt gct cac tgc aga      480
Phe Gly Val Tyr Ser Asn Ser Tyr Gly Pro Glu Phe Ala His Cys Arg
145    150    155    160

gaa ata cag tgg aat tgc ctg ggc aat ggt ttg gct tat gaa gac ttt      528
Glu Ile Gln Trp Asn Ser Leu Gly Asn Gly Leu Ala Tyr Glu Asp Phe
165    170    175

agt ttc ccc atc ttt ctt ctt gaa gat gaa aat gaa acc aaa gtc atc      576
Ser Phe Pro Ile Phe Leu Leu Glu Asp Glu Asn Glu Thr Lys Val Ile
180    185    190

aag cag tgc tat caa gat cac aac ctg agt cag aat ggc tca gca cca      624
Lys Gln Cys Tyr Gln Asp His Asn Leu Ser Gln Asn Gly Ser Ala Pro
195    200    205

acc ttc cca cta tgt gcc atg cag ctc ttt tca cac atg cat gct gtc      672
Thr Phe Pro Leu Cys Ala Met Gln Leu Phe Ser His Met His Ala Val
210    215    220

atc agc act gcc acc tgc atg cgg cgc agc tcc atc caa agc acc ttc      720
Ile Ser Thr Ala Thr Cys Met Arg Arg Ser Ser Ile Gln Ser Thr Phe
225    230    235    240

agc atc aac cca gaa atc gtc tgt gac ccc ctg tct gat tac aat gtg      768
Ser Ile Asn Pro Glu Ile Val Cys Asp Pro Leu Ser Asp Tyr Asn Val
245    250    255

tgg agc atg cta aag cct ata aat aca act ggg aca tta aag cct gac      816
Trp Ser Met Leu Lys Pro Ile Asn Thr Thr Gly Thr Leu Lys Pro Asp
260    265    270

gac agg gtt gtg gtt gct gcc acc cgg ctg gat agt cgt tcc ttt ttc      864
Asp Arg Val Val Val Ala Ala Thr Arg Leu Asp Ser Arg Ser Phe Phe
275    280    285

tgg aat gtg gcc cca ggg gct gaa agc gca gtg gct tcc ttt gtc acc      912
Trp Asn Val Ala Pro Gly Ala Glu Ser Ala Val Ala Ser Phe Val Thr
290    295    300

cag ctg gct gct gct gaa gct ttg caa aag gca cct gat gtg acc acc      960
Gln Leu Ala Ala Ala Glu Ala Leu Gln Lys Ala Pro Asp Val Thr Thr
305    310    315    320

ctg ccc cgc aat gtc atg ttt gtc ttc ttt caa ggg gaa act ttt gac      1008
Leu Pro Arg Asn Val Met Phe Val Phe Phe Gln Gly Glu Thr Phe Asp
325    330    335

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tac att ggc agc tcg agg atg gtc tac gat atg gag aag ggc aag ttt Tyr Ile Gly Ser Ser Arg Met Val Tyr Asp Met Glu Lys Gly Lys Phe 340 345 350	1056
ccc gtg cag tta gag aat gtt gac tca ttt gtg gag ctg gga cag gtg Pro Val Gln Leu Glu Asn Val Asp Ser Phe Val Glu Leu Gly Gln Val 355 360 365	1104
gcc tta aga act tca tta gag ctt tgg atg cac aca gat cct gtt tct Ala Leu Arg Thr Ser Leu Glu Leu Trp Met His Thr Asp Pro Val Ser 370 375 380	1152
cag aaa aat gag tct gta cgg aac cag gtg gag gat ctc ctg gcc aca Gln Lys Asn Glu Ser Val Arg Asn Gln Val Glu Asp Leu Leu Ala Thr 385 390 395 400	1200
ttg gag aag agt ggt gct ggt gtc cct gct gtc atc ctc agg agg cca Leu Glu Lys Ser Gly Ala Gly Val Pro Ala Val Ile Leu Arg Arg Pro 405 410 415	1248
aat cag tcc cag cct ctc cca cca tct tcc ctg cag cga ttt ctt cga Asn Gln Ser Gln Pro Leu Pro Pro Ser Ser Leu Gln Arg Phe Leu Arg 420 425 430	1296
gct cga aac atc tct ggc gtt gtt ctg gct gac cac tct ggt gcc ttc Ala Arg Asn Ile Ser Gly Val Val Leu Ala Asp His Ser Gly Ala Phe 435 440 445	1344
cat aac aaa tat tac cag agt att tac gac act gct gag aac att aat His Asn Lys Tyr Tyr Gln Ser Ile Tyr Asp Thr Ala Glu Asn Ile Asn 450 455 460	1392
gtg agc tat ccc gaa tgg ctg agc cct gaa gag gac ctg aac ttt gta Val Ser Tyr Pro Glu Trp Leu Ser Pro Glu Glu Asp Leu Asn Phe Val 465 470 475 480	1440
aca gac act gcc aag gcc ctg gca gat gtg gcc acg gtg ctg gga cgt Thr Asp Thr Ala Lys Ala Leu Ala Asp Val Ala Thr Val Leu Gly Arg 485 490 495	1488
gct ctg tat gag ctt gca gga gga acc aac ttc agc gac aca gtt cag Ala Leu Tyr Glu Leu Ala Gly Gly Thr Asn Phe Ser Asp Thr Val Gln 500 505 510	1536
gct gat ccc caa acg gtt acc cgc ctg ctc tat ggg ttc ctg att aaa Ala Asp Pro Gln Thr Val Thr Arg Leu Leu Tyr Gly Phe Leu Ile Lys 515 520 525	1584
gcc aac aac tca tgg ttc cag tct atc ctc agg cag gac cta agg tcc Ala Asn Asn Ser Trp Phe Gln Ser Ile Leu Arg Gln Asp Leu Arg Ser 530 535 540	1632
tac ttg ggt gac ggg cct ctt caa cat tac atc gct gtc tcc aqc ccc Tyr Leu Gly Asp Gly Pro Leu Gln His Tyr Ile Ala Val Ser Ser Pro 545 550 555 560	1680
acc aac acc act tat gtt gta cag tat gcc ttg gca aat ttg act ggc Thr Asn Thr Thr Tyr Val Val Gln Tyr Ala Leu Ala Asn Leu Thr Gly 565 570 575	1728
aca gtg gtc aac ctc acc cga gag cag tgc cag gat cca agt aaa gtc Thr Val Val Asn Leu Thr Arg Glu Gln Cys Gln Asp Pro Ser Lys Val 580 585 590	1776
cca agt gaa aac aag gat ctg tat gag tac tca tgg gtc cag ggc cct Pro Ser Glu Asn Lys Asp Leu Tyr Glu Tyr Ser Trp Val Gln Gly Pro 595 600 605	1824
ttg cat tct aat gag acg gac cga ctc ccc cgg tgt gtg cgt tct act Leu His Ser Asn Glu Thr Asp Arg Leu Pro Arg Cys Val Arg Ser Thr 610 615 620	1872
gca cga tta gcc agg gcc ttg tct cct gcc ttt gaa ctg agt cag tgg Ala Arg Leu Ala Arg Ala Leu Ser Pro Ala Phe Glu Leu Ser Gln Trp 625 630 635 640	1920
agc tct act gaa tac tct aca tgg act gag agc cgc tgg aaa gat atc Ser Ser Thr Glu Tyr Ser Thr Trp Thr Glu Ser Arg Trp Lys Asp Ile 645 650 655	1968
cgt gcc cgg ata ttt ctc atc gcc agc aaa gag ctt gag ttg atc acc Arg Ala Arg Ile Phe Leu Ile Ala Ser Lys Glu Leu Glu Leu Ile Thr 660 665 670	2016
ctg aca gtg ggc ttc ggc atc ctc atc ttc tcc ctc atc gtc acc tac Leu Thr Val Gly Phe Gly Ile Leu Ile Phe Ser Leu Ile Val Thr Tyr 675 680 685	2064
tgc atc aat gcc aaa gct gat gtc ctt ttc att gct ccc cgg gag cca Cys Ile Asn Ala Lys Ala Asp Val Leu Phe Ile Ala Pro Arg Glu Pro 690 695 700	2112
gga gct gtg tca tac tga Gly Ala Val Ser Tyr 705	2130

<210> 100

<211> 709

<212> PRT

<213> Homo sapiens

<400> 100

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Met Ala Thr Ala Gly Gly Gly Ser Gly Ala Asp Pro Gly Ser Arg Gly
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Leu Leu Arg Leu Leu Ser Phe Cys Val Leu Leu Ala Gly Leu Cys Arg
20     25     30

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

Pro Cys Val Arg Leu Leu Asn Ala Thr His Gln Ile Gly Cys Gln Ser
50     55     60

Ser Ile Ser Gly Asp Thr Gly Val Ile His Val Val Glu Lys Glu Glu
65     70     75     80

Asp Leu Gln Trp Val Leu Thr Asp Gly Pro Asn Pro Pro Tyr Met Val
85     90     95

Leu Leu Glu Ser Lys His Phe Thr Arg Asp Leu Met Glu Lys Leu Lys
100    105    110

Gly Arg Thr Ser Arg Ile Ala Gly Leu Ala Val Ser Leu Thr Lys Pro
115    120    125

Ser Pro Ala Ser Gly Phe Ser Pro Ser Val Gln Cys Pro Asn Asp Gly
130    135    140

Phe Gly Val Tyr Ser Asn Ser Tyr Gly Pro Glu Phe Ala His Cys Arg
145    150    155    160

Glu Ile Gln Trp Asn Ser Leu Gly Asn Gly Leu Ala Tyr Glu Asp Phe
165    170    175

Ser Phe Pro Ile Phe Leu Leu Glu Asp Glu Asn Glu Thr Lys Val Ile
180    185    190

Lys Gln Cys Tyr Gln Asp His Asn Leu Ser Gln Asn Gly Ser Ala Pro
195    200    205

Thr Phe Pro Leu Cys Ala Met Gln Leu Phe Ser His Met His Ala Val
210    215    220

Ile Ser Thr Ala Thr Cys Met Arg Arg Ser Ser Ile Gln Ser Thr Phe
225    230    235    240

Ser Ile Asn Pro Glu Ile Val Cys Asp Pro Leu Ser Asp Tyr Asn Val
245    250    255

Trp Ser Met Leu Lys Pro Ile Asn Thr Thr Gly Thr Leu Lys Pro Asp
260    265    270

Asp Arg Val Val Val Ala Ala Thr Arg Leu Asp Ser Arg Ser Phe Phe
275    280    285

Trp Asn Val Ala Pro Gly Ala Glu Ser Ala Val Ala Ser Phe Val Thr
290    295    300

Gln Leu Ala Ala Ala Glu Ala Leu Gln Lys Ala Pro Asp Val Thr Thr
305    310    315    320

Leu Pro Arg Asn Val Met Phe Val Phe Phe Gln Gly Glu Thr Phe Asp
325    330    335

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Tyr Ile Gly Ser Ser Arg Met Val Tyr Asp Met Glu Lys Gly Lys Phe
 340 345 350
 Pro Val Gln Leu Glu Asn Val Asp Ser Phe Val Glu Leu Gly Gln Val
 355 360 365
 Ala Leu Arg Thr Ser Leu Glu Leu Trp Met His Thr Asp Pro Val Ser
 370 375 380
 Gln Lys Asn Glu Ser Val Arg Asn Gln Val Glu Asp Leu Leu Ala Thr
 385 390 395 400
 Leu Glu Lys Ser Gly Ala Gly Val Pro Ala Val Ile Leu Arg Arg Pro
 405 410 415
 Asn Gln Ser Gln Pro Leu Pro Pro Ser Ser Leu Gln Arg Phe Leu Arg
 420 425 430
 Ala Arg Asn Ile Ser Gly Val Val Leu Ala Asp His Ser Gly Ala Phe
 435 440 445
 His Asn Lys Tyr Tyr Gln Ser Ile Tyr Asp Thr Ala Glu Asn Ile Asn
 450 455 460
 Val Ser Tyr Pro Glu Trp Leu Ser Pro Glu Glu Asp Leu Asn Phe Val
 465 470 475 480
 Thr Asp Thr Ala Lys Ala Leu Ala Asp Val Ala Thr Val Leu Gly Arg
 485 490 495
 Ala Leu Tyr Glu Leu Ala Gly Gly Thr Asn Phe Ser Asp Thr Val Gln
 500 505 510
 Ala Asp Pro Gln Thr Val Thr Arg Leu Leu Tyr Gly Phe Leu Ile Lys
 515 520 525
 Ala Asn Asn Ser Trp Phe Gln Ser Ile Leu Arg Gln Asp Leu Arg Ser
 530 535 540
 Tyr Leu Gly Asp Gly Pro Leu Gln His Tyr Ile Ala Val Ser Ser Pro
 545 550 555 560
 Thr Asn Thr Thr Tyr Val Val Gln Tyr Ala Leu Ala Asn Leu Thr Gly
 565 570 575
 Thr Val Val Asn Leu Thr Arg Glu Gln Cys Gln Asp Pro Ser Lys Val
 580 585 590
 Pro Ser Glu Asn Lys Asp Leu Tyr Glu Tyr Ser Trp Val Gln Gly Pro
 595 600 605
 Leu His Ser Asn Glu Thr Asp Arg Leu Pro Arg Cys Val Arg Ser Thr
 610 615 620
 Ala Arg Leu Ala Arg Ala Leu Ser Pro Ala Phe Glu Leu Ser Gln Trp
 625 630 635 640
 Ser Ser Thr Glu Tyr Ser Thr Trp Thr Glu Ser Arg Trp Lys Asp Ile
 645 650 655
 Arg Ala Arg Ile Phe Leu Ile Ala Ser Lys Glu Leu Glu Leu Ile Thr
 660 665 670
 Leu Thr Val Gly Phe Gly Ile Leu Ile Phe Ser Leu Ile Val Thr Tyr
 675 680 685
 Cys Ile Asn Ala Lys Ala Asp Val Leu Phe Ile Ala Pro Arg Glu Pro
 690 695 700
 Gly Ala Val Ser Tyr
 705

<210> 101

<211> 744

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(741)

<400> 101

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1      5      10      15

gcc ttc tcc ctt ttc ctg atc act gta gct gga gac cca ctt cgg gtt      96
Ala Phe Ser Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val
20      25      30

atc atc ctg gtg gcg gga gcc ttt ttc tgg ctg gtc tcc ctg ctc ttg      144
Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
35      40      45

gct tct gtg gtc tgg ttc atc ttg gtc cat gtg aca gac cga tca gat      192
Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
50      55      60

gca cgg ctc cag tat ggc ctc ctg att ttt ggt gct gct gtc tct gtc      240
Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
65      70      75      80

ctt cta cag gaa gtg ttc cgt ttt gct tac tac aag ctc ctt aag aag      288
Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
85      90      95

gca gat gag ggc tta gca tca ctg agt gag gac gga aga tca ccc atc      336
Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
100      105      110

tcc atc cga cag atg gcc tat gtt tct ggt ctg tcc ttc ggt atc atc      384
Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
115      120      125

agt ggt gtc ttc tct gtt atc aat att ttg gct gat gca ctt ggg cca      432
Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
130      135      140

ggt gtg gtt ggg atc cat gga gac tca ccc tat tac ttc ctg act tca      480
Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
145      150      155      160

gcc ttt ctg aca gca gcc att atc ctg ctc cac acc ttt tgg gga gtt      528
Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
165      170      175

gtg ttc ttt gat gcc tgt gag agg aga cgg tac tgg gct ttg ggc ctg      576
Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
180      185      190

gta gtt ggg agt cac ctt ctg aca tcg gga ctg aca ttc ctg aac ccc      624
Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
195      200      205

tgg tat gag gct agc ctg ctg ccc atc tat gca gtc acc gtt tcc atg      672
Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
210      215      220

ggg ctc tgg gcg ttc atc aca gcc gga gcc tcc ctc cga agt atc cag      720
Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
225      230      235      240

cgc agc ctt tcg tgt aag gac tga
Arg Ser Leu Ser Cys Lys Asp
245

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<210> 102

<211> 247

<212> PRT

<213> Mus musculus

<400> 102

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 20 25 30
 Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
 35 40 45
 Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
 50 55 60
 Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
 65 70 75 80
 Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
 85 90 95
 Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
 100 105 110
 Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
 115 120 125
 Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
 130 135 140
 Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
 145 150 155 160
 Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
 165 170 175
 Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
 180 185 190
 Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
 195 200 205
 Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
 210 215 220
 Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
 225 230 235 240
 Arg Ser Leu Ser Cys Lys Asp
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<210> 103

<211> 744

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(741)

<400> 103

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atc atc ctg gtg gcg gga gcc ttt ttc tgg ctg gtt tcc ctg ctc ttg Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu 35 40 45	144
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20      25      30

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ctt cta cag gag gtg ttc cgc ttt gcc tac tac aag ctg ctt aag aag      288
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85      90      95

gca gat gag ggg tta gca tcg ctg agt gag gac gga aga tca ccc atc      336
Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
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tcc atc cgc cag atg gcc tat gtt tct ggt ctc tcc ttc ggt atc atc      384
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Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
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Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
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Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
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          35          40          45

gag cag agc caa atc aaa ggc tat gtt tgg cgc tca gct gtg ggc ttc     192
Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
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Leu Phe Trp Val Ile Ile Leu Ala Thr Trp Ile Thr Ile Phe Gln Ile
          65          70          75          80

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          20          25          30

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Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
      50              55              60

ctc ttc tgg gtg att gtt ctc acc acc tgg atc acc atc ttc cag atc      240
Leu Phe Trp Val Ile Val Leu Thr Thr Trp Ile Thr Ile Phe Gln Ile
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tac cgg ccc cgc tgg ggt gct ctt ggg gac tac ctc tcc ttc acc att      288
Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
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      50      55      60

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Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
          20          25          30

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Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
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Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
          50          55          60

ctc ttc tgg gtg ata gtg ctc acc tcc tgg atc acc atc ttc cag atc     240
Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
          65          70          75          80

tac cgg ccc cgc tgg ggt gcc ctt ggg gac tac ctc tcc ttc acc ata     288
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          85          90          95

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          35          40          45

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          50          55          60

Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
          65          70          75          80

Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
          85          90          95

Pro Leu Gly Thr Pro
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REFERENCES CITED IN THE DESCRIPTION

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Patentkrav

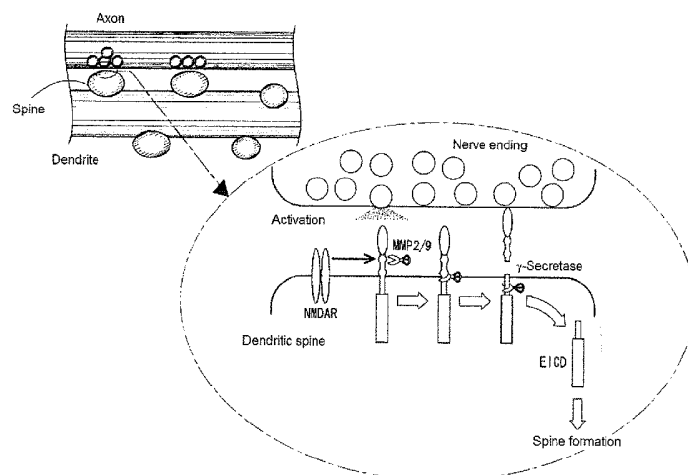
1. In vitro-fremgangsmåde til screening for et stof, der påvirker gelatinase-medieret Eph-receptor-A4-spaltning, som omfatter trinene:
- (a) etablering af kontakt mellem en første biologisk sammensætning, der indeholder gelatinase, og en anden biologisk sammensætning, der indeholder EphA4, ved tilstedeværelse og fravær af et kandidatstof;
 - (b) måling af tilstedeværelse eller mængden af EphA4-ektodomæne- og/eller endodomænefragmentet; og
 - (c) selektion af kandidatstoffet som et stof, der påvirker gelatinase-medieret EphA4-spaltning, hvis resultaterne i trin (b) målt i nærvær af kandidatstoffet er ændret i forhold til resultaterne i trin (b) målt i fravær af kandidatstoffet.
2. Fremgangsmåde ifølge krav 1, hvor trin (c) omfatter identificering af kandidatstoffet som et stof, der fremmer gelatinase-medieret EphA4-spaltning, hvis EphA4-endodomæne- og/eller ektodomænefragmentet målt i nærvær af kandidatstoffet i trin (b) er forøget sammenlignet med EphA4-endodomæne- og/eller ektodomænefragmentet målt i fravær af kandidatstoffet i trin (b).
3. Fremgangsmåde ifølge krav 1, hvor trin (c) omfatter identificering af kandidatstoffet som et stof, der hæmmer gelatinase-medieret EphA4-spaltning, hvis EphA4-endodomæne- og/eller ektodomænefragmentet målt i nærvær af kandidatstoffet i trin (b) er reduceret sammenlignet med EphA4-endodomæne- og/eller ektodomænefragmentet målt i fravær af kandidatstoffet i trin (b).
4. Fremgangsmåde ifølge krav 2, hvor stoffet, der fremmer gelatinase-medieret EphA4-spaltning, yderligere evalueres som et stof, der fremmer γ -secretase-medieret EphA4-spaltningsreaktion.
5. Fremgangsmåde ifølge krav 3, hvor stoffet, der hæmmer

gelatinase-medieret EphA4-spaltning, yderligere evalueres som et stof, der hæmmer γ -secretase-medieret EphA4-spaltningsreaktion.

- 5 6. Fremgangsmåde ifølge krav 2, hvor stoffet, der fremmer gelatinase-medieret EphA4-spaltning, yderligere evalueres som et stof, der fremmer spina-dannelsesreaktion medieret af det intracellulære EphA4-fragment.
- 10 7. Fremgangsmåde ifølge krav 3, hvor stoffet, der hæmmer gelatinase-medieret EphA4-spaltning, yderligere evalueres som et stof, der hæmmer spina-dannelsesreaktion medieret af det intracellulære EphA4-fragment.
- 15 8. Anvendelse af gelatinase til spaltning af ektodomænet af EphA4.
9. Anvendelse af et analysekit, der omfatter en første biologisk sammensætning, der indeholder gelatinase, og en
20 anden biologisk sammensætning, der indeholder EphA4, til måling af gelatinase-medieret EphA4-spaltning.

DRAWINGS

[Figure 1]



[Figure 2]

