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(54) Title: ISOLATED LAMININ 10

(57) Abstract: The present invention provides isolated laminin 10, methods for making recombinant laminin 10, host cells that express recombinant laminin 10, and methods for using the recombinant laminin 10 to accelerate the healing of injuries to vascular tissue, and to promote cell attachment and migration. The present invention also provides nucleic acid sequences encoding full length human laminin α5 chain, expression vectors and host cells thereof, and isolated full length human laminin α5 polypeptide chain.

ISOLATED LAMININ 10

Field of the Invention

This application relates to cell biology, molecular biology, proteins, nucleic acids, and laminins.

Background of the Invention

Basal laminae (basement membranes) are sheet-like, cell-associated extracellular matrices that play a central role in cell growth, tissue development, and tissue maintenance. They are present in virtually all tissues, and appear in the earliest stages of embryonic development.

Basal laminae are central to a variety of architectural and cell-interactive functions (See for example, Malinda and Kleinman, Int. J. Biochem. Cell Biol. 28:957-959 (1996); Aumailley and Krieg, J. Invest. Dermatology 106:209-214 (1996)). For example:

1. They serve as architectural supports for tissues, providing adhesive substrata for cells.
2. They create perm-selective barriers between tissue compartments that impede the migration of cells and passively regulate the exchange of macromolecules. These properties are illustrated by the kidney glomerular basement membrane, which functions as an important filtration structure, creating an effective blood-tissue barrier that is not permeable to most proteins and cells.
3. Basal laminae create highly interactive surfaces that can promote cell migration and cell elongation during embryogenesis and wound repair.

Following an injury, they provide a surface upon which cells regenerate to restore normal tissue function.

4. Basal laminae present information encoded in their structure to contacting cells that is important for differentiation and tissue maintenance. This information is communicated to the cells through various receptors that include the integrins, dystroglycan, and cell surface proteoglycans. Signaling is dependent not only on the presence of matrix ligands and corresponding receptors that interact with sufficient affinities, but also on such topographical factors as ligand density in a three-dimensional matrix "landscape", and on the ability of basal lamina components to cluster receptors. Because these matrix proteins can be long-lived, basal laminae create a "surface memory" in the basal lamina for resident and transient cells.

The basal lamina is largely composed of laminin and type IV collagen heterotrimers that in turn become organized into complex polymeric structures. To date, six type IV collagen chains and at least twelve laminin subunits have been identified. These chains possess shared and unique functions and are expressed with specific temporal (developmental) and spatial (tissue-site specific) patterns.

Laminins are a family of heterotrimeric glycoproteins that reside primarily in the basal lamina. They function via binding interactions with neighboring cell receptors, and by forming laminin networks, and they are important signaling molecules that can strongly influence cellular function. Laminins are important in both maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair and development.

Laminins are large, multi-domain proteins, with a common structural organization. The laminin molecule integrates various matrix and cell interactive functions into one molecule.

A laminin molecule is comprised of an α-, β-, and γ-chain subunit joined together through a coiled-coil domain. Within this structure are identifiable domains that possess binding activity towards other laminin and basal lamina molecules, and membrane-bound receptors. Domains VI, IVb, and IVa form globular structures, and domains V, IIIb, and IIIa (which contain cysteine-rich EGF-like elements) form rod-like structures (Kamiguchi et al., Ann. Rev. Neurosci.

21:97-125 (1998)). Domains I and II of the three chains participate in the formation of a triple-stranded coiled-coil structure (the long arm).

Table 1 shows the individual chains that each laminin type is composed of:

TABLE 1. Known laminin family members

Protein	*Chains*
Laminin-1	α1β1γ1
Laminin-2	α2β1γ1
Laminin 3	α1β2γ1
Laminin-4	α2β2γ1
Laminin-5	α3β3γ2
Laminin-6	α3β1γ1
Laminin-7	α3β2γ1
Laminin-8	α4β1γ1
Laminin-9	α4β2γ1
Laminin-10	α5β1γ1
Laminin-11	α5β2γ1
Laminin-12	α2β1γ3

Four structurally-defined family groups of laminins have been identified. The first group of five identified laminin molecules, including laminin 10 all share the β1 and γ1 chains, and vary by their α-chain composition (α1 to α5 chain). The second group of five identified laminin molecules all share the β2 and γ1 chain, and again vary by their α-chain composition. The third group of identified laminin molecules has one identified member, laminin 5, with a chain composition of α3β3γ2. The fourth group of identified laminin molecules has one identified member, laminin 12, with the newly identified γ3 chain (α2β1γ3).

Some progress has been made in elucidating the relationship between domain structure and function (See, for example, Wewer and Engvall, Neuromusc. Disord. 6:409-418 (1996)). The overall sequence similarity among the homologous domains in different chains varies, but it is highest in domain VI (thought to play a key role in laminin polymerization), followed by domains V (possibly involved in protein-protein interactions) and III (entactin/nidogen binding; possible cell adhesion sites), and is lowest in domains I, II (both thought to be involved in intermolecular assembly, and containing possible cell adhesion sites), and G. Not all domains are present in all 3 types of chains. The globular G domain (thought to be involved in cell receptor binding) is present only in the α chains. Other domains may not be present in all chains within a certain chain type. For example, domain VI is absent from α3, α4, and γ2 chains (Wewer and Engvall, 1996).

As a result of their large size (>600 kD) and unique structure, the laminin molecules can be resolved in the electron microscope (Wewer and Engvall, 1996). Typically, laminins appear as cross-shaped molecules in an EM. The three short arms of the cross represent the amino terminal portions of each of the three separate laminin chains (one short arm per chain). The long arm of the cross is composed of the C-terminal parts of the three chains, which together form a coiled coil structure (Wewer and Engvall, 1996). The long arm ends with the globular G domain.

The coiled-coil domain of the long arm is crucial for assembly of the three chains of laminin (Yurchenco et al., Proc. Natl. Acad. Sci. 94:10189-10194 (1997)). Disulfide bonds bridge and stabilize all three chains in the most proximal region of the long arm and join the β and γ chains in the most distal region of the long arm.

A model of laminin receptor-facilitated self-assembly, based on studies conducted with cultured skeletal myotubes and Schwann cells, predicts that laminins bind to their receptors, which freely diffuse in a fluidic membrane, when ligand-free. Receptor engagement forces the laminins into a high local two-dimensional concentration, facilitating their mass-action driven assembly into ordered surface polymers. In this process, the engaged receptors are also reorganized, accompanied by cytoskeletal rearrangements (Colognato, J. Cell Biol. 145:619-631 (1999)). This reorganization activates the receptors, causing signal transduction with the alteration of cell expression, shape and/or behavior. The evidence is that laminins must possess both cell-interacting and architecture-forming sites, which are located in different protein domains and on different subunits.

One class of laminin receptors are the integrins, which are cell surface receptors that mediate many cell-matrix and cell-cell interactions. Integrins are heterodimers, consisting of an α and a β subunit. 16 α- and 8 β-subunits are known, and at least 22 combinations of α and β subunits have been identified to date. Some integrins have only one or a few known ligands, whereas others appear to be very promiscuous. Binding to integrins is generally of low affinity, and is dependent on divalent cations. Integrins, activated through binding to their ligands, transduce signals via kinase activation cascades, such as focal adhesion and mitogen-activated kinases. Several different integrins bind different laminin isoforms more or less specifically (Aumailley et al., In The Laminins, Timpl and Ekblom, eds., Harwood Academic Publishers, Amsterdam. pp. 127-158 (1996)).

Laminin isoforms are expressed in tissue-specific and developmentally regulated patterns and they play significant roles in adhesion, migration, proliferation and differentiation of many cell types (Timpl, R., and Brown, J.C. (1994) *Matrix Biol.* 14(4), 275-81.; Ekblom, P., Timpl, R. (ed) (1996) *The laminins* Vol. 2. Cell Adhesion & Communication. Edited by Goridis, C., Harwood Academic Publishers GmbH, Amsterdam; Sorokin, L. M., et al. (1997) *Dev.Biol.* 189(2), 285-300.; Aumailley, M., and Smyth, N. (1998) *J. Anat.* 193(Pt 1), 1-21).

The laminin α5 chain, a component of laminin-10 (α5β1γ1) and laminin-11 (α5β2γ1), is expressed widely in adult tissues including placenta, heart, lung, skeletal muscle, kidney, and pancreas (Sorokin, L. M., et al. (1997) *Dev. Biol.* 189(2), 285-300; Patton, B. L., et al. (1997) *J. Cell Biol.* 139(6), 1507-21; Miner, J. H., et al. (1997) *J. Cell Biol.* 137(3), 685-701; Miner, J. H., et al. (1995) J. Biol. Chem. 270(48), 28523-6; Sorokin, L. M., et al. (1997) Dev. *Dyn.* 210(4), 446-62). Embryos lacking laminin α5 exhibit several developmental abnormalities, such as exencephaly and syndactyly, as well as dysmorphogenesis of the placental labyrinth and die late in embryogenesis (Miner, J. H., et al. (2000) *Dev.* Biol. 217(2), 278-89; Miner, J. H., et al. (1998) *J.Cell Biol.* 143(6), 1713-23). Laminin α5 chain-containing isoforms may therefore be important in placental endothelial cell migration and blood vessel branching, and in formation of proper basal laminae.

Integrin-mediated recognition of ECM molecules results in intracellular signaling that affects a range of cell behaviors (Clark, E. A. et al., Science 268(5208), 233-9 (1995)). In endothelial cells, these signals affect focal adhesions and cytoskeletal organization. Therefore, integrin-mediated endothelial cell recognition of laminin and other BM molecules may determine cell-to-matrix adhesiveness and mediate signals that are essential for the maintenance and normal functioning of blood vessels (Davis, G. E. et al., Exp. Cell Res. 216(1), 113-23 (1995); Dejana, E. et al., Kidney Int. 43(1), 61-5 (1993); and Shattil, S.J. et al., J. Clin. Invest. 100(11 Suppl), S91-5 (1997)). Laminin-8 and laminin-10 are secreted by endothelial cells, and are major components of the subendothelial basement membrane (Sorokin, L.M. et al., Dev. Biol. 189(2), 285-300 (1997); Iivanainen, A. et al., J. Biol. Chem. 272(44), 27862-8 (1997); Patton, B. L. et al., J. Cell Biol. 139(6), 1507-21 (1997), Miner, J.H. et al., J. Cell Biol. 137(3), 685-701 (1997); Sorokin, L. et al., Eur. J. Biochem. 223(2), 603-10 (1994); and Tokida, Y. et al., J. Biol. Chem. 265(30), 18123-9 (1990)).

There have been no reports of isolated laminin 10 that is free of other laminin chains. Studies on the function of laminin-10 have frequently used commercial preparations, which are normally prepared using proteolytic digestion and subsequent immunoaffinity chromatography resulting in a truncated mixture of α5-chain containing laminin isoforms (Sixt, M. et al., J. Biol. Chem. 276(22), 18878-87 (2001)). Attempts to purify laminin 10 from cell sources by affinity chromatography using laminin chain antibodies have been unsuccessful in eliminating, for example, laminin β2 chain, which is a component of laminin 11. (See, for example, Sixt, M. et al., J. Biol. Chem. 276(22), 18878-87 (2001)) Thus, such preparations represent a mixture of laminin 10 and laminin 11.

Despite the broad tissue distribution of the laminin α5 chain and laminin 10, the full length human laminin α5 chain sequence is not known, nor is there a means to isolate laminin 10 away from other laminins, nor has a means for recombinant expression of laminin 10 previously been developed. Isolated laminin 10 would have numerous research and therapeutic purposes including, but are not limited to, treating injuries to vascular tissue, promoting cell attachment and migration, ex vivo cell therapy, improving the biocompatibility of medical devices, and preparing improved cell culture devices and media.

Thus, there is a need in the art for isolated laminin-10 for research and therapeutic purposes, and methods for making isolated laminin 10.

Summary of the Invention

In one aspect, the present invention provides an isolated nucleic acid encoding a full-length human laminin α5 chain consisting of the nucleic acid sequence of SEQ ID NO:1, or the complement thereof, as well as vectors comprising the sequence, and host cells transfected with such vectors. In another aspect, the present invention provides isolated laminin α5 chain protein consisting of the amino acid sequence of SEQ ID NO:2.

In another aspect, the present invention provides isolated laminin 10, and methods for producing isolated laminin 10. In a further aspect, the present invention provides recombinant host cells that express laminin 10 chains and secrete recombinant laminin 10.

In a further aspect, the present invention provides pharmaceutical compositions, comprising isolated laminin 10 together with a pharmaceutically acceptable carrier. Such pharmaceutical compositions can optionally be provided with other extracellular matrix components.

In another aspect, the present invention provides methods and kits for accelerating the healing of injuries to vascular tissue, and for improving the biocompatibility of grafts used for treating such injuries. In specific examples, laminin 10 or pharmaceutical compositions thereof are used to:

a. promote re-endothelialization at the site of vascular injuries;

b. improve the "take" of grafts;

c. improve the biocompatibility of medical devices; and/or

d. promote cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration.

by providing an amount effective of isolated laminin 10 for the various methods. In preferred embodiments of all of these methods, recombinant laminin 10 is used. The kits comprise an amount of isolated laminin 10, or pharmaceutical compositions thereof, effective for the desired effect, and instructions for the use thereof.

In a further aspect, the present invention provides improved medical devices and grafts, wherein the improvement comprises providing medical devices and grafts with an amount effective of isolated laminin 10, or a pharmaceutical composition of the invention.

In a further aspect, the invention provides improved cell culture devices, and methods for preparing improved cell culture devices, for the growth and maintenance of cells in culture, by providing an amount effective to a cell culture device of isolated laminin 10 for cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration.

Brief Description of the Figures

Figure 1. cDNA-derived amino acid sequence of the human laminin 5 chain and alignment with the mouse chain. Upper sequence, human α5 chain; Lower sequence, mouse sequence. Domain boundaries are depicted, and adhesive tripeptide

sequences RGD and LRE are boxed. The potential cleavage site of the signal peptide is indicated by a solid triangle (Predicted by PSORT II). The five possible polymorphisms are shown as bold italic characters above the human sequence. The sequence submitted to GenBank by the Human Genome Project (accession NM_005560 (May 30, 2001)) differed from the present sequence at a few sites, indicated above the sequence in the figure. At these sites, the present sequence did not differ from the incomplete genomic sequences reported by Celera.

Figure 2. Characterization of r-laminin-10 using SDS-PAGE. (A) Silver stain: Conditioned medium of triple-transfected HEK293 cells (CM) and recombinant purified laminin-10 (r-laminin-10), were analyzed by SDS-PAGE on 4-15% gradient gels under reducing conditions; (B) Immunoblot of CM and r-laminin-10 under reducing conditions: Separated proteins on 5% gels were transferred onto PVDF membranes followed by staining with mAbs against laminin α5 (15H5), β1 (DG10), γ1 (clone 22) and FLAG-M2.; (C) Silver stain and immunoblot of rLN-10 under non-reducing conditions: Separated proteins on 5% gels were visualized by silver staining or transferred onto PVDF membranes followed by staining with mAbs against laminin α5 (15H5), β1 (DG10), γ1 (2E8). The positions of molecular size markers are shown.

Figure 3. Cell adhesion activity of recombinant laminin-10 (rLN-10) and other proteins. (A) HT-1080 cell adhesion to rLN-10, recombinant laminin-8 (rLN-8), laminin-1/nidogen complex (LN-1/Nd), and fibronectin (FN) coated at increasing concentrations.; (B) IBE cell adhesion to rLN-10, rLN-8, LN-1/Nd, and FN coated at increasing concentrations.; (C) HSVEC adhesion to rLN-10 and rLN-8 coated at 3 and 10 mg/ml, and LN-1/Nd, commercial laminin-10/11 (LN-10/11), collagen type IV (Col IV) and FN coated at 10 mg/ml. N.T. means not-tested. Bound cells were quantitated spectrophometrically using adhesion to BSA as blank. Error bars indicate S.D.

Figure 4. HT-1080 cell and HSVEC adhesion assays on laminins coated at 10 g/ml. Text under columns indicate the integrin subunit mAbs used or other added

substances. Adhesion shown is relative to control, designated 100. Adhesion to BSA was designated zero. Error bars indicate S.D.

Figure 5. HSVEC migration (endothelialization) on plastic coated with laminin-10 and other proteins. Migration of HSVECs into the cell free area coated with BSA, laminin-1/ nidogen complex (LN-1/Nd), recombinant laminin-8 (rLN-8), recombinant laminin-10 (rLN-10), fibronectin (FN), commercial laminin-10/11 (LN-10/11), gelatin, and collagen type IV (Col IV) was measured. The distance covered by cells from three different donors. N.T. means not-tested.

Table 2: **Primers used in laminin 5 expression construct preparation.**
Upper row, forward primer; Lower row, reverse primer.

plasmid	primer	primer sequence
KBX3	KZK1	5'-gccaccatggcgaagcggctctg-3' (SEQ ID NO.:21)
	Ba3r	5'-aagggcaggatccactgggg-3' (SEQ ID NO.:22)
BBL3	Bam4	5'-ctactgcgaagctggctctt-3' (SEQ ID NO.:23)
	Bcl1r	5'-ccaggtggtcctgggtatc-3' (SEQ ID NO.:24)
BNK2'	Bcl2	5'-gcgacaactgcctcctctac-3' (SEQ ID NO.:25)
	Not4r	5'-agtgggttcccaaagaatcc-3' (SEQ ID NO.:26)
BNL12	Bpu1F	5'-cctctgtgacgagctcacg-3' (SEQ ID NO.:27)
	Not4r	5'-agtgggttcccaaagaatcc-3' (SEQ ID NO.:26)
D29D30l	D29	5'-gatgtgtcccttgtcagtgccat-3' (SEQ ID NO.:28)
	D30l	5'-tgtcgtgttcagccgcttgaggt-3' (SEQ ID NO.:29)
NSK5	Not3	5'-ctctcagtgccttccaacaac-3' (SEQ ID NO.:30)
	Sal4r	5'-ctgactgtcgaagctgatgc-3' (SEQ ID NO.:31)
SFK2	Sal5	5'-ggaggtggtcagcctctaca-3' (SEQ ID NO.:32)
	FLAG1	5'-ttacttgtcatcgtcgtccttgtagtcggcggctgggcag-3' (SEQ ID NO.:33)
SFL13	Sal5	5'-ggaggtggtcagcctctaca-3' (SEQ ID NO.:32)
	m19R	5'-aatggtgccagactcagg-3' (SEQ ID NO.:34)

Detailed Description of the Preferred Embodiments

All references, patents and patent applications are hereby incorporated by reference in their entirety.

Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in *Methods in Enzymology* (M.P. Deutshcer, ed., (1990) Academic Press, Inc.); *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, CA), *Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed.* (R.I. Freshney. 1987. Liss, Inc. New York, NY), *Gene Transfer and Expression Protocols*, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 1998 Catalog (Ambion, Austin, TX).

In one aspect, the present invention provides an isolated nucleic acid encoding a full length laminin α5 chain polypeptide consisting of the amino acid sequence of SEQ ID NO:2. In a preferred embodiment, the isolated nucleic acid consists of the sequence of SEQ ID NO:1, the complement thereof, or the RNA expression product thereof.

In an additional aspect, the present invention provides an isolated nucleic acid comprising a nucleic acid sequence encoding the 2,743 N-terminal amino acids (SEQ ID NO:36) of the human laminin α5 chain, which has not previously been reported. In a preferred embodiment, the isolated nucleic acid consists of the sequence of SEQ ID NO:35, the complements thereof, or the RNA expression product thereof.

An used herein, an "isolated nucleic acid sequence" refers to a nucleic acid sequence that is free of gene sequences which naturally flank the nucleic acid in the genomic DNA of the organism from which the nucleic acid is derived (i.e., genetic sequences that are located adjacent to the gene for the isolated nucleic molecule in the genomic DNA of the organism from which the nucleic acid is derived). An "isolated" laminin α5 chain nucleic acid sequence according to the present invention may, however, be linked to other nucleotide sequences that do not normally flank the recited sequence, such as a heterologous promoter sequence, or other vector sequences. It is not necessary for the isolated nucleic acid sequence to be free of other cellular material to be considered "isolated", as a nucleic acid sequence

according to the invention may be part of an expression vector that is used to transfect host cells (see below).

In another aspect, the present invention provides recombinant expression vectors comprising a full length laminin α5 chain nucleic acid sequence, or a nucleic acid sequence expressing the 2,743 N-terminal amino acids (SEQ ID NO:36) of the human laminin α5 chain. In one embodiment, the expression vectors comprise a nucleic acid encoding a polypeptide selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:36, operatively linked to a heterologous (i.e.: is not the naturally occurring α5 laminin chain promoter) promoter. In a preferred embodiment, the isolated nucleic acid consists of a sequence selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:35. A promoter and a laminin α5 chain nucleic acid sequence are "operatively linked" when the promoter is capable of driving expression of the laminin α5 chain DNA into RNA.

As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA into which additional DNA segments may be cloned. Another type of vector is a viral vector, wherein additional DNA segments may be cloned into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors), are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" or simply "expression vectors". In the present invention, the expression of the laminin polypeptide sequence is directed by the promoter sequences of the invention, by operatively linking the promoter sequences of the invention to the gene to be expressed. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" may be used interchangeably, as the plasmid is the most commonly used form of vector. However, the invention is intended to include other forms of expression vectors, such as viral

vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The vector may also contain additional sequences, such as a polylinker for subcloning of additional nucleic acid sequences, or a polyadenylation signal to effect proper polyadenylation of the transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and any such sequence may be employed, including but not limited to the SV40 and bovine growth hormone poly-A sites. Also contemplated as an element of the vector is a termination sequence, which can serve to enhance message levels and to minimize read through from the construct into other sequences. Additionally, expression vectors typically have selectable markers, often in the form of antibiotic resistance genes, that permit selection of cells that carry these vectors.

In a further embodiment, the present invention provides host cells transfected with the laminin $\alpha 5$ chain-expressing recombinant expression vectors disclosed herein. As used herein, the term "host cell" is intended to refer to a cell into which a nucleic acid of the invention, such as a recombinant expression vector of the invention, has been introduced. Such cells may be prokaryotic, which can be used, for example, to rapidly produce a large amount of the expression vectors of the invention, or may be eukaryotic, for functional studies.

The terms "host cell" and "recombinant host cell" are used interchangeably herein. It should be understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

The host cells can be transiently or stably transfected with one or more of the expression vectors of the invention. Such transfection of expression vectors into prokaryotic and eukaryotic cells can be accomplished via any technique known in the art, including but not limited to standard bacterial transformations, calcium phosphate co-precipitation, electroporation, or liposome mediated-, DEAE dextran mediated-, polycationic mediated-, or viral mediated transfection. (See, for example, *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press; *Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed.* (R.I. Freshney. 1987. Liss, Inc. New York, NY).

In another aspect, the present invention provides an isolated full length human laminin α5 chain polypeptide consisting of amino acid sequence of SEQ ID NO:2. In a further embodiment, of this aspect, the invention provides an isolated polypeptide consisting of the 2,743 N-terminal amino acids (SEQ ID NO:36) of the human laminin α5 chain.

As used herein, an "isolated polypeptide" refers to a polypeptide that is substantially free of other proteins, including other laminin chains, and gel agents, such as polyacrylamide and agarose. In a preferred embodiment, the isolated laminin polypeptide is free of detectable contaminating laminin chains. Thus, the protein can either be isolated from natural sources, or recombinant protein can be isolated from the transfected host cells disclosed above.

In a further aspect, the invention provides methods for detecting the presence of the laminin α5 chain in a protein sample, comprising providing a protein sample to be screened, contacting the protein sample to be screened with an antibody against the 2,743 N-terminal amino acids (SEQ ID NO:36) of the human laminin α5 chain, or fragments thereof, and detecting the formation of antibody-antigen complexes.

The antibody can be either polyclonal or monoclonal, although monoclonal antibodies are preferred. As used herein, the term "protein sample" refers to any sample that may contain the laminin α5 chain, including but not limited to tissues and portions thereof, tissue sections, intact cells, cell extracts, purified or partially purified protein samples, bodily fluids, nucleic acid expression libraries. Accordingly, this aspect of the present invention is useful for a variety of purposes including, but not limited to, immunolocalization, immunofluorescence analysis, Western blot analysis, ELISAs, and nucleic acid expression library screening. In one embodiment, the techniques may determine only the presence or absence of the human laminin α5 chain. Alternatively, the techniques may be quantitative, and provide information about the relative amount of laminin α5 chain in the sample. For quantitative purposes, ELISAs are preferred.

Detection of immunocomplex formation between the human laminin α5 chain and antibodies or fragments thereof directed against an amino acid sequence of SEQ ID NO:36, or fragments thereof, can be accomplished by standard detection techniques. For example, detection of immunocomplexes can be accomplished by using labeled antibodies or secondary antibodies.

Antibodies can be made by well-known methods, such as described in Harlow and Lane, Antibodies; A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., (1988). For example, all or a portion of the amino acid sequence of SEQ ID NO:36, together with an appropriate adjuvant, can be injected into an animal in an amount and at intervals sufficient to elicit an immune response. Animals are bled at regular intervals, preferably weekly, to determine antibody titer. Polyclonal antibodies against laminin α5 chain can then be purified directly by passing serum collected from the animal through a column to which non-antigen-related proteins prepared from the same expression system without laminin α5 chain bound.

Monoclonal antibodies can be produced by obtaining spleen cells from the animal. (See Kohler and Milstein, Nature 256, 495-497 (1975)). In one example, monoclonal antibodies (mAb) of interest are prepared by immunizing inbred mice with peptide fragments of the amino acid sequence of SEQ ID NO:36. The mice are immunized by the IP or SC route in an amount and at intervals sufficient to elicit an immune response. The mice receive an initial immunization on day 0 and are rested for about 3 to about 30 weeks. Immunized mice are given one or more booster immunizations of by the intravenous (IV) route. Lymphocytes, from antibody positive mice are obtained by removing spleens from immunized mice by standard procedures known in the art. Hybridoma cells are produced by mixing the splenic lymphocytes with an appropriate fusion partner under conditions which will allow the formation of stable hybridomas. The antibody producing cells and fusion partner cells are fused in polyethylene glycol at concentrations from about 30% to about 50%. Fused hybridoma cells are selected by growth in hypoxanthine, thymidine and aminopterin supplemented Dulbecco's Modified Eagles Medium (DMEM) by procedures known in the art. Supernatant fluids are collected from growth positive wells and are screened for antibody production by an immunoassay such as solid phase immunoradioassay. Hybridoma cells from antibody positive wells are cloned by a technique such as the soft agar technique of MacPherson, Soft Agar Techniques, in Tissue Culture Methods and Applications, Kruse and Paterson, Eds., Academic Press, 1973.

In yet another aspect, the invention provides methods for detecting the presence in a sample of nucleic acid sequences encoding the human laminin α5 chain, comprising

providing a nucleic acid sample to be screened, contacting the sample with a nucleic acid probe consisting of the nucleic acid sequence of SEQ ID NO:35 or fragments thereof, and detecting complex formation.

As used herein, the term "sample" refers to any sample that may contain nucleic acid sequences encoding the human laminin α5 chain, including but not limited to tissues and portions thereof, tissue sections, intact cells, cell extracts, purified or partially purified nucleic acid samples, DNA libraries, and bodily fluids. Accordingly, this aspect of the present invention may be used to test for the presence of laminin α5 chain mRNA or DNA in these various samples by standard techniques including, but not limited to, in situ hybridization, Northern blotting, Southern blotting, DNA library screening, polymerase chain reaction (PCR) or reverse transcription-PCR (RT-PCR). In one embodiment, the techniques may determine only the presence or absence of the nucleic acid of interest. Alternatively, the techniques may be quantitative, and provide information about the relative amount of the nucleic acid of interest in the sample. For quantitative purposes, quantitative PCR and RT-PCR are preferred. Thus, in one example, RNA is isolated from a sample, and contacted with an oligonucleotide derived from the nucleic acid sequence of SEQ ID NO:35, or its complement, together with reverse transcriptase under suitable buffer and temperature conditions to produce cDNAs from the laminin α5 chain RNA. The cDNA is then subjected to PCR using primer pairs derived from the nucleic acid sequence of interest. For detecting laminin α5 chain nucleic acid sequences, standard labeling techniques can be used to label the probe, the nucleic acid of interest, or the complex between the probe and the nucleic acid of interest, including, but not limited to radio-, enzyme-, chemiluminescent-, or avidin or biotin-labeling techniques, all of which are well known in the art. (See, for example, *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA); *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, CA)).

In another aspect, the present invention provides isolated laminin 10. As used herein "laminin 10" encompasses both r-laminin 10 and heterotrimeric laminin

10 from naturally occurring sources. In a preferred embodiment, the laminin 10 comprises recombinant laminin 10 (or "r-laminin 10").

As used herein, the term "r-laminin 10" refers to recombinant heterotrimeric laminin 10, expressed by a host cell that has been transfected with one or more expression vectors comprising at least one nucleic acid sequence encoding a laminin 10 chain selected from the α5, β1 and γ1 chains, or processed/secreted forms thereof. Such r-laminin 10 can thus comprise α5, β1, and γ1 sequences from a single organism, or from different organisms. Various laminin 10 chain DNA sequences are known in the art, and the use of each to prepare the r-laminin 10 of the invention is contemplated. (See, for example, Pouliot, N. et al., Experimental Cell Research 261(2):360-71, (2000); Kikkawa, Y. et al., Journal of Cell Science 113 (Pt 5):869-76, (2000); Church, HJ. et al., Biochemical Journal 332 (Pt 2):491-8, (1998); Sorokin, LM. et al., Developmental Biology 189(2):285-300, (1997); Miner, JH. et al., Journal of Biological Chemistry 270(48):28523-6, (1995); Sorokin, L. et al., European Journal of Biochemistry 223(2):603-10, (1994); all references incorporated by reference herein in their entirety). In a preferred embodiment, the r-laminin 10 comprises recombinant human α5, β1, and γ1 polypeptide chains.

As used herein, "isolated" means that the laminin 10 is substantially free of other proteins, including the laminin β2 chain polypeptide chain, and gel agents, such as polyacrylamide and agarose. In a preferred embodiment, the isolated laminin 10 is free of detectable laminin β2 polypeptide chains.

The invention encompasses those laminin molecules wherein one or two chains that make up the recombinant heterotrimeric laminin 10 are encoded by endogenous laminin 10 chains. In a preferred embodiment, each of the α5, β1, and γ1 polypeptide chains are expressed recombinantly.

Laminin 10 is a secreted protein, which is capable of being directed to the endoplasmic reticulum (ER), secretory vesicles, and the extracellular space as a result of a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Such processing event can be variable, and thus may yield different versions of the final "mature protein". The isolated laminin 10 of the present invention includes heterotrimers comprising both the full length and any such processed laminin 10 polypeptide chains.

As used herein, a laminin 10 polypeptide chain refers to a polypeptide chain according to one or more of the following:

(a) comprises a polypeptide structure selected from the group consisting of:

1. R1-R2-R3
2. R1-R2-R3(e)
3. R3
4. R3(e)
5. R1-R3
6. R1-R3(e)
7. R2-R3
8. R2-R3(e)

wherein R1 is an amino terminal methionine; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, or an artificial sequence; R3 is a secreted laminin chain selected from group consisting of the α5, β1, and γ1 chains; and R3(e) is a secreted laminin chain selected from the α5, β1, and γ1 chains that further comprises an epitope tag (such as those described below), which can be placed at any position within the laminin chain amino acid sequence; and/or

(b) is encoded by a polynucleotide that hybridizes under high or low stringency conditions to the coding regions, or portions thereof, of one or more of the recombinant laminin 10 chain DNA sequences disclosed herein (SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, and SEQ ID NO:35), or complementary sequences thereof; and/or

(c) has at least 70% identity to one or more of the disclosed laminin 10 polypeptide chain amino acid sequences (SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, and SEQ ID NO:36), preferably at least 80% identity, and most preferably at least about 90% identity.

"Stringency of hybridization" is used herein to refer to conditions under which nucleic acid hybrids are stable. The invention also includes nucleic acids that hybridize under high stringency conditions (as defined herein) to all or a portion of

the coding sequences of the laminin chain polynucleotides disclosed herein, or their complements. The hybridizing portion of the hybridizing nucleic acids is typically at least 50 nucleotides in length. As known to those of skill in the art, the stability of hybrids is reflected in the melting temperature (T_M) of the hybrids. T_M decreases approximately 1-1.5°C with every 1% decrease in sequence homology. In general, the stability of a hybrid is a function of sodium ion concentration and temperature. Typically, the hybridization reaction is performed under conditions of lower stringency, followed by washes of varying, but higher, stringency. Reference to hybridization stringency relates to such washing conditions. Thus, as used herein, high stringency refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are laminin 10-encoding nucleic acid sequences that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH_2PO_4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

As used herein, "percent identity" of two amino acids or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12, to determine nucleotide sequences identity to the nucleic acid molecules of the invention. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3, to determine an amino acid sequence identity to a polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids. Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. See http://www.ncbi.nlm.nih.gov.

Further embodiments of the present invention include polynucleotides encoding laminin 10 chain polypeptides having at least 70% identity, preferably at least 80% identity, and most preferably at least 90% identity to one or more of the polypeptide sequences contained in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, and SEQ ID NO:36 .

As used herein, "α5 polynucleotide" refers to polynucleotides encoding an laminin α5 chain of the same name. Such polynucleotides can be characterized by one or more of the following: (a) polynucleotides that encode polypeptides which share at least 70% identity, preferably 80% identity, and most preferably at least 90% identity with one or more sequences selected from the group consisting of SEQ ID NO: 2 and SEQ ID NO:4; (b) the α5 polynucleotides hybridize under low or high stringency conditions to one or more coding sequences selected from the group consisting of SEQ ID NO: 1 or SEQ ID NO:3; complementary sequences thereof; or (c) the α5 polynucleotides encode a laminin α5 chain polypeptide with a general structure selected from the group consisting of (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e); wherein R1 and R2 are as described above, and R3 and R3(e) are as described above but comprise secreted α5 chain polypeptides.

As used herein, "β1 polynucleotides" refers to polynucleotides encoding a β1 laminin chain of the same name. Such polynucleotides can be characterized by one or more of the following: (a) polynucleotides that encode polypeptides which share at least 70% identity, preferably at least 80%, and most preferably at least 90% identity with one or more of the sequences selected from the group consisting of SEQ ID NO: 6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12; (b) the β1 polynucleotides hybridize under low or high stringency conditions to one or more coding sequences selected from the group consisting of SEQ ID NO: 5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, or complementary sequences thereof; or (c) the β1 polynucleotides encode a polypeptide with a general structure selected from (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e); wherein R1 and R2 are as described above, and R3 and R3(e) are as described above but comprise secreted β1 chain polypeptides.

As used herein, "γ1 polynucleotides" refers to polynucleotides encoding a γ1 laminin chain of the same name. Such polynucleotides can be characterized by one or more of the following: (a) polynucleotides that encode polypeptides which share at least 70% identity, preferably at least 80%, and most preferably at least 90% identity with one or more of the sequences selected from the group consisting of SEQ ID NO: 14, SEQ ID NO:16, SEQ ID NO:18, or SEQ ID NO:20; (b) the γ1 polynucleotides hybridize under low or high stringency conditions to one or more of the coding sequence selected from the group consisting of SEQ ID NO: 13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19 or complementary sequences thereof; or (c) the γ1 polynucleotides encode a polypeptide with a general structure selected from (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e); wherein R1 and R2 are as described above, and R3 and R3(e) are as described above but comprise secreted γ1 chain polypeptides.

As used herein, the term "epitope tag" refers to a polypeptide sequence that is expressed as part of a chimeric protein, where the epitope tag serves as a recognition site for binding of antibodies generated against the epitope tag, or for binding of other molecules that can be used for affinity purification of sequences containing the tag.

In a preferred embodiment, cDNAs encoding the laminin α5, β1 and γ1 chains, or fragments thereof, are subcloned into an expression vector. Alternatively,

laminin α5, β1 and/or γ1 gene sequences, including one or more introns, can be used for sub-cloning into an expression vector.

In another aspect, the present invention provides laminin 10 expressing-cells that have been transfected with an expression vector containing promoter sequences that are operatively linked to nucleic acid sequences encoding at least one polypeptide sequence comprising a sequence selected from the group consisting of the α5, β1 and γ1 chains of laminin 10, wherein the transfected cells secrete heterotrimeric laminin 10 containing the recombinant laminin chain. In a preferred embodiment, the cells are systematically transfected with recombinant expression vectors containing promoter sequences that are operatively linked to nucleic acid sequences encoding polypeptide sequences comprising the α5, β1 and γ1 chains of laminin 10, even more preferably, all human chains. After the multiple transfections, the cells express recombinant laminin 10 chains, which form the heterotrimeric r-laminin 10.

Transfection of the expression vectors into eukaryotic cells can be accomplished via any technique known in the art, including but not limited to calcium phosphate co-precipitation, electroporation, or liposome mediated-, DEAE dextran mediated-, polycationic mediated-, or viral mediated transfection. Transfection of bacterial cells can be done by standard methods.

In a preferred embodiment, the cells are stably transfected. Methods for stable transfection and selection of appropriate transfected cells are known in the art. In another preferred embodiment, a CMV promoter driven expression vector is used in a human kidney embryonic 293 cell line.

Any cell capable of expressing and secreting the r-laminin 10 can be used. Preferably, eukaryotic cells are used, and most preferably mammalian cells are used, including but not limited to kidney and epithelial cell lines. The promoter sequence used to drive expression of the individual chains or r-laminin 10 may be constitutive (driven by any of a variety of promoters, including but not limited to, CMV, SV40, RSV, actin, EF) or inducible (driven by any of a number of inducible promoters including, but not limited to, tetracycline, ecdysone, steroid-responsive). Carbohydrate and disulfide post-translational modifications are believed to be required for laminin 10 protein folding and function. This makes the use of eukaryotic cells preferable for producing functional r-laminin 10, although other systems are useful for obtaining, for example, antigens for antibody production. In a

most preferred embodiment, the mammalian cells do not express the laminin β2 chain endogenously. In another preferred embodiment, the cells do not express all of the laminin 10 chains endogenously.

The protein may comprise additional sequences useful for promoting purification of the protein, such as epitope tags and transport signals. Examples of such epitope tags include, but are not limited to FLAG (Sigma Chemical, St. Louis, MO), myc (9E10) (Invitrogen, Carlsbad, CA), 6-His (Invitrogen; Novagen, Madison, WI), and HA (Boehringer Manheim Biochemicals). Examples of such transport signals include, but are not limited to, export signals, secretory signals, nuclear localization signals, and plasma membrane localization signals.

In one embodiment, at least one of the laminin chain polypeptide sequences, or fragments thereof, is operatively linked to a nucleic acid sequence encoding an "epitope tag", so that at least one of the chains is expressed as a fusion protein with an expressed epitope tag. The epitope tag may be expressed as the amino terminus, the carboxy terminus, or internal to any of the polypeptide chains comprising r-laminin 10, so long as the resulting r-laminin 10 remains functional.

In another embodiment, one of the r-laminin 10 chains is expressed as a fusion protein with a first epitope tag, and at least one other r-laminin chain is expressed as a fusion protein with a second epitope tag. This permits multiple rounds of purification to be carried out. Alternatively, the same epitope tag can be used to create fusion proteins with more than one of the r-laminin chains.

In a further embodiment, the epitope tag can be engineered to be cleavable from the r-laminin 10 chain(s). Alternatively, no epitope tag is fused to any of the r-laminin 10 chains, and the r-laminin 10 is isolated by standard techniques, including but not limited to affinity chromatography using laminin 10 specific antibodies or other laminin 10 binding molecules.

Media from cells transfected with a single laminin chain are initially analyzed on Western blots using laminin chain-specific antibodies. The expression of single laminin chains following transfection is generally intracellular. Clones showing reactivity against individual transfected chain(s) are verified by any appropriate method, such as PCR, reverse transcription-PCR, or nucleic acid hybridization, to confirm incorporation of the transfected gene. Preferably, analysis of genomic DNA preparations from such clones is done by PCR using laminin chain-specific primer pairs. Media from transfected clones producing all three chains are further analyzed

for r-laminin 10 secretion and/or activity, by any appropriate method, including Western blot analysis and cell binding assays. Activity of the r-laminin 10 is preferably analyzed in a cell adhesion assay.

In a preferred embodiment, purification of r-laminin 10 is accomplished by passing media from the transfected cells through an antibody affinity column. In one embodiment, antibodies against a peptide epitope expressed on at least one of the recombinant chains are attached to an affinity column, and bind the r-laminin 10 that has been secreted into the media. The r-laminin 10 is removed from the column by passing excess peptide over the column. Eluted fractions are analyzed by any appropriate method, including gel electrophoresis and Western blot analysis. In a further embodiment, the peptide epitope can be cleaved after purification. In other embodiments, two or three separate r-laminin chains are expressed as fusion proteins, each with a different epitope tag, permitting two or three rounds of purification and a doubly or triply isolated r-laminin 10. The epitope tag can be engineered so as to be cleavable from the r-laminin 10 chain(s) after purification. Alternatively, no epitope tag is fused to any of the r-laminin 10 chains, and the r-laminin 10 is isolated by standard techniques, including but not limited to affinity chromatography using laminin 10 specific antibodies or other laminin 10 binding molecules.

The laminin 10 polypeptide chains of the present invention also include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more amino acid residues having substituents groups, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340

(1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

The present invention further provides pharmaceutical compositions comprising isolated laminin 10 and a pharmaceutically acceptable carrier. In a preferred embodiment, the pharmaceutical composition comprises isolated r-laminin 10. According to this aspect of the invention, other agents can be included in the pharmaceutical compositions, depending on the condition being treated. The pharmaceutical composition may further comprise one or more other compounds, including but not limited to any of the collagens, other laminin types, fibronectin, vitronectin, cadherins, integrins, α-dystroglycan, entactin/nidogen, α-dystroglycan, glycoproteins, proteoglycans, heparan sulfate proteoglycan, glycosaminoglycans, epidermal growth factor, vascular endothelial growth factor, fibroblast growth factor, or nerve growth factors, and peptide fragments thereof.

Pharmaceutical preparations comprising isolated laminin 10 can be prepared in any suitable form, and generally comprise the isolated laminin 10 in combination with any of the well known pharmaceutically acceptable carriers. The carriers can be injectable carriers, topical carriers, transdermal carriers, and the like. The preparation may advantageously be in a form for topical administration, such as an ointment, gel, cream, spray, dispersion, suspension or paste. The preparations may further advantageously include preservatives, antibacterials, antifungals, antioxidants, osmotic agents, and similar materials in composition and quantity as is conventional. Suitable solutions for use in accordance with the invention are sterile, are not harmful for the proposed application, and may be subjected to conventional pharmaceutical operations such as sterilization and/or may contain conventional adjuvants, such as preservatives, stabilizers, wetting agents, emulsifiers, buffers etc. For assistance in formulating the compositions of the present invention, one may refer to Remington's Pharmaceutical Sciences, 15th Ed., Mack Publishing Co., Easton, Pa. (1975).

In further aspect, the present invention provides methods and kits comprising isolated laminin 10, or pharmaceutical compositions thereof (and instructions for using the isolated laminin 10 in the kits) for accelerating the healing of injuries to vascular tissue, and for improving the biocompatibility of grafts used for treating such injuries. In a preferred embodiment of each of the methods disclosed below, isolated

laminin 10 is used. In specific examples, isolated laminin 10, isolated r-laminin 10, or pharmaceutical compositions thereof are used to:

a. promote re-endothelialization at the site of vascular injuries;

b. improve the "take" of grafts;

c. improve the biocompatibility of medical devices;

d. promote cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration

by providing an amount effective of isolated laminin 10 or pharmaceutical compositions thereof for the various methods.

Endothelial cells normally rest on a subendothelium, composed of collagen type I/III, elastin, fibronectin, glycosaminoglycans, and a basement membrane, mainly consisting of laminin and type IV collagen. Several of the invasive treatments used in the repair of vascular occlusive diseases, or the disease itself, may cause large areas of endothelial cell-denudation in the vessel wall. Endothelialization is, in part, dependent upon the underlying matrix, as subendothelial proteins have been shown to be important modulators of endothelial cell function (Madri, J.A. et al., Am. J. Pathol. 132(1), 18-27 (1988); and Madri, J.A. et al., J. Cell Biochem. 45(2), 123-30 (1991). In an effort to enhance endothelialization of grafts in humans, extensive research has been devoted to identifying substances that promote endothelial cell migration. Endothelial cell migration is a key element of endothelialization of vascular grafts, whether by anastomotic ingrowth, transmural capillary ingrowth, adherence of circulating cells, or *ex vivo* cell seeding. Ultimately, it is desirable to encourage spontaneous migration *in vivo* because this would minimize the need for *ex vivo* graft and cell manipulation. In addition, retention of cells on the vascular surface is necessary prior to migration (Dixit, P. et al., J. Biomed. Mater. Res. 56(4), 545-55 (2001)). Pretreatment of the graft with an adhesive substrate significantly enhances endothelial cell attachment to graft samples.

Laminin-8 and laminin-10 are secreted by endothelial cells, and are major components of the subendothelial basement membrane (Sorokin, L.M. et al., Dev. Biol. 189(2), 285-300 (1997); Iivanainen, A. et al., J. Biol. Chem. 272(44), 27862-8 (1997); Patton, B. L. et al., J. Cell Biol. 139(6), 1507-21 (1997), Miner, J.H. et al., J. Cell Biol. 137(3), 685-701 (1997); Sorokin, L. et al., Eur. J. Biochem. 223(2), 603-10 (1994); and Tokida, Y. et al., J. Biol. Chem. 265(30), 18123-9 (1990)). The data

presented below demonstrates that isolated laminin 10 promotes endothelial cell attachment and migration.

Thus, in one embodiment the isolated laminin 10 is used to promote re-endothelialization, and to thus inhibit abnormal smooth muscle cell proliferation, at the site of a vascular injury. In another embodiment, isolated laminin 10 is coated onto grafts to improve the "take" of grafts. As used herein the term "graft" refers to both natural and prosthetic grafts and implants.

In a further aspect, the present invention comprises medical devices with improved biocompatibility, wherein the devices are coated with isolated laminin 10 or pharmaceutical compositions thereof, alone or in combination with other proteins or agents that serve to increase the biocompatibility of the device surface. The coated device stimulates cell attachment (such as endothelial cell attachment), and provides for diminished inflammation and/or infection at the site of entry of the appliance.

Such medical devices can be of any material used for implantation into the body, and preferably are made of or coated with a biocompatible metal that may be either stainless steel or titanium. Alternatively, the device is made of or coated with a ceramic material, or a polymer including but not limited to polyester, polyglycolic acid or a polygalactose-polyglycolic acid copolymer.

One particular use of the present invention is to increase cell adhesion to target surfaces, including but not limited to endothelial cell adhesion. For example, vascular grafts and stents may be coated with isolated laminin 10 or pharmaceutical compositions thereof to stimulate endothelial cell attachment.

If the device is made of a natural or synthetic biodegradable material in the form of a mesh, sheet or fabric, isolated laminin 10 or pharmaceutical compositions thereof may be applied directly to the surface thereof. Appropriate cells may then be cultured on the matrix to form transplantable or implantable devices, including dental abutment pieces, needles, metal pins or rods, indwelling catheters, colostomy tubes, surgical meshes and any other appliance for which coating with isolated laminin 10 is desirable. Alternatively, the devices may be implanted and cells may be permitted to attach in vivo.

Coupling of the isolated laminin 10 may be non-covalent (such as by adsorption), or by covalent means. The device may be immersed in, incubated in, or sprayed with the isolated laminin 10 or pharmaceutical compositions thereof.

The dosage regimen for various treatments using the isolated laminin 10 of the present invention is based on a variety of factors, including the type of injury or condition, the age, weight, sex, medical condition of the individual, the severity of the condition, and the route of administration. Thus, the dosage regimen may vary widely, but can be determined routinely by a physician using standard methods. Laminins are extremely potent molecules, and one or a few molecules per cell could produce an effect. Thus, effective doses in the pico-gram per milliliter range are possible if the delivery is optimized. Laminins are sometimes present in an insoluble form in the basement membrane and have the capability of polymerizing at concentrations as low as about 50 μg/ml, depending on the laminin isoform and the conditions. Laminins can also polymerize into a gel at a concentration of about 2-3 mg/ml. Dosage levels of the order of between 1 ng/ml and 10 mg/ml are thus useful for all methods disclosed herein, preferably between about 1 μg/ml and about 3 mg/ml.

The present invention also provides a method for inducing cell attachment to the device (as disclosed above), comprising coating the appliance with isolated laminin 10 or pharmaceutical compositions thereof prior to incubation with cells appropriate for the desired application.

In another aspect of the present invention, isolated laminin 10 is used for the culture of cells, including but not limited to endothelial cells, by contacting the cells with an amount effective of isolated laminin 10 to stimulate cell attachment and subsequent cell stasis, proliferation, differentiation, and/or migration. The isolated laminin 10 can either be provided in the cell culture medium, or as a cell culture medium supplement, or may be coated on the surface of a cell growth substrate. In a preferred embodiment, the method further includes contacting the cells with other compounds, including but not limited to any of the collagens, other laminin types, fibronectin, α-dystroglycan, cadherins, integrins, entactin/nidogen, α-dystroglycan, glycoproteins, proteoglycans, heparan sulfate proteoglycan, glycosaminoglycans, epidermal growth factor or nerve growth factors, vascular endothelial growth factor, fibroblast growth factor, and peptide fragments thereof.

The cells may comprise primary cells or cell culture cell lines. The methods of this aspect of the invention can be used in vivo, or in vitro.

In a preferred embodiment, isolated laminin 10 is used to coat the surface of a substrate, to promote cell adhesion to the substrate. The substrate used herein may be any desired substrate. For laboratory use, the substrate may be as simple as glass or plastic. For use in vivo, the substrate may be any biologically compatible material capable of supporting cell adhesion. Suitable substrate materials include shaped articles made of or coated with such materials as collagen, regenerated collagen, polyglycolic acid, polygalactose, polylactic acid or derivatives thereof; biocompatible metals such as titanium and stainless steel; ceramic materials including prosthetic material such as hydroxylapatite; synthetic polymers including polyesters and nylons; polystyrene; polyacrylates; polytetrafluoroethylene and virtually any other material to which biological molecules can readily adhere. The determination of the ability of a particular material to support adhesion of the isolated laminin 10 of the invention requires only routine experimentation by the skilled artisan.

In a further aspect, the present invention provides cell growth substrates for adhesion and culturing of cells, by providing an amount effective of isolated laminin 10 for the attachment of cells to a cell culture device. The substrates may comprise any of the substrates discussed above.

In another aspect of the present invention, an improved cell culture medium is provided, wherein the improvement comprises addition to the cell culture medium of an effective amount of isolated laminin 10 to the cell culture medium to promote the adherence, proliferation, and/or maintenance of cells. Any cell culture media that can support the growth of cells can be used with the present invention. Such cell culture media include, but are not limited to Basal Media Eagle, Dulbecco's Modified Eagle Medium, Iscove's Modified Dulbecco's Medium, McCoy's Medium, Minimum Essential Medium, F-10 Nutrient Mixtures, Opti-MEM® Reduced-Serum Medium, RPMI Medium, and Macrophage-SFM Medium or combinations thereof.

The improved cell culture medium can be supplied in either a concentrated (ie: 10X) or non-concentrated form, and may be supplied as either a liquid, a powder, or a lyophilizate. The cell culture may be either chemically defined, or may contain a serum supplement. Culture media is commercially available from many sources, such as GIBCO BRL (Gaithersburg, MD) and Sigma (St. Louis, MO).In an alternative embodiment, the laminin 10 is used as a cell culture supplement.

The present invention may be better understood with reference to the accompanying examples that are intended for purposes of illustration only and should

not be construed to limit the scope of the invention, as defined by the claims appended hereto.

Examples

Cloning of the Human Laminin α5 cDNA

The previously published mouse laminin α5 sequence (SEQ ID NO.:3) was used to search EST-databases. Based upon sequences of the identified ESTs, oligonucleotide primers were synthesized and used for PCR amplification of several human α5 specific probes with λgt11 cDNA library (Clontech) as template. These probes were used for screening of λgt11 cDNA libraries (Clontech) from human lung, fetal lung and fetal kidney. This resulted in the isolation of several clones, and further screening was performed with PCR amplified selected regions of these clones. This walk generated clones covering 2134 base pair of coding sequence and 195 base pairs of 3'UTR in the C-terminal part, and 5354 base pairs in the N-terminal part, but lacking a translation initiation start site. The center part, comprising base pairs 5582-9316, was obtained by PCR amplification from a Human Lung MARATHON READY™ cDNA-mix (Clontech). The remaining 296 base pairs of coding sequence and a 67 base pair 5'UTR end was obtained with SMART™ RACE cDNA Amplification Kit (Clontech) using poly-A RNA purified with QuickPrep mRNA Purification Kit (Pharmacia Biotech) from HEK293 cell lysate. The reverse transcription was performed with the MMLV reverse transcriptase SuperscriptII (Life Technologies), and subsequent PCR amplification was performed with Advantage®-GC 2 PCR kit (Clontech). This 363 base pair N-terminal sequence was confirmed by sequencing genomic P1-clone (GenomeSystems) obtained by screening with a PCR generated probe from nucleotides 344-452. This generated a full-length sequence, but most of the sequence was only covered by a single λ-clone or PCR fragment. To further confirm the sequence, we used PCR amplification of SMART™RACE-generated cDNA-mixes from HEK293 cells, human placenta total RNA and from Human Lung Marathon Ready™ cDNA-mix. This generated new clones so that all regions of the cDNA were covered by more than one clone from different sources. In the case of suspected polymorphisms, several clones from different sources were compared. Sequencing was performed on an ABI PRISM™ 310 Genetic Analyzer

(Perkin Elmer) using ABI PRISM®BigDye™ Terminator Cycle Sequencing kit (PE Applied Biosystems). Sequence analysis was performed with AutoAssembler™ (PE Applied Biosystems) and sequence comparative analysis with the GCG-software (Group, G.C. et al., *Program for the GCG* Package, Version 10.1, Genetics Computer Group, Madison, WI (2000)).

Expression Constructs

For expression of the human laminin α5 chain containing a C-terminal FLAG epitope, the full-length cDNA was constructed as follows. To obtain overlapping cDNA clones, PCR amplification of SMART™ RACE-generated cDNA-mixes from HEK293 cells, human placenta total RNA, and Human Lung MARATHON READψ™ cDNA-mix was performed using ADVANTAGE®-GC 2 PCR kit and Pfu Turbo polymerase (Boeringer-Mannheim). All PCR derived cDNA fragments were cloned into the pCR2.1-TOPO vector (Invitrogen) and sequenced (AmpliTag FS on an ABI310 sequencer, Perkin-Elmer) to ensure that no mutations had occurred during amplification. All primers for PCR and pCR2.1-TOPO™ plasmids into which the PCR derived cDNA fragments were cloned are shown in Table I. To ensure efficient and correct translation initiation, the Kozak sequence (accgcc, (Kozak, M., *J. Cell Biol.* 115(4), 997-903 (1991)) was edited to match the consensus. Primer KZK1 contained modified Kozak sequence and primer FLAG1 contained the FLAG sequence encoding the FLAG epitope (N-Asp-Tyr-Lys-Asp-Asp- Asp-Asp-Lys-C). (SEQ ID NO:37)

The EcoRI-BamHI insert from KBX3 was cloned into EcoRI-BamHI digested pUC18 vector to make KBX4. The BamHI-XbaI fragment from BBL3 was ligated into BamHI-XbaI sites of KBX4 to make KBY1'. The BNK2' BclI-NotI fragment was cloned into KBY1' BclI-NotI sites to make KNX3. The 1.2 kilobase Bpu10I-NotI fragment of KNX3, which contained unwanted mutation was corrected by replacing the mutated fragment with non-mutated Bpu10I-NotI fragment from BNL12 to make KNX4'. The 1.8 kilobase BbvCI-SalI fragment of NSK5 was replaced by D29D30lII BbvCI-SalI fragment to make NSX1. The NotI-SalI fragment from NSX1 and AscI-EcoRI fragment containing FLAG epitope from SFK2 were cloned into SFL12 to make NFX4. The 5.3 kilobase NotI-HindIII fragment from NFX4 was ligated into NotI-HindIII sites of KNX4' to make KFX5 with full-length cDNA. The final

expression construct named HLN5Full.pcDNA was made by inserting the KFX5 EcoRI fragment into the EcoRI sites of pcDNA3.1/Zeo(-) mammalian expression vector (Invitrogen) in correct orientation. The construct used for expression of human laminin β1 was constructed from a baculovirus expression vector (Pikkarainen, T. et al., *Eur. J. Biochem.* 209(2), 571-82 (1992)) by ligation of the insert into pIRES-vector (Clontech). The construct used for expression of laminin γ1 (HG1) has been described previously (Kortesmaa, J. et al., *J. Biol. Chem.* 275(20), 14853-9 (2000)).

Antibodies and Control Proteins

Anti-laminin α5 (15H5, (Kikkawa, Y. et al., *J. Bio. Chem.* 273(25), 15854-9 (1998)) monoclonal antibody (mAb) was kindly provided by Dr. K. Sekiguchi. Anti-laminin β1 (DG10,Virtanen, I. et al., Am. J. Pathol. 150(4), 1421-31 (1997)) mAb was kindly provided by Dr. I. Virtanen. Anti-laminin β1 (2E8, Engvall, E. et al., J. Cell Biol. 103(6 Pt 1), 2457-65 (1986)) mAb was kindly provided by Dr. E. Engvall. Anti-FLAG M2 mAb, purified control mouse IgG, collagen type I from calfskin, collagen type IV (Col IV) from mouse-EHS- tumor and heparin (grade I-A) were purchased from Sigma. Anti-laminin γ1 (clone 22) mAb was purchased from Transduction Laboratories. Mouse mAb against integrin α6 (BQ16) was purchased from Alexis Biochemicals. Mouse function blocking mAbs against integrin α1 (FB12), α2 (P1E6), α3 (P1B5), αv (NKI-M9), αϖβ3 (ΛM609), mouse mAb against integrin β4 (ASC-3) and control rat IgG2a were obtained from Chemicon. Rat function blocking mAbs against integrin α6 (GoH3), mouse function blocking mAbs against integrin β1 (4B4) and mouse mAbs against integrin α4 (HP2/1), αv (AMF-7), and β3 (SZ-21) were obtained from Coulter. Secondary Ab conjugates anti-mouse IgG-horseradish peroxidase (HRP) and FITC-conjugated F(ab)2 fragments of rabbit anti-mouse immunoglobulin were purchased from Dako. RGDS-peptide, cyclical RGDS-peptide, control RAGS-peptide, mouse mAb against integrin α5 (P1D6) and human vitronectin from plasma were purchased from Life Technologies. Human fibronectin (FN) from plasma was obtained from Roche. EHS-derived laminin-1/nidogen complex (laminin-1/Nd) was kindly provided by Dr. J. Engel.

Production and Purification of Recombinant Laminin-10

r-laminin-10 was produced in human embryonic kidney cells (HEK293, ATCC CRL-1573) cultured in DMEM, pyruvate, 10% FCS in humidified 5% CO_2 atmosphere at 37°C. Wild-type cells were transfected using the standard calcium-phosphate method with the HG1 construct and stable colonies were selected using 100 mg/ml hygromycin (Cayla). All further cell culture and clonal expansion was carried out in continuous presence of relevant selection antibiotics. A highly expressing clone was then transfected with the human laminin β1 construct and stable clones were selected using 500 mg/ml G418 (Life Technologies). A clone highly expressing both laminin γ1 and laminin β1 was finally transfected with HLN5Full.pcDNA and stable colonies were selected using 200 mg/ml zeocin (Cayla). The clones showing the highest secretion were expanded further.

For production of r-laminin-10, confluent cells were cultured in DMEM supplemented with 1mM pyruvate and insulin-transferrin-selen supplement (Sigma) for up to five days. r-laminin-10 was affinity purified using anti-FLAG M2 matrix (Sigma). The collected medium was incubated in batch mode with the matrix overnight at 4°C with agitation. Bound r-laminin-10 was competitively eluted with 50 mg/ml FLAG peptide (Sigma) in TBS/E (50 mM Tris-Cl, pH 7.5, 150 mM NaCl, 1 mM EDTA) at room temperature. The elute was concentrated and the buffer was replaced by PBS using 30 kD cut-off ultrafiltration (Millipore). Finally the concentrated solution was passed through 0.2 mm filter to remove self-aggregated polymers. Recombinant human laminin-8 (r-laminin -8) was produced in HEK293 cells and isolated using anti-FLAG matrix and ion-exchange chromatography.

Characterization of Recombinant Laminin-10

Secreted laminin in medium and after purification was characterized using 5% SDS-PAGE and 4-15% gradient SDS-PAGE. Proteins were visualized using silver staining or transferred onto PVDF. The membranes were probed with mAbs described above. After washing, the membranes were incubated with HRP-conjugated goat anti-mouse antibody. The immunoreactivity was detected by a chemiluminescent kit (Life Science Products) according to the manufacturer's instructions.

Electron microscopy was performed by the rotary shadowing technique as described previously (Engel, J., Methods Enzymol. 245, 469-88 (1994)). Briefly,

protein (25-50 mg/ml) in 0.2 M ammonium bicarbonate, pH 7.4, or 0.1 M acetic acid was mixed with an equal volume of glycerol and sprayed onto freshly cleaved mica discs. These were dried in high vacuum, shadowed with platinum/carbon at an angle of 9° and replicated. Negative staining was performed at neutral pH in order to avoid dissociation of aggregates by the acid pH in the routine procedure. Ten ml of a solution in PBS was put on a glow discharged collodium and carbon grid and 5 ml of a 2% sodium phosphotungstate solution of pH 7 was added. After removal of the first stain, incubation was repeated for 2 min.

Cell Culture and HSVEC isolation

Human fibrosarcoma HT-1080 (CCL-121) cells were from ATCC. Immortomouse brain capillary endothelial (Kanda, S. et al Exp. Cell Res. 248(1), 203-13 (1999)) cells were kindly provided by Dr. L. Claesson-Welsh. All cells were cultured in humidified 5% CO_2 atmosphere. HT-1080 cells were cultured in DMEM, 10% FCS, pyruvate at 37°C. IBE cells were cultured in F-12, 10% FCS, 2 units/ml γ-interferon on gelatin-coated plastic at 33°C. Prior to assay, the IBE cells were cultured in serum-free F-12 at 37°C without γ-interferon for 24 hours.

As approved by the ethical committee at the Karolinska Hospital, Stockholm, Sweden, residual segments of the great saphenous vein were collected from patients undergoing coronary bypass surgery. HSVECs were isolated as previously described (Haegerstrand, A. et al., J. Vasc. Surg. 16(2), 280-5 (1992)). Briefly, veins were rinsed with MEM (Life Technologies) and filled with 0.1% collagenase and 0.16% dispase (Boehringer Mannheim) in MEM for 20 min at 37°C in an 8% CO2-humidified atmosphere. Cells were cultured in MEM containing 40% heat-inactivated pooled human serum (HS), 1 nmol/L choleratoxin (CT; Sigma), 33 mmol/L isobutylmethylxantine (IBMX; Sigma), and antibiotics. HSVECs were seeded on gelatin-coated plates and passaged (1:3). HSVECs were characterized with monoclonal anti-human von Willebrand factor-related antigen (Dako) and HSVECs between passages 4 and 7 were used in the experiments.

Cell Adhesion Assays

Adhesion assay was performed as described previously (Kortesmaa, J. et al., J. Biol. Chem. 275(20), 14853-9 (2000)). Briefly, 96-well plates (Maxi-Sorp, Nunc)

were coated with proteins overnight at 4°C. The remaining protein binding capacity was saturated by addition of 2% heat-inactivated BSA in PBS.

For the assay, cells were suspended in buffered serum-free medium at $3x10^4$ cells/well. DMEM, 25mM Hepes, pyruvate was used for HT-1080 cells, F-12, 25 mM Hepes, 0.25% BSA for others. Antibodies or other test compounds were added to the cell suspension and the cells were allowed to recover at 37°C for 30 min. Integrin mAbs were used at 10 mg/ml, RGD-peptides at 0.25 mg/ml, heparin at 5 mg/ml, and EDTA at 5mM. The cells were then allowed to adhere for 60 min at 37°C. Bound cells were quantitated by crystal violet staining. None of the cell lines bound appreciably to BSA. When the quantitative results were calculated, binding to BSA was given a value of zero, while the relevant control was given the value 100. The mean and standard deviation (S.D.) were calculated from results obtained from parallel wells.

Immunofluorescence Flow Cytometry

Briefly, suspended HSVECs were incubated in PBS containing anti-integrin mAbs against α1-6, αv, β1, β3, and β4 for 30 min at 4°C. Following washing, cells were incubated with FITC-conjugated F(ab)2 fragments of rabbit anti-mouse immunoglobulin for 30 min at 4°C. Cells were then analyzed in a FACS can flow cytometer (Becton Dickinson). Mouse IgG was used as a negative control.

Cell Migration Assays

Cell migration assay was performed as described previously (Jansson, K. et al., Eur. J. Vasc. Endovasc. Surg. 16(4), 334-41 (1998)). Flat-bottom 24-well culture plates (Corning) were coated with proteins overnight at 4°C. The remaining protein binding capacity was saturated by addition of 2% heat-inactivated BSA in PBS. Thereafter a 4x10 mm stainless steel-weight was put on the center of well, before seeding HSVECs at $2x10^5$ cells/well. After adhesion for 2 days in MEM with 30% HS, the steel-weight was removed. A gap devoid of HSVECs was thus created, with two broad (10 mm) EC-edges facing each other at a distance of 4 mm. During endothelialization, HSVECs were incubated in MEM with 40% HS, CT and IBMX for 2 days after removing the steel-weight. The cells were visualized by 0.1% crystal violet staining.

Results

Sequence of Human Laminin Alpha 5 Chain

The full-length laminin α5 cDNA coding sequence (Fig. 1) (SEQ ID NO:1) consisted of 11,088 base pair with an open reading frame encoding 3696 amino acids (SEQ ID NO.:2). Compared to the previously reported mouse laminin α5 sequence (GENBANK™ accession number U37501; Miner, J.H. et al., J. Biol. Chem. 270(48), 28523-6 (1995)) (SEQ ID NO.:4), we obtained an additional 79 amino acids in the N-terminal end. The mouse sequence has an additional stretch of 20 amino acids in the C-terminus, compared to the human sequence. Alignment of mouse and human laminin LG5-modules with other published sequences (not shown) revealed similar C-terminal length in all cases except for the mouse α5. Comparison with the mouse laminin α5 showed an overall amino-acid identity of 79%. The previously reported adhesive tripeptide sequence LRE (Hunter, D.D. et al., Cell 59(5), 905-13 (1989)) was not conserved in the human chain (amino acid residues; 3176-3178 LQQ), while the two RGD-sequences were conserved (Fig. 1) . The human sequence contained two extra cysteines (amino acid residues; 3173 and 3663) and a hinge region between LG 3 and LG 4 that is seven residues longer than the mouse sequence. In addition, there was a stretch of four extra amino acids in domain IV (amino acid residues; 1680-1683) in the human sequence. We generated cDNAs from four different sources (placenta, HEK293 cells, and lung-marathon-ready-cDNA from two sources) and thereby detected four possible polymorphisms in domain IIIa; 5698:A-G (1900: Met-Val), 5722: G-A (1908: Ala-Thr), 6158: G-A (2053: Arg-Thr), 6184: A-G (2062: Asn-Asp) and one in the G domain; 9235:T-C (3079: Trp-Arg). The amino acids chosen for the r-laminin-10 construct at these possible polymorphic sites are those shown in Fig. 1.

Production and Characterization of Recombinant laminin-10

Conditioned medium from wild-type HEK293 cells did not react in western blotting with the anti-laminin α5, anti-laminin β1, anti-laminin γ1, or anti-FLAG Abs, indicating that these cells express endogenous laminins at very low amounts if at all (data not shown). After triple transfection, the best cell clone produced 2-3 mg of r-laminin-10 per liter of medium, which is quite high considering the size and complexity of the protein.

Immunoaffinity purification with anti-FLAG M2 matrix followed by competitive elution with FLAG-peptide resulted in highly purified protein as seen in silver stained SDS-PAGE gels (Fig 2a). Under reducing conditions, two bands were seen, a 400 kD band corresponding to the laminin α5 chain and a 200 kD band corresponding to the laminin β1 and γ1 chains, which have similar molecular weights (Fig. 2a). In western blotting of the conditioned medium, two bands of approximately 350 and 400 kD could be seen with the laminin α5 mAb (Fig. 2b). The anti-FLAG antibody reacted with a 400 kD and a 40 kD fragment (Fig 2b and not shown). Taken together, these data indicate that the 400 kD fragment is the intact laminin α5, the 350 kD is a N-terminal fragment and the 40 kD is a C-terminal fragment harboring the FLAG epitope. Under non-reducing conditions, most of the protein appeared at the top of the gel as a very high molecular weight band, which was immunoreactive with α5, FLAG, β1 and γ1 mAbs, showing that the r-laminin-10 was produced as disulfide-crosslinked heterotrimer (Fig. 2c). A minor band of approximately 400 kD was also seen in silver staining and in western blotting with α5, FLAG, β1 and γ1 mAbs. The non-covalently associated α5 chain had an apparent molecular weight similar to the β1/γ1 dimer, which explains the immunoreactivity of the minor band with α5 and FLAG mAbs.

Rotary shadowing EM revealed the r-laminin-10 protein as having three short arms and one long arm in accordance with the expected structure. Some monomers were shown to have an elongated globular domain in one of the short arms, which could be domain IVb. Oligomers dominated the preparation.

Cell Binding to r-laminin-10

Vascular endothelial cells undergo drastic morphological and functional changes during angiogenesis, and it is well established that the behavior of the cell is critically influenced by its interaction with components of the extracellular matrix. Because of this fact, endothelial cell attachment and migration on grafts used in vascular surgery might be improved if the surfaces of these non-biological materials would be pre-coated with ECM proteins, e. g. laminins. The ingrowth of endothelial cells on the surfaces of grafts, a process known as endothelialization, has been shown to be of critical importance for preventing thrombus formation on the graft material, and for reducing neointimal hyperplasia. Many adhesive substrate coatings to enhance

endothelial cell attachment have been tested (Dixit, P., et al. (2001) *J. Biomed. Mater. Res.* 56(4), 545-55), but the long term patency of small-diameter vascular grafts is still disappointing, primarily due to stenosis and thrombus formation (Pevec, W. C., et al. (1992) *J. Vasc. Surg.* 16(1), 60-5; Watelet, J., et al. (1997) *Ann. Vasc. Surg.* 11(5), 510-9).

To investigate the biological activity of r-laminin-10, we assayed it for cell adhesion properties. Cell adhesion onto the laminin coated substratum is mediated predominantly by the integrin family of adhesion receptors. Several integrins have been implicated as receptors for laminin-10 or laminin-10/ 11, including $\alpha 2\beta 1$, $\alpha 3\beta 1$, $\alpha 6\beta 1$, and $\alpha 6\beta 4$ (Kikkawa, Y. et al., J. Biol. Chem. 273(25), 15854-9 (1998); Kikkawa, Y. et al., J. Cell Sci. 113(Pt 5), 869-76 (2000); Ferletta, M. et al., J. Cell Sci. 112 (Pt 1), 1-10 (1999); Gu, Y. et al., Blood 93(8), 2533-42 (1999); Pouliot, N. et al., Exp. Cell Res. 261(2), 360-71 (2000); and Tani, T. et al., Exp. Cell Res. 248(1), 115-21 (1999)). In addition, Nielsen and co-workers recently demonstrated that domain IV of the laminin $\alpha 5$ chain is a binding site for integrin $\alpha 2\beta 1$, $\alpha 3\beta 1$, $\alpha 4\beta 1$, and $\alpha 6\beta 1$ (Nielsen, P.K. et al., J. Biol. Chem. 276(14), 10906-12 (2001)). As a general model, we used the HT-1080 fibrosarcoma cell line, which expresses a wide variety of integrin receptors such as $\alpha 2$, $\alpha 3$, $\alpha 5$, $\alpha 6$ and $\beta 1$ (Wayner, E.A. et al., J. Cell Biol. 121(5), 1141-52 (1993)). Different blocking anti-integrin antibodies were used to identify the integrin receptors mediating cell binding to r-laminin-10. Two endothelial cell types were also studied: HSVECs were used as model for macrovascular endothelial cells and IBE cells for microvascular endothelial cells. HT-1080 cells adhered to fibronectin equally strongly as to r-laminin-10 (Fig. 3a) while laminin-1 and r-laminin-8 were less effective in promoting cell adhesion (Fig. 3a). Similar results were obtained with IBE cells and HSVECs (Fig. 3b and c). Based on these results, further experiments with blocking integrin mAbs were performed using a coating concentration of 10 mg/ml.

Monoclonal Abs against either $\alpha 3$ or $\beta 1$ inhibited HT-1080 cell binding to r-laminin-10 by approximately 80%, indicating that integrin $\alpha 3\beta 1$ was a major mediator of adhesion to r-laminin-10 (Fig. 4). In addition, mAbs against integrin $\alpha 2$ had partial inhibitory effect on adhesion to r-laminin-10 (Fig. 4). Since some adhesion remained after blocking of the integrin $\beta 1$, other receptor classes besides $\beta 1$ could be involved in the cell adhesion. Monoclonal Abs against integrins $\alpha 6$ and αv had no effects on the

adhesion of HT-1080 cells to r-laminin-10 either alone (Fig. 4) or in various combinations ($\alpha3+\alpha6$, $\beta1+\alpha6$, $\beta1+\alpha v\beta3$, $\beta1+\alpha6+\alpha v\beta3$, $\beta1+\alpha6+\alpha v$; not shown). This indicates that $\alpha6$ integrins ($\alpha6\beta1$, $\alpha6\beta4$) or αv integrins ($\alpha v\beta1$, $\alpha v\beta3$ or $\alpha v\beta5$) were not mediating the cell adhesion.

HSVEC binding to the r-laminin-10 was also studied. To determine which integrins were present on the cell surface, we performed fluorescent cell sorting assay using mAbs against integrin subunits $\alpha1$, $\alpha2$, $\alpha3$, $\alpha4$, $\alpha5$, $\alpha6$, αv, $\beta1$, $\beta3$ and $\beta4$. From these results it can be concluded that HSVEC express large amounts of $\alpha2\beta1$, $\alpha5\beta1$ and $\alpha v\beta3$, moderate amounts of $\alpha3\beta1$, and small amounts of $\alpha1\beta1$, $\alpha6\beta1$ and $\alpha6\beta4$, but integrin $\alpha4\beta1$ was not detected. The HSVEC binding was most efficiently inhibited by mAbs against integrin $\alpha3$ and $\beta1$, but also against $\alpha2$ (Fig. 3) had partial effect, in a fashion similar to that observed for HT-1080 cells. Integrin $\alpha6$ was only weakly expressed on HSVECs and, consequently, mAbs against this integrin did not inhibit binding to r-laminin-10.

Cell adhesion to r-laminin-10 was found to be dependent of divalent cations since it could be abolished by 5 mM EDTA in both HT-1080 cells and HSVECs (Fig.3). Heparin, when used at 5 mg/ml, had no effect on the adhesion of either cell type (Fig. 3). Since the $\alpha5$-chain has conserved RGD-sequences, we tested the effect of RGD peptides, which are reported to block the function of various RGD-dependent integrins (such as $\alpha5\beta1$ and the αv family) (Pierschbacher, M.D. et al., Nature 309(5963), 30-3 (1984)). Neither linear nor cyclic RGD-peptides had any effect at 0.25 mg/ml concentration on adhesion of either HT-1080 cells or HSVECs to r-laminin-10 (Fig. 4). It was, furthermore, observed that the cell binding activity of r-laminin-10 was sensitive to air-drying, as we have previously reported for r-laminin-8 (Kortesmaa, J. et al., J. Biol. Chem. 275(20), 14853-9 (2000)). When the coated protein was allowed to air dry for 20 min at room temperature before adding the cells, the cell binding activity of r-laminin-10 was completely lost (data not shown).

Cell Migration

Laminins have been shown to stimulate cell migration during development, and in many pathological processes. We examined the ability to promote HSVEC migration on dishes coated with 10 mg/ml of r-laminin-10 or other adhesive proteins. The migration assay was repeated three times using HSVEC obtained from three

different donors. Among the seven different adhesive proteins examined, r-laminin-10 was the most potent in promoting HSVEC migration *in vitro*. In addition to r-laminin-10, type IV collagen was also quite potent in promoting HSVEC migration. Laminin N-1 and gelatin were of roughly equal potency but significantly lower than r-laminin-10, and r-laminin-8 was the least potent among the proteins examined.

Discussion

Several cell types have been tested for identification of the integrin receptors for laminin-10, but no report exists concerning endothelial cells. In this study, we demonstrated that HSVECs use integrins $\alpha 2\beta 1$ and $\alpha 3\beta 1$ to mediate cell adhesion to r laminin-10, and similar results were obtained for HT-1080 cells. An antibody against the integrin $\alpha 6$ subunit, either alone or combination with other mAbs ($\alpha 3+\alpha 6$, $\beta 1+\alpha 6$, $\beta 1+\alpha 6+\alpha v\beta 3$, $\beta 1+\alpha 6+\alpha v$), did not inhibit cell adhesion (Fig.4 and not shown), indicating that integrin $\alpha 6$ is not an important receptor in these cells for r laminin-10, although the $\alpha 6$ integrins have previously been implicated as receptors for laminins in general and laminin-10 in particular (Kikkawa, Y. et al., J. Cell Sci. 113(Pt 5), 869-76 (2000)).

HSVECs, as well as HT-1080 and IBE cells, attached to r-10 more strongly than to laminin-1 and r laminin-8. Poor adhesion of HSVECs to r laminin-8 is not surprising considering the fluorescent cell sorting data showing that the cells have little $\alpha 6$ integrins, which have previously been shown to be receptors for r-laminin-8 (Kortesmaa, J. et al., J. Biol. Chem. 275(20), 14853-9 (2000)). We can, therefore, conclude that the integrin-binding is distinctly different between the two main forms of endothelial laminins, as well as between different endothelial cell types, as we have previously shown that IBE and bovine capillary endothelial cell adhesion onto r-laminin-8 is mediated predominantly by $\alpha 6$ integrins (Kortesmaa, J. et al., J. Biol. Chem. 275(20), 14853-9 (2000)).

Cell migration-promoting activities of different laminins appear to be dependent on cell specific factors. Human glioblastoma cell line T98G showed best migration on laminin-8 (Fujiwara, H. et al., J. Biol. Chem. 276(20), 17550-8 (2001)) compared to laminin-2/4, laminin-5, laminin-10/11 and fibronectin, while LIM1215 carcinoma cells migrate more efficiently on laminin-10 than on collagen type I, type IV or laminin-1 (Pouliot, N. et al., Exp. Cell Res. 266(1), 1-10 (2001)). Here, we

demonstrated that r-laminin 10 was the most potent matrix of the components tested in promoting endothelial cell (HSVEC) migration *in vitro* (Fig. 5). Interestingly, HSVEC adhesion to commercial laminin-10/11 and to r-laminin-10 was equally strong, but the potency of laminin-10/11 in promoting HSVEC migration was much lower than that of r-laminin-10.

We claim:

1. An isolated nucleic acid consisting of a sequence that encodes a polypeptide with the amino acid sequence of SEQ ID NO:2.

2. The isolated nucleic acid of claim 1 wherein the nucleic acid consists of the sequence of SEQ ID NO:1.

3. A recombinant expression vector comprising the isolated nucleic acid sequence of claim 1 operatively linked to a promoter.

4. A host cell transfected with the recombinant expression vector of claim 3.

5. An isolated laminin α5 polypeptide, consisting of the amino acid sequence of SEQ ID NO:2.

6. Isolated laminin 10.

7. The isolated laminin 10 of claim 6, wherein the isolated laminin 10 is recombinant laminin 10.

8. The isolated recombinant laminin 10 of claim 7 comprising:

a first chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more sequence selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:3;

a second chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, and SEQ ID NO:11; and

a third chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more sequence selected from the group consisting of SEQ ID NO: 13, SEQ ID NO:15, SEQ ID NO:17, and SEQ ID NO:19;

wherein the first, second, and third chains are assembled into recombinant laminin 10.

9. The isolated recombinant laminin 10 of claim 7 comprising:

a first chain comprising a polypeptide at least 70% identical to one or more polypeptide sequences selected from the group consisting of SEQ ID NO:2, and SEQ ID NO:4;

a second chain comprising a polypeptide at least 70% identical to one or more polypeptide sequences selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, and SEQ ID NO:12; and

a third chain comprising a polypeptide at least 70% identical to one or more polypeptide sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, and SEQ ID NO:20;

wherein the first, second, and third chains are assembled into recombinant laminin 10.

10. The isolated recombinant laminin 10 of claim 7 comprising a first, second, and third polypeptide chain, wherein the first, second, and third polypeptide chains each comprise a general structure selected from the group consisting of: (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e)

wherein R1 is an amino terminal methionine; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, or it may be an artificial sequence; R3 is a secreted $\alpha 5$ laminin chain for the first polypeptide chain, a secreted $\beta 1$ laminin chain for the second polypeptide chain, and a secreted $\gamma 1$ laminin chain for the third polypeptide chain; and R3(e) is identical to R3, but further comprises an epitope tag.

11. Recombinant laminin 10-expressing host cells.

12. The recombinant laminin 10-expressing host cells of claim 11, wherein the recombinant laminin 10 comprises:

a first chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more sequence selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:3;

a second chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, and SEQ ID NO:11; and

a third chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more sequence selected from the group consisting of SEQ ID NO: 13, SEQ ID NO:15, SEQ ID NO:17, and SEQ ID NO:19;

wherein the first, second, and third chains are assembled into recombinant laminin 10.

13. The isolated recombinant laminin 10-expressing host cells of claim 11, wherein the recombinant laminin 10 comprises:

a first chain comprising a polypeptide at least 70% identical to one or more polypeptide sequences selected from the group consisting of SEQ ID NO:2, and SEQ ID NO:4;

a second chain comprising a polypeptide at least 70% identical to one or more polypeptide sequences selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, and SEQ ID NO:12; and

a third chain comprising a polypeptide at least 70% identical to one or more polypeptide sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, and SEQ ID NO:20;

wherein the first, second, and third chains are assembled into recombinant laminin 10.

14. The host cells of claim 11, wherein the host cell is a mammalian cell.

15. The host cells of claim 13, wherein at least one of the first, second, or third chains is expressed as a fusion protein with an epitope tag.

16. A method of isolating recombinant laminin 10, comprising:

a. providing the host cells of claim 13;

b. growing the cells in cell culture medium under conditions to stimulate expression of the recombinant laminin 10 chains;

c. passing the cell culture medium through an affinity chromatography column, wherein the column contains a compound that binds to the recombinant laminin 10;

d. washing the affinity column to remove unbound materials; and

e. eluting the bound recombinant laminin 10 from the column.

17. Isolated recombinant laminin 10 isolated according to the method of claim 16.

18. A method to improve the biocompatibility of a medical device or graft, comprising contacting the medical device or graft with an amount effective of isolated laminin 10 to improve the biocompatibility of the medical device or graft.

19. An improved medical device or graft, wherein the improvement consists of providing a medical device or graft with an amount effective of isolated laminin 10 to improve the biocompatibility of the medical device or graft.

20. A method to promote cell adhesion and/or cell migration to a surface, comprising contacting cells with an amount effective of isolated laminin 10 to promote cell adhesion and/or cell migration to the surface.

21. An improved cell growth substrate, wherein the improvement consists of providing a cell growth substrate that has been coated with an amount effective of laminin 10 to promote cell attachment to the cell growth substrate.

22. A method to accelerate healing of a vascular tissue injury in a subject, comprising contacting the site of the vascular tissue injury of the subject with an amount effective of laminin 10 to promote re-endothelialization at the vascular tissue injury site.

23. A pharmaceutical composition comprising:

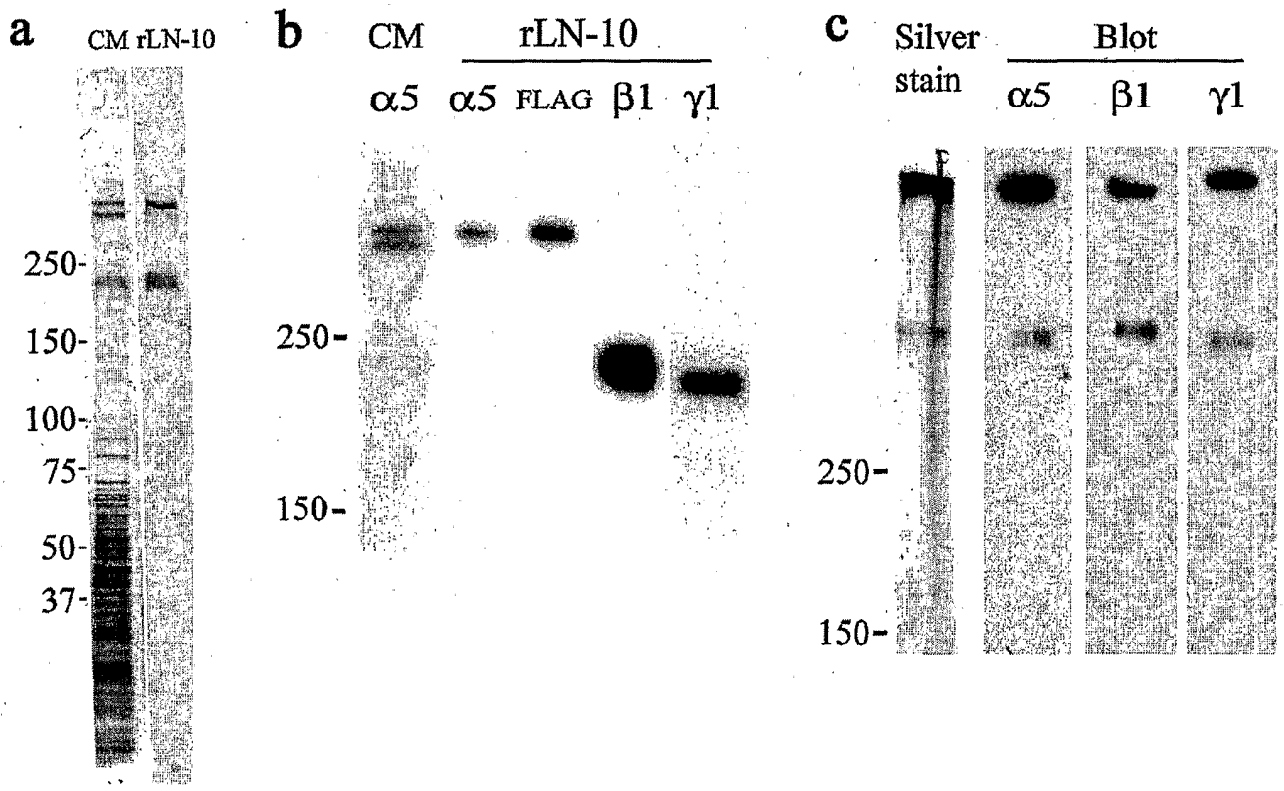
a) the isolated laminin 10 of claim 6; and

b) a pharmaceutically acceptable carrier.

Fig. 1


domain VI
domain V
domain IVb
domain IIIb
domain IVa
domain IIIa
domain I/II
domain G

Fig. 2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150-
100-
75-
50-
37-
b
CM
rLN-10
α5
α5
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c
Silver stain
Blot
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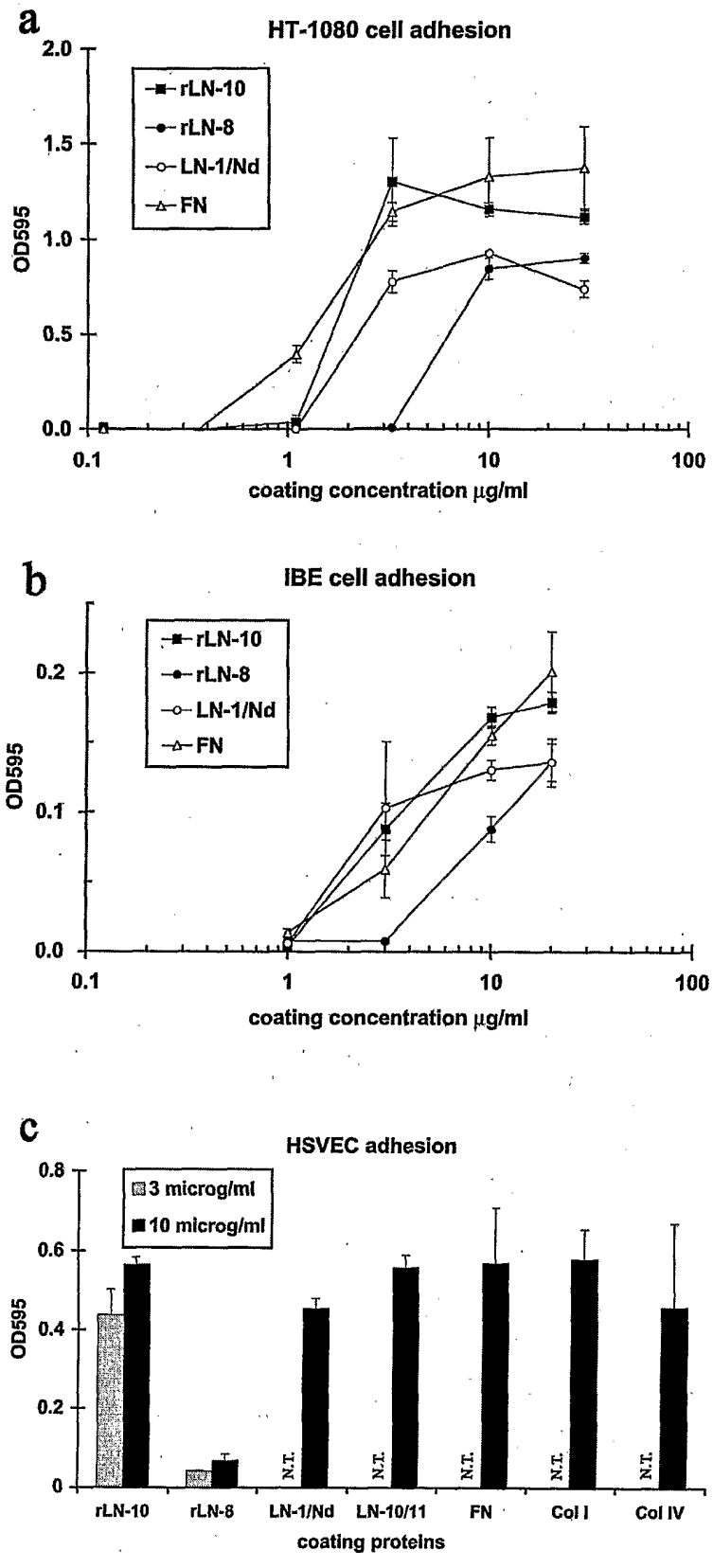
β1
γ1
250-
150-

Fig. 4 3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1.0
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0.1
1
10
100
coating concentration µg/ml
b
IBE cell adhesion
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rLN-8
LN-1/Nd
FN
OD595
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0.1
0.0
0.1
1
10
100
coating concentration µg/ml
c
HSVEC adhesion
3 microg/ml
10 microg/ml
OD595
0.8
0.6
0.4
0.2
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N.T.
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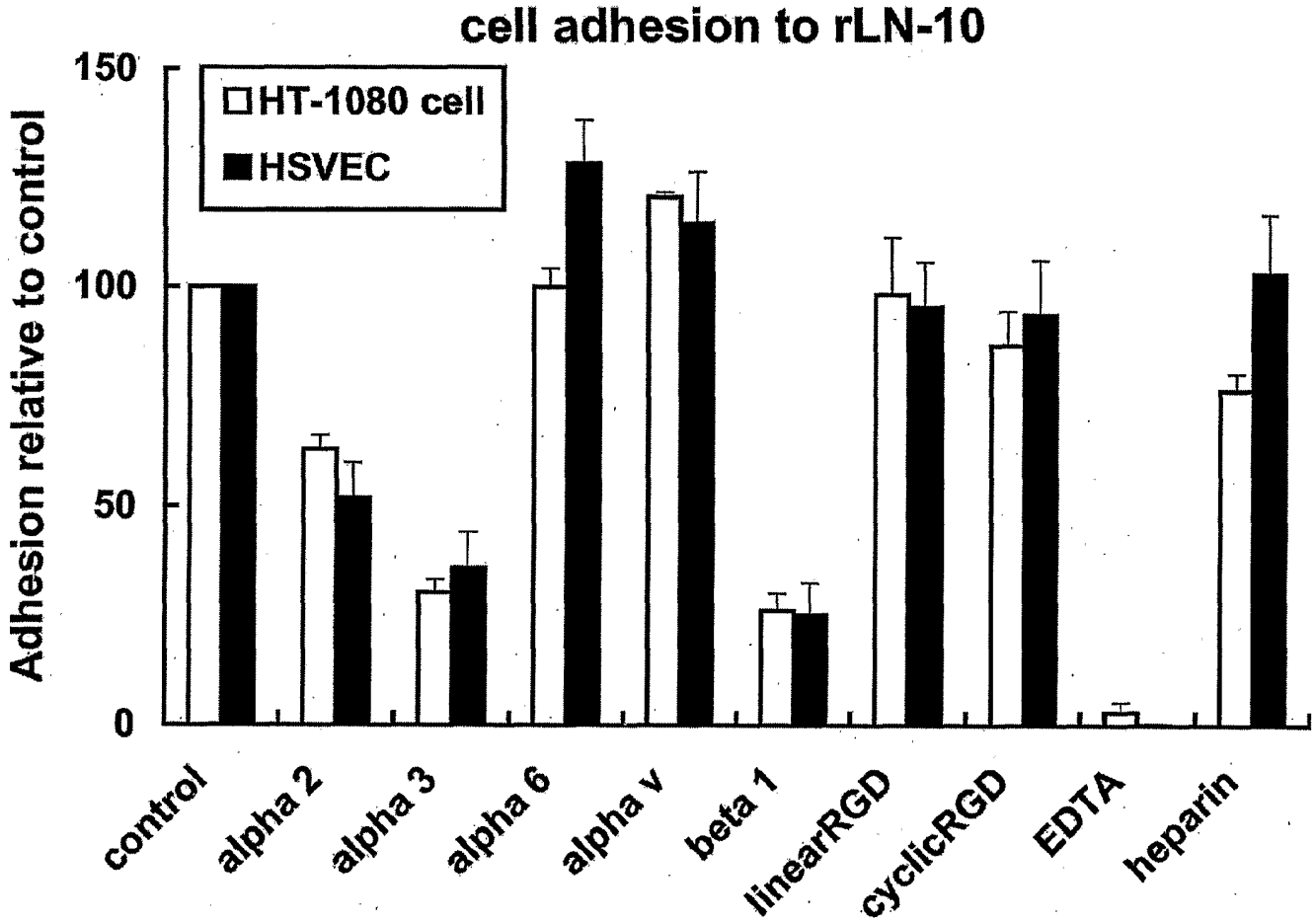
rLN-8
LN-1/Nd
LN-10/11
FN
Col I
Col IV
coating proteins

Fig. 6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HT-1080 cell
HSVEC
Adhesion relative to control
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0
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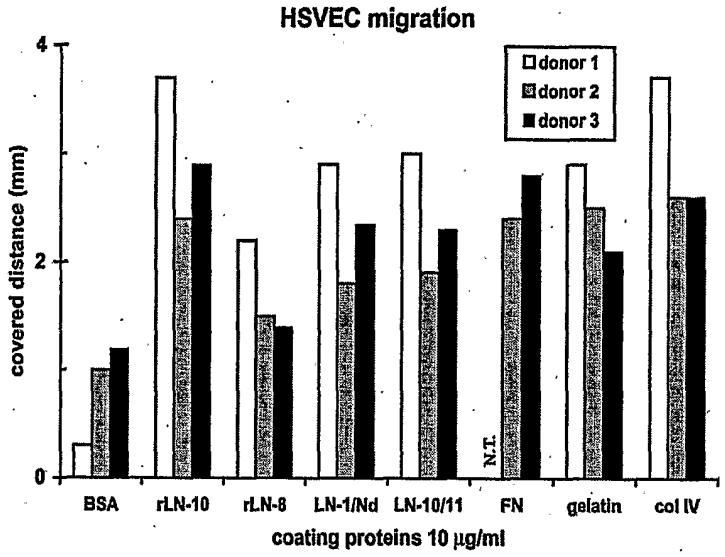
alpha 3
alpha 6
alpha v
beta 1
linearRGD
cyclicRGD
EDTA
heparin

5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donor 1
donor 2
donor 3
covered distance (mm)
4
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LN-1/Nd
LN-10/11
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SEQUENCE LISTING

<110> Tryggvason, Karl
Doi, Masayuki
Thyboll, Jill

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Met Ala Lys Arg Leu Cys Ala Gly Ser Ala Leu Cys Val Arg
1 5 10

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Gly Pro Arg Gly Pro Ala Pro Leu Leu Leu Val Gly Leu Ala Leu Leu
15 20 25 30

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Gly Ala Ala Arg Ala Arg Glu Glu Ala Gly Gly Gly Phe Ser Leu His
35 40 45

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Pro Pro Tyr Phe Asn Leu Ala Glu Gly Ala Arg Ile Ala Ala Ser Ala
50 55 60

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Thr Cys Gly Glu Glu Ala Pro Ala Arg Gly Ser Pro Arg Pro Thr Glu
65 70 75

gac ctt tac tgc aag ctg gta ggg ggc ccc gtg gcc ggc ggc gac ccc 349
Asp Leu Tyr Cys Lys Leu Val Gly Gly Pro Val Ala Gly Gly Asp Pro

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 95                 100                 105                 110

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Ser Asn Lys Ala His Pro Ala Ser Asn Ala Ile Asp Gly Thr Glu Arg
                115                 120                 125

tgg tgg cag agt cca ccg ctg tcc cgc ggc ctg gag tac aac gag gtc   493
Trp Trp Gln Ser Pro Pro Leu Ser Arg Gly Leu Glu Tyr Asn Glu Val
            130                 135                 140

aac gtc acc ctg gac ctg ggc cag gtc ttc cac gtg gcc tac gtc ctc   541
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atc aag ttt gcc aac tca ccc cgg ccg gac ctc tgg gtg ctg gag cgg   589
Ile Lys Phe Ala Asn Ser Pro Arg Pro Asp Leu Trp Val Leu Glu Arg
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tcc atg gac ttc ggc cgc acc tac cag ccc tgg cag ttc ttt gcc tcc   637
Ser Met Asp Phe Gly Arg Thr Tyr Gln Pro Trp Gln Phe Phe Ala Ser
175                 180                 185                 190

tct aag agg gac tgt ctg gag cgg ttc ggg cca cag acg ctg gag cgc   685
Ser Lys Arg Asp Cys Leu Glu Arg Phe Gly Pro Gln Thr Leu Glu Arg
                195                 200                 205

atc aca cgg gac gac gca gcc atc tgc acc acc gag tac tca cgc atc   733
Ile Thr Arg Asp Asp Ala Ala Ile Cys Thr Thr Glu Tyr Ser Arg Ile
            210                 215                 220

gtg ccc ctg gag aac gga gag atc gtg gtg tcc ctg gtg aac gga cgt   781
Val Pro Leu Glu Asn Gly Glu Ile Val Val Ser Leu Val Asn Gly Arg
        225                 230                 235

ccg ggc gcc atg aat ttc tcc tac tcg ccg ctg cta cgt gag ttc acc   829
Pro Gly Ala Met Asn Phe Ser Tyr Ser Pro Leu Leu Arg Glu Phe Thr
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aag gcc acc aac gtc cgc ctg cgc ttc ctg cgt acc aac acg ctg ctg   877
Lys Ala Thr Asn Val Arg Leu Arg Phe Leu Arg Thr Asn Thr Leu Leu
255                 260                 265                 270

ggc cat ctc atg ggg aag gcg ctg cgg gac ccc acg gtc acc cgc cgg   925
Gly His Leu Met Gly Lys Ala Leu Arg Asp Pro Thr Val Thr Arg Arg
                275                 280                 285

tat tat tac agc atc aag gat atc agc atc gga ggc cgc tgt gtc tgc   973
Tyr Tyr Tyr Ser Ile Lys Asp Ile Ser Ile Gly Gly Arg Cys Val Cys
            290                 295                 300

cac ggc cac gcg gat gcc tgc gat gcc aaa gac ccc acg gac ccg ttc   1021
His Gly His Ala Asp Ala Cys Asp Ala Lys Asp Pro Thr Asp Pro Phe
        305                 310                 315

agg ctg cag tgc acc tgc cag cac aac acc tgc ggg ggc acc tgc gac   1069
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Asn Ser Ala Asn Glu Cys Gln Ser Cys Asn Cys Tyr Gly His Ala Thr
                355                 360                 365

gac tgt tac tac gac cct gag gtg gac cgg cgc cgc gcc agc cag agc   1213
Asp Cys Tyr Tyr Asp Pro Glu Val Asp Arg Arg Arg Ala Ser Gln Ser
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Leu Asp Gly Thr Tyr Gln Gly Gly Gly Val Cys Ile Asp Cys Gln His
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cac acc gcc ggc gtc aac tgt gag cgc tgc ctg ccc ggc ttc tac cgc   1309
His Thr Ala Gly Val Asn Cys Glu Arg Cys Leu Pro Gly Phe Tyr Arg
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tct ccc aac cac cct ctc gac tcg ccc cac gtc tgc cgc cgc tgc aac   1357
Ser Pro Asn His Pro Leu Asp Ser Pro His Val Cys Arg Arg Cys Asn
415                 420                 425                 430

tgc gag tcc gac ttc acg gat ggc acc tgc gag gac ctg acg ggt cga   1405
Cys Glu Ser Asp Phe Thr Asp Gly Thr Cys Glu Asp Leu Thr Gly Arg
                435                 440                 445

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Cys Tyr Cys Arg Pro Asn Phe Ser Gly Glu Arg Cys Asp Val Cys Ala
            450                 455                 460

gag ggc ttc acg ggc ttc cca agc tgc tac ccg acg ccc tcg tcc tcc   1501
Glu Gly Phe Thr Gly Phe Pro Ser Cys Tyr Pro Thr Pro Ser Ser Ser
        465                 470                 475

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    480                 485                 490

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495                 500                 505                 510

agg gtg gga cgc tgt ctg tgc aaa ccc aac ttc caa ggc acc cat tgt   1645
Arg Val Gly Arg Cys Leu Cys Lys Pro Asn Phe Gln Gly Thr His Cys
                515                 520                 525

gag ctc tgc gcg cca ggg ttc tac ggc ccc ggc tgc cag ccc tgc cag   1693
Glu Leu Cys Ala Pro Gly Phe Tyr Gly Pro Gly Cys Gln Pro Cys Gln
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Cys Ser Ser Pro Gly Val Ala Asp Asp Arg Cys Asp Pro Asp Thr Gly
        545                 550                 555

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cct gca gga acc ttg ccc gag ggc tgc gat gag gcc ggc cgc tgc cta   1885
Pro Ala Gly Thr Leu Pro Glu Gly Cys Asp Glu Ala Gly Arg Cys Leu
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tgc cag cct gag ttt gct gga cct cat tgt gac cgg tgc cgc cct ggc   1933
Cys Gln Pro Glu Phe Ala Gly Pro His Cys Asp Arg Cys Arg Pro Gly
            610                 615                 620

tac cat ggt ttc ccc aac tgc caa gca tgc acc tgc gac cct cgg gga   1981
Tyr His Gly Phe Pro Asn Cys Gln Ala Cys Thr Cys Asp Pro Arg Gly
        625                 630                 635

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Ala Leu Asp Gln Leu Cys Gly Ala Gly Gly Leu Cys Arg Cys Arg Pro
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Phe Pro Ser Cys Val Pro Cys His Cys Ser Ala Glu Gly Ser Leu His
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Ala Ala Cys Asp Pro Arg Ser Gly Gln Cys Ser Cys Arg Pro Arg Val
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Thr Gly Leu Arg Cys Asp Thr Cys Val Pro Gly Ala Tyr Asn Phe Pro
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Tyr Cys Glu Ala Gly Ser Cys His Pro Ala Gly Leu Ala Pro Val Asp
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cct gcc ctt cct gag gca cag gtt ccc tgt atg tgc cgg gct cac gtg   2317
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735                 740                 745                 750

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Thr Leu Gly Gly Val Ala Glu Cys Gln Pro Gly Thr Gly Gln Cys Phe
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Val Cys Arg Cys Arg Pro Asn Thr Gln Gly Pro Thr Cys Ser Glu Pro
            850                 855                 860

gcg agg gac cac tac ctc ccg gac ctg cac cac ctg cgc ctg gag ctg   2701
Ala Arg Asp His Tyr Leu Pro Asp Leu His His Leu Arg Leu Glu Leu
        865                 870                 875

gag gag gct gcc aca cct gag ggt cac gcc gtg cgc ttt ggc ttc aac   2749
Glu Glu Ala Ala Thr Pro Glu Gly His Ala Val Arg Phe Gly Phe Asn
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ccc ctc gag ttc gag aac ttc agc tgg agg ggc tac gcg cag atg gca   2797
Pro Leu Glu Phe Glu Asn Phe Ser Trp Arg Gly Tyr Ala Gln Met Ala
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cct gtc cag ccc agg atc gtg gcc agg ctg aac ctg acc tcc ccc gac   2845
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cct gcc ttc atc acc gtg ccc cag agg ggc ttc gga gag ccc ttt gtg   3037
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975                 980                 985                 990

ctg aac cct ggc acc tgg gcc ctg cgt gtg gag gcc gaa ggg gtg ctc   3085
Leu Asn Pro Gly Thr Trp Ala Leu Arg Val Glu Ala Glu Gly Val Leu
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ctg gac tac gtg gtt ctg ctg cct agc gca tac tac gag gcg gcg ctc   3133
Leu Asp Tyr Val Val Leu Leu Pro Ser Ala Tyr Tyr Glu Ala Ala Leu
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Leu Gln Leu Arg Val Thr Glu Ala Cys Thr Tyr Arg Pro Ser Ala Gln
       1025                1030                1035

cag tct ggc gac aac tgc ctc ctc tac aca cac ctc ccc ctg gat ggc   3229
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Pro Leu Thr His Ala Gln Asp Leu Thr Pro Ala Thr Ser Pro Ala Gly
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        1265                1270                1275

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Leu Leu Arg Glu Pro Gln Ala Thr Val Val Phe Thr Thr His Val Pro
    1280                1285                1290

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Thr Leu Gly Arg Tyr Ala Phe Leu Leu His Gly Tyr Gln Pro Ala His
1295                1300                1305                1310
```

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ccc acc ttc ccc gtg gaa gtc ctc atc aac gcc ggc cgc gtg tgg cag   4045
Pro Thr Phe Pro Val Glu Val Leu Ile Asn Ala Gly Arg Val Trp Gln
               1315                1320                1325

ggc cac gcc aac gcc agc ttc tgt cca cat ggc tac ggc tgc cgc acc   4093
Gly His Ala Asn Ala Ser Phe Cys Pro His Gly Tyr Gly Cys Arg Thr
           1330                1335                1340

ctg gtg gtg tgt gag ggc cag gcc ctg ctg gac gtg acc cac agc gag   4141
Leu Val Val Cys Glu Gly Gln Ala Leu Leu Asp Val Thr His Ser Glu
       1345                1350                1355

ctc act gtg acc gtg cgt gtg ccc gag ggc cgg tgg ctc tgg ctg gat   4189
Leu Thr Val Thr Val Arg Val Pro Glu Gly Arg Trp Leu Trp Leu Asp
   1360                1365                1370

tat gta ctc gtg gtc cct gag aac gtc tac agc ttt ggc tac ctc cgg   4237
Tyr Val Leu Val Val Pro Glu Asn Val Tyr Ser Phe Gly Tyr Leu Arg
1375                1380                1385                1390

gag gag ccc ctg gat aaa tcc tat gac ttc atc agc cac tgc gca gcc   4285
Glu Glu Pro Leu Asp Lys Ser Tyr Asp Phe Ile Ser His Cys Ala Ala
               1395                1400                1405

cag ggc tac cac atc agc ccc agc agc tca tcc ctg ttc tgc cga aac   4333
Gln Gly Tyr His Ile Ser Pro Ser Ser Ser Ser Leu Phe Cys Arg Asn
           1410                1415                1420

gct gct gct tcc ctc tcc ctc ttc tat aac aac gga gcc cgt cca tgt   4381
Ala Ala Ala Ser Leu Ser Leu Phe Tyr Asn Asn Gly Ala Arg Pro Cys
       1425                1430                1435

ggc tgc cac gaa gta ggt gct aca ggc ccc acg tgt gag ccc ttc ggg   4429
Gly Cys His Glu Val Gly Ala Thr Gly Pro Thr Cys Glu Pro Phe Gly
   1440                1445                1450

ggc cag tgt ccc tgc cat gcc cat gtc att ggc cgt gac tgc tcc cgc   4477
Gly Gln Cys Pro Cys His Ala His Val Ile Gly Arg Asp Cys Ser Arg
1455                1460                1465                1470

tgt gcc acc gga tac tgg ggc ttc ccc aac tgc agg ccc tgt gac tgc   4525
Cys Ala Thr Gly Tyr Trp Gly Phe Pro Asn Cys Arg Pro Cys Asp Cys
               1475                1480                1485

ggt gcc cgc ctc tgt gac gag ctc acg ggc cag tgc atc tgc ccg cca   4573
Gly Ala Arg Leu Cys Asp Glu Leu Thr Gly Gln Cys Ile Cys Pro Pro
           1490                1495                1500

cgc acc atc ccg ccc gac tgc ctg ctg tgc cag ccc cag acc ttt ggc   4621
Arg Thr Ile Pro Pro Asp Cys Leu Leu Cys Gln Pro Gln Thr Phe Gly
       1505                1510                1515

tgc cac ccc ctg gtc ggc tgt gag gag tgt aac tgc tca ggg ccc ggc   4669
Cys His Pro Leu Val Gly Cys Glu Glu Cys Asn Cys Ser Gly Pro Gly
   1520                1525                1530

atc cag gag ctc aca gac cct acc tgt gac aca gac agc ggc cag tgc   4717
Ile Gln Glu Leu Thr Asp Pro Thr Cys Asp Thr Asp Ser Gly Gln Cys
1535                1540                1545                1550
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aag tgc aga ccc aac gtg act ggg cgc cgc tgt gat acc tgc tct ccg   4765
Lys Cys Arg Pro Asn Val Thr Gly Arg Arg Cys Asp Thr Cys Ser Pro
               1555                1560                1565

ggc ttc cat ggc tac ccc cgc tgc cgc ccc tgt gac tgt cac gag gcg   4813
Gly Phe His Gly Tyr Pro Arg Cys Arg Pro Cys Asp Cys His Glu Ala
           1570                1575                1580

ggc act gcg cct ggc gtg tgt gac ccc ctc aca ggg cag tgc tac tgt   4861
Gly Thr Ala Pro Gly Val Cys Asp Pro Leu Thr Gly Gln Cys Tyr Cys
       1585                1590                1595

aag gag aac gtg cag ggc ccc aaa tgt gac cag tgc agc ctt ggg acc   4909
Lys Glu Asn Val Gln Gly Pro Lys Cys Asp Gln Cys Ser Leu Gly Thr
   1600                1605                1610

ttc tca ctg gat gct gcc aac ccc aaa ggt tgc acc cgc tgc ttc tgc   4957
Phe Ser Leu Asp Ala Ala Asn Pro Lys Gly Cys Thr Arg Cys Phe Cys
1615                1620                1625                1630

ttt ggg gcc acg gag cgc tgc cgg agc tcg tcc tac acc cgc cag gag   5005
Phe Gly Ala Thr Glu Arg Cys Arg Ser Ser Ser Tyr Thr Arg Gln Glu
               1635                1640                1645

ttc gtg gat atg gag gga tgg gtg ctg ctg agc act gac cgg cag gtg   5053
Phe Val Asp Met Glu Gly Trp Val Leu Leu Ser Thr Asp Arg Gln Val
           1650                1655                1660

gtg ccc cac gag cgg cag cca ggg acg gag atg ctc cgt gca gac ctg   5101
Val Pro His Glu Arg Gln Pro Gly Thr Glu Met Leu Arg Ala Asp Leu
       1665                1670                1675

cgg cac gtg cct gag gct gtg ccc gag gct ttc ccc gag ctg tac tgg   5149
Arg His Val Pro Glu Ala Val Pro Glu Ala Phe Pro Glu Leu Tyr Trp
   1680                1685                1690

cag gcc cca ccc tcc tac ctg ggg gac cgg gtg tca tcc tac ggt ggg   5197
Gln Ala Pro Pro Ser Tyr Leu Gly Asp Arg Val Ser Ser Tyr Gly Gly
1695                1700                1705                1710

acc ctc cgt tat gaa ctg cac tca gag acc cag cgg gga gat gtc ttt   5245
Thr Leu Arg Tyr Glu Leu His Ser Glu Thr Gln Arg Gly Asp Val Phe
               1715                1720                1725

gtc ccc atg gag agc agg ccg gat gtg gtg ctg cag ggc aac cag atg   5293
Val Pro Met Glu Ser Arg Pro Asp Val Val Leu Gln Gly Asn Gln Met
           1730                1735                1740

agc atc aca ttc ctg gag ccg gca tac ccc acg cct ggc cac gtt cac   5341
Ser Ile Thr Phe Leu Glu Pro Ala Tyr Pro Thr Pro Gly His Val His
       1745                1750                1755

cgt ggg cag ctg cag ctg gtg gag ggg aac ttc cgg cat acg gag act   5389
Arg Gly Gln Leu Gln Leu Val Glu Gly Asn Phe Arg His Thr Glu Thr
   1760                1765                1770

cgc aac act gtg tcc cgc gag gag ctc atg atg gtg ctg gcc agc ctg   5437
Arg Asn Thr Val Ser Arg Glu Glu Leu Met Met Val Leu Ala Ser Leu
1775                1780                1785                1790

gag cag ctg cag atc cgt gcc ctc ttc tca cag atc tcc tcg gct gtc   5485
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Glu Gln Leu Gln Ile Arg Ala Leu Phe Ser Gln Ile Ser Ser Ala Val
               1795                1800                1805

tcc ctg cgc agg gtg gca ctg gag gtg gcc agc cca gca ggc cag ggg   5533
Ser Leu Arg Arg Val Ala Leu Glu Val Ala Ser Pro Ala Gly Gln Gly
           1810                1815                1820

gcc ctg gcc agc aat gtg gag ctg tgc ctg tgc ccc gcc agc tac cgg   5581
Ala Leu Ala Ser Asn Val Glu Leu Cys Leu Cys Pro Ala Ser Tyr Arg
       1825                1830                1835

ggg gac tca tgc cag gaa tgt gcc ccc ggc ttc tat cgg gac gtc aaa   5629
Gly Asp Ser Cys Gln Glu Cys Ala Pro Gly Phe Tyr Arg Asp Val Lys
   1840                1845                1850

ggt ctc ttc ctg ggc cga tgt gtc cct tgt cag tgc cat gga cac tca   5677
Gly Leu Phe Leu Gly Arg Cys Val Pro Cys Gln Cys His Gly His Ser
1855                1860                1865                1870

gac cgc tgc ctc cct ggc tct ggc gtc tgt gtg gac tgc cag cac aac   5725
Asp Arg Cys Leu Pro Gly Ser Gly Val Cys Val Asp Cys Gln His Asn
               1875                1880                1885

acc gaa ggg gcc cac tgt gag cgc tgc cag gct ggc ttc atg agc agc   5773
Thr Glu Gly Ala His Cys Glu Arg Cys Gln Ala Gly Phe Met Ser Ser
           1890                1895                1900

agg gac gac ccc agc gcc ccc tgt gtc agc tgc ccc tgc ccc ctc tca   5821
Arg Asp Asp Pro Ser Ala Pro Cys Val Ser Cys Pro Cys Pro Leu Ser
       1905                1910                1915

gtg cct tcc aac aac ttc gcc gag ggc tgt gtc ctg cga ggc ggc cgc   5869
Val Pro Ser Asn Asn Phe Ala Glu Gly Cys Val Leu Arg Gly Gly Arg
   1920                1925                1930

acc cag tgc ctc tgc aaa cct ggt tat gca ggt gcc tcc tgc gag cgg   5917
Thr Gln Cys Leu Cys Lys Pro Gly Tyr Ala Gly Ala Ser Cys Glu Arg
1935                1940                1945                1950

tgt gcg ccc gga ttc ttt ggg aac cca ctg gtg ctg ggc agc tcc tgc   5965
Cys Ala Pro Gly Phe Phe Gly Asn Pro Leu Val Leu Gly Ser Ser Cys
               1955                1960                1965

cag cca tgc gac tgc agc ggc aac ggt gac ccc aac ttg ctc ttc agc   6013
Gln Pro Cys Asp Cys Ser Gly Asn Gly Asp Pro Asn Leu Leu Phe Ser
           1970                1975                1980

gac tgc gac ccc ctg acg ggc gcc tgc cgt ggc tgc ctg cgc cac acc   6061
Asp Cys Asp Pro Leu Thr Gly Ala Cys Arg Gly Cys Leu Arg His Thr
       1985                1990                1995

act ggg ccc cgc tgc gag atc tgt gcc ccc ggc ttc tac ggc aac gcc   6109
Thr Gly Pro Arg Cys Glu Ile Cys Ala Pro Gly Phe Tyr Gly Asn Ala
   2000                2005                2010

ctg ctg ccc ggc aac tgc acc cgg tgc gac tgt acc cca tgt ggg aca   6157
Leu Leu Pro Gly Asn Cys Thr Arg Cys Asp Cys Thr Pro Cys Gly Thr
2015                2020                2025                2030

gag gcc tgc gac ccc cac agc ggg cac tgc ctg tgc aag gcg ggc gtg   6205
Glu Ala Cys Asp Pro His Ser Gly His Cys Leu Cys Lys Ala Gly Val
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                2035                2040                2045

act ggg cgg cgc tgt gac cgc tgc cag gag gga cat ttt ggt ttc aat   6253
Thr Gly Arg Arg Cys Asp Arg Cys Gln Glu Gly His Phe Gly Phe Asn
            2050                2055                2060

ggc tgc ggg ggc tgc cgc ccg tgt gct tgt gga ccg gcc gcc gag ggc   6301
Gly Cys Gly Gly Cys Arg Pro Cys Ala Cys Gly Pro Ala Ala Glu Gly
        2065                2070                2075

tcc gag tgc cac ccc cag agc gga cag tgc cac tgc cga cca ggg acc   6349
Ser Glu Cys His Pro Gln Ser Gly Gln Cys His Cys Arg Pro Gly Thr
    2080                2085                2090

atg gga ccc cag tgc cgc gag tgt gcc cct ggc tac tgg ggg ctc cct   6397
Met Gly Pro Gln Cys Arg Glu Cys Ala Pro Gly Tyr Trp Gly Leu Pro
2095                2100                2105                2110

gag cag ggc tgc agg cgc tgc cag tgc cct ggg ggc cgc tgt gac cct   6445
Glu Gln Gly Cys Arg Arg Cys Gln Cys Pro Gly Gly Arg Cys Asp Pro
                2115                2120                2125

cac acg ggc cgc tgc aac tgc ccc ccg ggg ctc agc ggg gag cgc tgc   6493
His Thr Gly Arg Cys Asn Cys Pro Pro Gly Leu Ser Gly Glu Arg Cys
            2130                2135                2140

gac acc tgc agc cag cag cat cag gtg cct gtt cca ggc ggg cct gtg   6541
Asp Thr Cys Ser Gln Gln His Gln Val Pro Val Pro Gly Gly Pro Val
        2145                2150                2155

ggc cac agc atc cac tgt gaa gtg tgt gac cac tgt gtg gtc ctg ctc   6589
Gly His Ser Ile His Cys Glu Val Cys Asp His Cys Val Val Leu Leu
    2160                2165                2170

ctg gat gac ctg gaa cgg gcc ggc gcc ctc ctc ccc gcc att cac gag   6637
Leu Asp Asp Leu Glu Arg Ala Gly Ala Leu Leu Pro Ala Ile His Glu
2175                2180                2185                2190

caa ctg cgt ggc atc aat gcc agc tcc atg gcc tgg gcc cgt ctg cac   6685
Gln Leu Arg Gly Ile Asn Ala Ser Ser Met Ala Trp Ala Arg Leu His
                2195                2200                2205

agg ctg aac gcc tcc atc gct gac ctg cag agc cag ctc cgg agc ccc   6733
Arg Leu Asn Ala Ser Ile Ala Asp Leu Gln Ser Gln Leu Arg Ser Pro
            2210                2215                2220

ctg ggc ccc cgc cat gag acg gca cag cag ctg gag gtg ctg gag cag   6781
Leu Gly Pro Arg His Glu Thr Ala Gln Gln Leu Glu Val Leu Glu Gln
        2225                2230                2235

cag agc aca agc ctc ggg cag gac gca cgg cgg cta ggc ggc cag gcc   6829
Gln Ser Thr Ser Leu Gly Gln Asp Ala Arg Arg Leu Gly Gly Gln Ala
    2240                2245                2250

gtg ggg acc cga gac cag gcg agc caa ttg ctg gcc ggc acc gag gcc   6877
Val Gly Thr Arg Asp Gln Ala Ser Gln Leu Leu Ala Gly Thr Glu Ala
2255                2260                2265                2270

aca ctg ggc cat gcg aag acg ctg ttg gcg gcc atc cgg gct gtg gac   6925
Thr Leu Gly His Ala Lys Thr Leu Leu Ala Ala Ile Arg Ala Val Asp
                2275                2280                2285
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cgc acc ctg agc gag ctc atg tcc cag acg ggc cac ctg ggg ctg gcc   6973
Arg Thr Leu Ser Glu Leu Met Ser Gln Thr Gly His Leu Gly Leu Ala
          2290                2295                2300

aat gcc tcg gct cca tca ggt gag cag ctg ctc cgg aca ctg gcc gag   7021
Asn Ala Ser Ala Pro Ser Gly Glu Gln Leu Leu Arg Thr Leu Ala Glu
       2305                2310                2315

gtg gag cgg ctg ctc tgg gag atg cgg gcc cgg gac ctg ggg gcc ccg   7069
Val Glu Arg Leu Leu Trp Glu Met Arg Ala Arg Asp Leu Gly Ala Pro
   2320                2325                2330

cag gca gca gct gag gct gag ttg gct gca gca cag aga ttg ctg gcc   7117
Gln Ala Ala Ala Glu Ala Glu Leu Ala Ala Ala Gln Arg Leu Leu Ala
2335                2340                2345                2350

cgg gtg cag gag cag ctg agc agc ctc tgg gag gag aac cag gca ctg   7165
Arg Val Gln Glu Gln Leu Ser Ser Leu Trp Glu Glu Asn Gln Ala Leu
               2355                2360                2365

gcc aca caa acc cgc gac cgg ctg gcc cag cac gag gcc ggc ctc atg   7213
Ala Thr Gln Thr Arg Asp Arg Leu Ala Gln His Glu Ala Gly Leu Met
          2370                2375                2380

gac ctg cga gag gct ttg aac cgg gca gtg gac gcc aca cgg gag gcc   7261
Asp Leu Arg Glu Ala Leu Asn Arg Ala Val Asp Ala Thr Arg Glu Ala
       2385                2390                2395

cag gag ctc aac agc cgc aac cag gag cgc ctg gag gaa gcc ctg caa   7309
Gln Glu Leu Asn Ser Arg Asn Gln Glu Arg Leu Glu Glu Ala Leu Gln
   2400                2405                2410

agg aag cag gag ctg tcc cgg gac aat gcc acc ctg cag gcc act ctg   7357
Arg Lys Gln Glu Leu Ser Arg Asp Asn Ala Thr Leu Gln Ala Thr Leu
2415                2420                2425                2430

cat gcg gct agg gac acc ctg gcc agc gtc ttc aga ttg ctg cac agc   7405
His Ala Ala Arg Asp Thr Leu Ala Ser Val Phe Arg Leu Leu His Ser
               2435                2440                2445

ctg gac cag gct aag gag gag ctg gag cgc ctc gcc gcc agc ctg gac   7453
Leu Asp Gln Ala Lys Glu Glu Leu Glu Arg Leu Ala Ala Ser Leu Asp
          2450                2455                2460

ggg gct cgg acc cca ctg ctg cag agg atg cag acc ttc tcc ccg gcg   7501
Gly Ala Arg Thr Pro Leu Leu Gln Arg Met Gln Thr Phe Ser Pro Ala
       2465                2470                2475

ggc agc aag ctg cgt cta gtg gag gcc gcc gag gcc cac gca cag cag   7549
Gly Ser Lys Leu Arg Leu Val Glu Ala Ala Glu Ala His Ala Gln Gln
   2480                2485                2490

ctg ggc cag ctg gca ctc aat ctg tcc agc atc atc ctg gac gtc aac   7597
Leu Gly Gln Leu Ala Leu Asn Leu Ser Ser Ile Ile Leu Asp Val Asn
2495                2500                2505                2510

cag gac cgc ctc acc cag agg gcc atc gag gcc tcc aac gcc tac agc   7645
Gln Asp Arg Leu Thr Gln Arg Ala Ile Glu Ala Ser Asn Ala Tyr Ser
               2515                2520                2525
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cgc atc ctg cag gcc gtg cag gct gcc gag gat gct gct ggc cag gcc   7693
Arg Ile Leu Gln Ala Val Gln Ala Ala Glu Asp Ala Ala Gly Gln Ala
          2530                2535                2540

ctg cag cag gcg gac cac acg tgg gcg acg gtg gtg cgg cag ggc ctg   7741
Leu Gln Gln Ala Asp His Thr Trp Ala Thr Val Val Arg Gln Gly Leu
       2545                2550                2555

gtg gac cga gcc cag cag ctc ctg gcc aac agc act gca cta gaa gag   7789
Val Asp Arg Ala Gln Gln Leu Leu Ala Asn Ser Thr Ala Leu Glu Glu
   2560                2565                2570

gcc atg ctc cag gaa cag cag agg ctg ggc ctt gtg tgg gct gcc ctc   7837
Ala Met Leu Gln Glu Gln Gln Arg Leu Gly Leu Val Trp Ala Ala Leu
2575                2580                2585                2590

cag ggt gcc agg acc cag ctc cga gat gtc cgg gcc aag aag gac cag   7885
Gln Gly Ala Arg Thr Gln Leu Arg Asp Val Arg Ala Lys Lys Asp Gln
               2595                2600                2605

ctg gag gcg cac atc cag gcg gcg cag gcc atg ctt gcc atg gac aca   7933
Leu Glu Ala His Ile Gln Ala Ala Gln Ala Met Leu Ala Met Asp Thr
          2610                2615                2620

gac gag aca agc aag aag atc gca cat gcc aag gct gtg gct gct gaa   7981
Asp Glu Thr Ser Lys Lys Ile Ala His Ala Lys Ala Val Ala Ala Glu
       2625                2630                2635

gcc cag gac acc gcc acc cgt gtg cag tcc cag ctg cag gcc atg cag   8029
Ala Gln Asp Thr Ala Thr Arg Val Gln Ser Gln Leu Gln Ala Met Gln
   2640                2645                2650

gag aat gtg gag cgg tgg cag ggc cag tac gag ggc ctg cgg ggc cag   8077
Glu Asn Val Glu Arg Trp Gln Gly Gln Tyr Glu Gly Leu Arg Gly Gln
2655                2660                2665                2670

gac ctg ggc cag gca gtg ctt gac gca ggc cac tca gtg tcc acc ctg   8125
Asp Leu Gly Gln Ala Val Leu Asp Ala Gly His Ser Val Ser Thr Leu
               2675                2680                2685

gag aag acg ctg ccc cag ctg ctg gcc aag ctg agc atc ctg gag aac   8173
Glu Lys Thr Leu Pro Gln Leu Leu Ala Lys Leu Ser Ile Leu Glu Asn
          2690                2695                2700

cgt ggg gtg cac aac gcc agc ctg gcc ctg tcc gcc agc att ggc cgc   8221
Arg Gly Val His Asn Ala Ser Leu Ala Leu Ser Ala Ser Ile Gly Arg
       2705                2710                2715

gtg cga gag ctc att gcc cag gcc cgg ggg gct gcc agt aag gtc aag   8269
Val Arg Glu Leu Ile Ala Gln Ala Arg Gly Ala Ala Ser Lys Val Lys
   2720                2725                2730

gtg ccc atg aag ttc aac ggg cgc tca ggg gtg cag ctg cgc acc cca   8317
Val Pro Met Lys Phe Asn Gly Arg Ser Gly Val Gln Leu Arg Thr Pro
2735                2740                2745                2750

cgg gat ctt gcc gac ctt gct gcc tac act gcc ctc aag ttc tac ctg   8365
Arg Asp Leu Ala Asp Leu Ala Ala Tyr Thr Ala Leu Lys Phe Tyr Leu
               2755                2760                2765

cag ggc cca gag cct gag cct ggg cag ggt acc gag gat cgc ttt gtg   8413
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Gln Gly Pro Glu Pro Glu Pro Gly Gln Gly Thr Glu Asp Arg Phe Val
          2770                2775                2780

atg tac atg ggc agc cgc cag gcc act ggg gac tac atg ggt gtg tct   8461
Met Tyr Met Gly Ser Arg Gln Ala Thr Gly Asp Tyr Met Gly Val Ser
       2785                2790                2795

ctg cgt gac aag aag gtg cac tgg gtg tat cag ctg ggt gag gcg ggc   8509
Leu Arg Asp Lys Lys Val His Trp Val Tyr Gln Leu Gly Glu Ala Gly
   2800                2805                2810

cct gca gtc cta agc atc gat gag gac att ggg gag cag ttc gca gct   8557
Pro Ala Val Leu Ser Ile Asp Glu Asp Ile Gly Glu Gln Phe Ala Ala
2815                2820                2825                2830

gtc agc ctg gac agg act ctc cag ttt ggc cac atg tcc gtc aca gtg   8605
Val Ser Leu Asp Arg Thr Leu Gln Phe Gly His Met Ser Val Thr Val
               2835                2840                2845

gag aga cag atg atc cag gaa acc aag ggt gac acg gtg gcc cct ggg   8653
Glu Arg Gln Met Ile Gln Glu Thr Lys Gly Asp Thr Val Ala Pro Gly
          2850                2855                2860

gca gag ggg ctg ctc aac ctg cgg cca gac gac ttc gtc ttc tac gtc   8701
Ala Glu Gly Leu Leu Asn Leu Arg Pro Asp Asp Phe Val Phe Tyr Val
       2865                2870                2875

ggg ggg tac ccc agt acc ttc acg ccc cct ccc ctg ctt cgc ttc ccc   8749
Gly Gly Tyr Pro Ser Thr Phe Thr Pro Pro Pro Leu Leu Arg Phe Pro
   2880                2885                2890

ggc tac cgg ggc tgc atc gag atg gac acg ctg aat gag gag gtg gtc   8797
Gly Tyr Arg Gly Cys Ile Glu Met Asp Thr Leu Asn Glu Glu Val Val
2895                2900                2905                2910

agc ctc tac aac ttc gag agg acc ttc cag ctg gac acg gct gtg gac   8845
Ser Leu Tyr Asn Phe Glu Arg Thr Phe Gln Leu Asp Thr Ala Val Asp
               2915                2920                2925

agg cct tgt gcc cgc tcc aag tcg acc ggg gac ccg tgg ctc acg gac   8893
Arg Pro Cys Ala Arg Ser Lys Ser Thr Gly Asp Pro Trp Leu Thr Asp
          2930                2935                2940

ggc tcc tac ctg gac ggc acc ggc ttc gcc cgc atc agc ttc gac agt   8941
Gly Ser Tyr Leu Asp Gly Thr Gly Phe Ala Arg Ile Ser Phe Asp Ser
       2945                2950                2955

cag atc agc acc acc aag cgc ttc gag cag gag ctg cgg ctc gtg tcc   8989
Gln Ile Ser Thr Thr Lys Arg Phe Glu Gln Glu Leu Arg Leu Val Ser
   2960                2965                2970

tac agc ggg gtg ctc ttc ttc ctg aag cag cag agc cag ttc ctg tgc   9037
Tyr Ser Gly Val Leu Phe Phe Leu Lys Gln Gln Ser Gln Phe Leu Cys
2975                2980                2985                2990

ttg gcc gtg caa gaa ggc agc ctc gtg ctg ttg tat gac ttt ggg gct   9085
Leu Ala Val Gln Glu Gly Ser Leu Val Leu Leu Tyr Asp Phe Gly Ala
               2995                3000                3005

ggc ctg aaa aag gcc gtc cca ctg cag ccc cca ccg ccc ctg acc tcg   9133
Gly Leu Lys Lys Ala Val Pro Leu Gln Pro Pro Pro Pro Leu Thr Ser
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          3010                3015                3020

gcc agc aag gcg atc cag gtg ttc ctg ctg ggg ggc agc cgc aag cgt   9181
Ala Ser Lys Ala Ile Gln Val Phe Leu Leu Gly Gly Ser Arg Lys Arg
       3025                3030                3035

gtg ctg gtg cgt gtg gag cgg gcc acg gtg tac agc gtg gag cag gac   9229
Val Leu Val Arg Val Glu Arg Ala Thr Val Tyr Ser Val Glu Gln Asp
   3040                3045                3050

aat gat ctg gag ctg gcc gac gcc tac tac ctg ggg ggc gtg ccg ccc   9277
Asn Asp Leu Glu Leu Ala Asp Ala Tyr Tyr Leu Gly Gly Val Pro Pro
3055                3060                3065                3070

gac cag ctg ccc ccg agc ctg cga tgg ctc ttc ccc acc gga ggc tca   9325
Asp Gln Leu Pro Pro Ser Leu Arg Trp Leu Phe Pro Thr Gly Gly Ser
               3075                3080                3085

gtc cgt ggc tgc gtc aaa ggc atc aag gcc ctg ggc aag tat gtg gac   9373
Val Arg Gly Cys Val Lys Gly Ile Lys Ala Leu Gly Lys Tyr Val Asp
           3090                3095                3100

ctc aag cgg ctg aac acg aca ggc gtg agc gcc ggc tgc acc gcc gac   9421
Leu Lys Arg Leu Asn Thr Thr Gly Val Ser Ala Gly Cys Thr Ala Asp
       3105                3110                3115

ctg ctg gtg ggg cgc gcc atg act ttc cat ggc cac ggc ttc ctt cgc   9469
Leu Leu Val Gly Arg Ala Met Thr Phe His Gly His Gly Phe Leu Arg
   3120                3125                3130

ctg gcg ctc tcg aac gtg gca ccg ctc act ggc aac gtc tac tcc ggc   9517
Leu Ala Leu Ser Asn Val Ala Pro Leu Thr Gly Asn Val Tyr Ser Gly
3135                3140                3145                3150

ttc ggc ttc cac agc gcc cag gac agt gcc ctg ctc tac tac cgg gcg   9565
Phe Gly Phe His Ser Ala Gln Asp Ser Ala Leu Leu Tyr Tyr Arg Ala
               3155                3160                3165

tcc ccg gat ggg cta tgc cag gtg tcc ctg cag cag ggc cgt gtg agc   9613
Ser Pro Asp Gly Leu Cys Gln Val Ser Leu Gln Gln Gly Arg Val Ser
           3170                3175                3180

cta cag ctc ctg agg act gaa gtg aaa act caa gcg ggc ttc gcc gat   9661
Leu Gln Leu Leu Arg Thr Glu Val Lys Thr Gln Ala Gly Phe Ala Asp
       3185                3190                3195

ggt gcc ccc cat tac gtc gcc ttc tac agc aat gcc acg gga gtc tgg   9709
Gly Ala Pro His Tyr Val Ala Phe Tyr Ser Asn Ala Thr Gly Val Trp
   3200                3205                3210

ctg tat gtc gat gac cag ctc cag cag atg aag ccc cac cgg gga cca   9757
Leu Tyr Val Asp Asp Gln Leu Gln Gln Met Lys Pro His Arg Gly Pro
3215                3220                3225                3230

ccc ccc gag ctc cag ccg cag cct gag ggg ccc ccg agg ctc ctc ctg   9805
Pro Pro Glu Leu Gln Pro Gln Pro Glu Gly Pro Pro Arg Leu Leu Leu
               3235                3240                3245

gga ggc ctg cct gag tct ggc acc att tac aac ttc agt ggc tgc atc   9853
Gly Gly Leu Pro Glu Ser Gly Thr Ile Tyr Asn Phe Ser Gly Cys Ile
           3250                3255                3260
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agc aac gtc ttc gtg cag cgg ctc ctg ggc cca cag cgc gta ttt gat   9901
Ser Asn Val Phe Val Gln Arg Leu Leu Gly Pro Gln Arg Val Phe Asp
       3265                3270                3275

ctg cag cag aac ctg ggc agc gtc aat gtg agc acg ggc tgt gca ccc   9949
Leu Gln Gln Asn Leu Gly Ser Val Asn Val Ser Thr Gly Cys Ala Pro
   3280                3285                3290

gcc ctg caa gcc cag acc ccg ggc ctg ggg cct aga gga ctg cag gcc   9997
Ala Leu Gln Ala Gln Thr Pro Gly Leu Gly Pro Arg Gly Leu Gln Ala
3295                3300                3305                3310

acc gcc cgg aag gcc tcc cgc cgc agc cgt cag ccc gcc cgg cat cct   10045
Thr Ala Arg Lys Ala Ser Arg Arg Ser Arg Gln Pro Ala Arg His Pro
               3315                3320                3325

gcc tgc atg ctg ccc cca cac ctc agg acc acc cga gac tcc tac cag   10093
Ala Cys Met Leu Pro Pro His Leu Arg Thr Thr Arg Asp Ser Tyr Gln
           3330                3335                3340

ttt ggg ggt tcc ctg tcc agt cac ctg gag ttt gtg ggc atc ctg gcc   10141
Phe Gly Gly Ser Leu Ser Ser His Leu Glu Phe Val Gly Ile Leu Ala
       3345                3350                3355

cga cat agg aac tgg ccc agt ctc tcc atg cac gtc ctc ccg cga agc   10189
Arg His Arg Asn Trp Pro Ser Leu Ser Met His Val Leu Pro Arg Ser
   3360                3365                3370

tcc cga ggc ctc ctc ctc ttc act gcc cgt ctg agg ccc ggc agc ccc   10237
Ser Arg Gly Leu Leu Leu Phe Thr Ala Arg Leu Arg Pro Gly Ser Pro
3375                3380                3385                3390

tcc ctg gcg ctc ttc ctg agc aat ggc cac ttc gtt gca cag atg gaa   10285
Ser Leu Ala Leu Phe Leu Ser Asn Gly His Phe Val Ala Gln Met Glu
               3395                3400                3405

ggc ctc ggg act cgg ctc cgc gcc cag agc cgc cag cgc tcc cgg cct   10333
Gly Leu Gly Thr Arg Leu Arg Ala Gln Ser Arg Gln Arg Ser Arg Pro
           3410                3415                3420

ggc cgc tgg cac aag gtc tcc gtg cgc tgg gag aag aac cgg atc ctg   10381
Gly Arg Trp His Lys Val Ser Val Arg Trp Glu Lys Asn Arg Ile Leu
       3425                3430                3435

ctg gtg acg gac ggg gcc cgg gcc tgg agc cag gag ggg ccg cac cgg   10429
Leu Val Thr Asp Gly Ala Arg Ala Trp Ser Gln Glu Gly Pro His Arg
   3440                3445                3450

cag cac cag ggg gca gag cac ccc cag ccc cac acc ctc ttt gtg ggc   10477
Gln His Gln Gly Ala Glu His Pro Gln Pro His Thr Leu Phe Val Gly
3455                3460                3465                3470

ggc ctc ccg gcc agc agc cac agc tcc aaa ctt ccg gtg acc gtc ggg   10525
Gly Leu Pro Ala Ser Ser His Ser Ser Lys Leu Pro Val Thr Val Gly
               3475                3480                3485

ttc agc ggc tgt gtg aag aga ctg agg ctg cac ggg agg ccc ctg ggg   10573
Phe Ser Gly Cys Val Lys Arg Leu Arg Leu His Gly Arg Pro Leu Gly
           3490                3495                3500
```

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gcc ccc aca cgg atg gca ggg gtc aca ccc tgc atc ttg ggc ccc ctg   10621
Ala Pro Thr Arg Met Ala Gly Val Thr Pro Cys Ile Leu Gly Pro Leu
       3505                3510                3515

gag gcg ggc ctg ttc ttc cca ggc agc ggg gga gtt atc act tta gac   10669
Glu Ala Gly Leu Phe Phe Pro Gly Ser Gly Gly Val Ile Thr Leu Asp
   3520                3525                3530

ctc cca gga gct aca ctg cct gat gtg ggc ctg gaa ctg gag gtg cgg   10717
Leu Pro Gly Ala Thr Leu Pro Asp Val Gly Leu Glu Leu Glu Val Arg
3535                3540                3545                3550

ccc ctg gca gtc acc gga ctg atc ttc cac ttg ggc cag gcc cgg acg   10765
Pro Leu Ala Val Thr Gly Leu Ile Phe His Leu Gly Gln Ala Arg Thr
               3555                3560                3565

ccc ccc tac ttg cag ttg cag gtg acc gag aag caa gtc ctg ctg cgg   10813
Pro Pro Tyr Leu Gln Leu Gln Val Thr Glu Lys Gln Val Leu Leu Arg
           3570                3575                3580

gcg gat gac gga gca ggg gag ttc tcc acg tca gtg acc cgc ccc tca   10861
Ala Asp Asp Gly Ala Gly Glu Phe Ser Thr Ser Val Thr Arg Pro Ser
       3585                3590                3595

gtg ctg tgt gat ggc cag tgg cac cgg cta gcg gtg atg aaa agc ggg   10909
Val Leu Cys Asp Gly Gln Trp His Arg Leu Ala Val Met Lys Ser Gly
   3600                3605                3610

aat gtg ctc cgg ctg gag gtg gac gcg cag agc aac cac acc gtg ggc   10957
Asn Val Leu Arg Leu Glu Val Asp Ala Gln Ser Asn His Thr Val Gly
3615                3620                3625                3630

ccc ttg ctg gcg gct gca gct ggt gcc cca gcc cct ctg tac ctc ggg   11005
Pro Leu Leu Ala Ala Ala Ala Gly Ala Pro Ala Pro Leu Tyr Leu Gly
               3635                3640                3645

ggc ctg cct gag ccc atg gcc gtg cag ccc tgg ccc ccc gcc tac tgc   11053
Gly Leu Pro Glu Pro Met Ala Val Gln Pro Trp Pro Pro Ala Tyr Cys
           3650                3655                3660

ggc tgc atg agg agg ctg gcg gtg aac cgg tcc ccc gtc gcc atg act   11101
Gly Cys Met Arg Arg Leu Ala Val Asn Arg Ser Pro Val Ala Met Thr
       3665                3670                3675

cgc tct gtg gag gtc cac ggg gca gtg ggg gcc agt ggc tgc cca gcc   11149
Arg Ser Val Glu Val His Gly Ala Val Gly Ala Ser Gly Cys Pro Ala
   3680                3685                3690

gcc taggacacag ccaaccccgg cccctggtca ggcccctgca gctgcctcac        11202
Ala
3695

accgcccctt gtgctcgcct cataggtgtc tatttggact ctaagctcta cgggtgacag 11262

atcttgtttc tgaagatggt ttaagttata gcttcttaaa cgaaagaata aaatactgca 11322

aaatgccgga attcgatatc aagcttat                                    11350


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<211> 3695
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<212> PRT
<213> Homo sapiens

<400> 2

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

Arg Gly Pro Ala Pro Leu Leu Leu Val Gly Leu Ala Leu Leu Gly Ala
             20                  25                  30

Ala Arg Ala Arg Glu Glu Ala Gly Gly Gly Phe Ser Leu His Pro Pro
         35                  40                  45

Tyr Phe Asn Leu Ala Glu Gly Ala Arg Ile Ala Ala Ser Ala Thr Cys
     50                  55                  60

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

Tyr Cys Lys Leu Val Gly Gly Pro Val Ala Gly Gly Asp Pro Asn Gln
                 85                  90                  95

Thr Ile Arg Gly Gln Tyr Cys Asp Ile Cys Thr Ala Ala Asn Ser Asn
            100                 105                 110

Lys Ala His Pro Ala Ser Asn Ala Ile Asp Gly Thr Glu Arg Trp Trp
        115                 120                 125

Gln Ser Pro Pro Leu Ser Arg Gly Leu Glu Tyr Asn Glu Val Asn Val
    130                 135                 140

Thr Leu Asp Leu Gly Gln Val Phe His Val Ala Tyr Val Leu Ile Lys
145                 150                 155                 160

Phe Ala Asn Ser Pro Arg Pro Asp Leu Trp Val Leu Glu Arg Ser Met
                165                 170                 175

Asp Phe Gly Arg Thr Tyr Gln Pro Trp Gln Phe Phe Ala Ser Ser Lys
            180                 185                 190

Arg Asp Cys Leu Glu Arg Phe Gly Pro Gln Thr Leu Glu Arg Ile Thr
        195                 200                 205

Arg Asp Asp Ala Ala Ile Cys Thr Thr Glu Tyr Ser Arg Ile Val Pro
    210                 215                 220

Leu Glu Asn Gly Glu Ile Val Val Ser Leu Val Asn Gly Arg Pro Gly
225                 230                 235                 240

Ala Met Asn Phe Ser Tyr Ser Pro Leu Leu Arg Glu Phe Thr Lys Ala
                245                 250                 255

Thr Asn Val Arg Leu Arg Phe Leu Arg Thr Asn Thr Leu Leu Gly His
            260                 265                 270

Leu Met Gly Lys Ala Leu Arg Asp Pro Thr Val Thr Arg Arg Tyr Tyr
        275                 280                 285

Tyr Ser Ile Lys Asp Ile Ser Ile Gly Gly Arg Cys Val Cys His Gly
    290                 295                 300
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His Ala Asp Ala Cys Asp Ala Lys Asp Pro Thr Asp Pro Phe Arg Leu
305                 310                 315                 320

Gln Cys Thr Cys Gln His Asn Thr Cys Gly Gly Thr Cys Asp Arg Cys
                325                 330                 335

Cys Pro Gly Phe Asn Gln Gln Pro Trp Lys Pro Ala Thr Ala Asn Ser
            340                 345                 350

Ala Asn Glu Cys Gln Ser Cys Asn Cys Tyr Gly His Ala Thr Asp Cys
        355                 360                 365

Tyr Tyr Asp Pro Glu Val Asp Arg Arg Arg Ala Ser Gln Ser Leu Asp
    370                 375                 380

Gly Thr Tyr Gln Gly Gly Gly Val Cys Ile Asp Cys Gln His His Thr
385                 390                 395                 400

Ala Gly Val Asn Cys Glu Arg Cys Leu Pro Gly Phe Tyr Arg Ser Pro
                405                 410                 415

Asn His Pro Leu Asp Ser Pro His Val Cys Arg Arg Cys Asn Cys Glu
            420                 425                 430

Ser Asp Phe Thr Asp Gly Thr Cys Glu Asp Leu Thr Gly Arg Cys Tyr
        435                 440                 445

Cys Arg Pro Asn Phe Ser Gly Glu Arg Cys Asp Val Cys Ala Glu Gly
    450                 455                 460

Phe Thr Gly Phe Pro Ser Cys Tyr Pro Thr Pro Ser Ser Ser Asn Asp
465                 470                 475                 480

Thr Arg Glu Gln Val Leu Pro Ala Gly Gln Ile Val Asn Cys Asp Cys
                485                 490                 495

Ser Ala Ala Gly Thr Gln Gly Asn Ala Cys Arg Lys Asp Pro Arg Val
            500                 505                 510

Gly Arg Cys Leu Cys Lys Pro Asn Phe Gln Gly Thr His Cys Glu Leu
        515                 520                 525

Cys Ala Pro Gly Phe Tyr Gly Pro Gly Cys Gln Pro Cys Gln Cys Ser
    530                 535                 540

Ser Pro Gly Val Ala Asp Asp Arg Cys Asp Pro Asp Thr Gly Gln Cys
545                 550                 555                 560

Arg Cys Arg Val Gly Phe Glu Gly Ala Thr Cys Asp Arg Cys Ala Pro
                565                 570                 575

Gly Tyr Phe His Phe Pro Leu Cys Gln Leu Cys Gly Cys Ser Pro Ala
            580                 585                 590

Gly Thr Leu Pro Glu Gly Cys Asp Glu Ala Gly Arg Cys Leu Cys Gln
        595                 600                 605

Pro Glu Phe Ala Gly Pro His Cys Asp Arg Cys Arg Pro Gly Tyr His
    610                 615                 620

Gly Phe Pro Asn Cys Gln Ala Cys Thr Cys Asp Pro Arg Gly Ala Leu
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625 630 635 640

Asp Gln Leu Cys Gly Ala Gly Gly Leu Cys Arg Cys Arg Pro Gly Tyr
645 650 655

Thr Gly Thr Ala Cys Gln Glu Cys Ser Pro Gly Phe His Gly Phe Pro
660 665 670

Ser Cys Val Pro Cys His Cys Ser Ala Glu Gly Ser Leu His Ala Ala
675 680 685

Cys Asp Pro Arg Ser Gly Gln Cys Ser Cys Arg Pro Arg Val Thr Gly
690 695 700

Leu Arg Cys Asp Thr Cys Val Pro Gly Ala Tyr Asn Phe Pro Tyr Cys
705 710 715 720

Glu Ala Gly Ser Cys His Pro Ala Gly Leu Ala Pro Val Asp Pro Ala
725 730 735

Leu Pro Glu Ala Gln Val Pro Cys Met Cys Arg Ala His Val Glu Gly
740 745 750

Pro Ser Cys Asp Arg Cys Lys Pro Gly Phe Trp Gly Leu Ser Pro Ser
755 760 765

Asn Pro Glu Gly Cys Thr Arg Cys Ser Cys Asp Leu Arg Gly Thr Leu
770 775 780

Gly Gly Val Ala Glu Cys Gln Pro Gly Thr Gly Gln Cys Phe Cys Lys
785 790 795 800

Pro His Val Cys Gly Gln Ala Cys Ala Ser Cys Lys Asp Gly Phe Phe
805 810 815

Gly Leu Asp Gln Ala Asp Tyr Phe Gly Cys Arg Ser Cys Arg Cys Asp
820 825 830

Ile Gly Gly Ala Leu Gly Gln Ser Cys Glu Pro Arg Thr Gly Val Cys
835 840 845

Arg Cys Arg Pro Asn Thr Gln Gly Pro Thr Cys Ser Glu Pro Ala Arg
850 855 860

Asp His Tyr Leu Pro Asp Leu His His Leu Arg Leu Glu Leu Glu Glu
865 870 875 880

Ala Ala Thr Pro Glu Gly His Ala Val Arg Phe Gly Phe Asn Pro Leu
885 890 895

Glu Phe Glu Asn Phe Ser Trp Arg Gly Tyr Ala Gln Met Ala Pro Val
900 905 910

Gln Pro Arg Ile Val Ala Arg Leu Asn Leu Thr Ser Pro Asp Leu Phe
915 920 925

Trp Leu Val Phe Arg Tyr Val Asn Arg Gly Ala Met Ser Val Ser Gly
930 935 940

Arg Val Ser Val Arg Glu Glu Gly Arg Ser Ala Ala Cys Ala Asn Cys
945 950 955 960

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Thr Ala Gln Ser Gln Pro Val Ala Phe Pro Pro Ser Thr Glu Pro Ala
                965                 970                 975

Phe Ile Thr Val Pro Gln Arg Gly Phe Gly Glu Pro Phe Val Leu Asn
            980                 985                 990

Pro Gly Thr Trp Ala Leu Arg Val Glu Ala Glu Gly Val Leu Leu Asp
        995                1000                1005

Tyr Val Val Leu Leu Pro Ser Ala Tyr Tyr Glu Ala Ala Leu Leu Gln
   1010                1015                1020

Leu Arg Val Thr Glu Ala Cys Thr Tyr Arg Pro Ser Ala Gln Gln Ser
1025                1030                1035                1040

Gly Asp Asn Cys Leu Leu Tyr Thr His Leu Pro Leu Asp Gly Phe Pro
               1045                1050                1055

Ser Ala Ala Gly Leu Glu Ala Leu Cys Arg Gln Asp Asn Ser Leu Pro
           1060                1065                1070

Arg Pro Cys Pro Thr Glu Gln Leu Ser Pro Ser His Pro Pro Leu Ile
       1075                1080                1085

Thr Cys Thr Gly Ser Asp Val Asp Val Gln Leu Gln Val Ala Val Pro
   1090                1095                1100

Gln Pro Gly Arg Tyr Ala Leu Val Val Glu Tyr Ala Asn Glu Asp Ala
1105                1110                1115                1120

Arg Gln Glu Val Gly Val Ala Val His Thr Pro Gln Arg Ala Pro Gln
               1125                1130                1135

Gln Gly Leu Leu Ser Leu His Pro Cys Leu Tyr Ser Thr Leu Cys Arg
           1140                1145                1150

Gly Thr Ala Arg Asp Thr Gln Asp His Leu Ala Val Phe His Leu Asp
       1155                1160                1165

Ser Glu Ala Ser Val Arg Leu Thr Ala Glu Gln Ala Arg Phe Phe Leu
   1170                1175                1180

His Gly Val Thr Leu Val Pro Ile Glu Glu Phe Ser Pro Glu Phe Val
1185                1190                1195                1200

Glu Pro Arg Val Ser Cys Ile Ser Ser His Gly Ala Phe Gly Pro Asn
               1205                1210                1215

Ser Ala Ala Cys Leu Pro Ser Arg Phe Pro Lys Pro Pro Gln Pro Ile
           1220                1225                1230

Ile Leu Arg Asp Cys Gln Val Ile Pro Leu Pro Pro Gly Leu Pro Leu
       1235                1240                1245

Thr His Ala Gln Asp Leu Thr Pro Ala Thr Ser Pro Ala Gly Pro Arg
   1250                1255                1260

Pro Arg Pro Pro Thr Ala Val Asp Pro Asp Ala Glu Pro Thr Leu Leu
1265                1270                1275                1280
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Arg Glu Pro Gln Ala Thr Val Val Phe Thr Thr His Val Pro Thr Leu
                1285                1290                1295

Gly Arg Tyr Ala Phe Leu Leu His Gly Tyr Gln Pro Ala His Pro Thr
            1300                1305                1310

Phe Pro Val Glu Val Leu Ile Asn Ala Gly Arg Val Trp Gln Gly His
        1315                1320                1325

Ala Asn Ala Ser Phe Cys Pro His Gly Tyr Gly Cys Arg Thr Leu Val
    1330                1335                1340

Val Cys Glu Gly Gln Ala Leu Leu Asp Val Thr His Ser Glu Leu Thr
1345                1350                1355                1360

Val Thr Val Arg Val Pro Glu Gly Arg Trp Leu Trp Leu Asp Tyr Val
                1365                1370                1375

Leu Val Val Pro Glu Asn Val Tyr Ser Phe Gly Tyr Leu Arg Glu Glu
            1380                1385                1390

Pro Leu Asp Lys Ser Tyr Asp Phe Ile Ser His Cys Ala Ala Gln Gly
        1395                1400                1405

Tyr His Ile Ser Pro Ser Ser Ser Ser Leu Phe Cys Arg Asn Ala Ala
    1410                1415                1420

Ala Ser Leu Ser Leu Phe Tyr Asn Asn Gly Ala Arg Pro Cys Gly Cys
1425                1430                1435                1440

His Glu Val Gly Ala Thr Gly Pro Thr Cys Glu Pro Phe Gly Gly Gln
                1445                1450                1455

Cys Pro Cys His Ala His Val Ile Gly Arg Asp Cys Ser Arg Cys Ala
            1460                1465                1470

Thr Gly Tyr Trp Gly Phe Pro Asn Cys Arg Pro Cys Asp Cys Gly Ala
        1475                1480                1485

Arg Leu Cys Asp Glu Leu Thr Gly Gln Cys Ile Cys Pro Pro Arg Thr
    1490                1495                1500

Ile Pro Pro Asp Cys Leu Leu Cys Gln Pro Gln Thr Phe Gly Cys His
1505                1510                1515                1520

Pro Leu Val Gly Cys Glu Glu Cys Asn Cys Ser Gly Pro Gly Ile Gln
                1525                1530                1535

Glu Leu Thr Asp Pro Thr Cys Asp Thr Asp Ser Gly Gln Cys Lys Cys
            1540                1545                1550

Arg Pro Asn Val Thr Gly Arg Arg Cys Asp Thr Cys Ser Pro Gly Phe
        1555                1560                1565

His Gly Tyr Pro Arg Cys Arg Pro Cys Asp Cys His Glu Ala Gly Thr
    1570                1575                1580

Ala Pro Gly Val Cys Asp Pro Leu Thr Gly Gln Cys Tyr Cys Lys Glu
1585                1590                1595                1600

Asn Val Gln Gly Pro Lys Cys Asp Gln Cys Ser Leu Gly Thr Phe Ser
```

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                1605                1610                1615

Leu Asp Ala Ala Asn Pro Lys Gly Cys Thr Arg Cys Phe Cys Phe Gly
            1620                1625                1630

Ala Thr Glu Arg Cys Arg Ser Ser Ser Tyr Thr Arg Gln Glu Phe Val
        1635                1640                1645

Asp Met Glu Gly Trp Val Leu Leu Ser Thr Asp Arg Gln Val Val Pro
    1650                1655                1660

His Glu Arg Gln Pro Gly Thr Glu Met Leu Arg Ala Asp Leu Arg His
1665                1670                1675                1680

Val Pro Glu Ala Val Pro Glu Ala Phe Pro Glu Leu Tyr Trp Gln Ala
                1685                1690                1695

Pro Pro Ser Tyr Leu Gly Asp Arg Val Ser Ser Tyr Gly Gly Thr Leu
            1700                1705                1710

Arg Tyr Glu Leu His Ser Glu Thr Gln Arg Gly Asp Val Phe Val Pro
        1715                1720                1725

Met Glu Ser Arg Pro Asp Val Val Leu Gln Gly Asn Gln Met Ser Ile
    1730                1735                1740

Thr Phe Leu Glu Pro Ala Tyr Pro Thr Pro Gly His Val His Arg Gly
1745                1750                1755                1760

Gln Leu Gln Leu Val Glu Gly Asn Phe Arg His Thr Glu Thr Arg Asn
                1765                1770                1775

Thr Val Ser Arg Glu Glu Leu Met Met Val Leu Ala Ser Leu Glu Gln
            1780                1785                1790

Leu Gln Ile Arg Ala Leu Phe Ser Gln Ile Ser Ser Ala Val Ser Leu
        1795                1800                1805

Arg Arg Val Ala Leu Glu Val Ala Ser Pro Ala Gly Gln Gly Ala Leu
    1810                1815                1820

Ala Ser Asn Val Glu Leu Cys Leu Cys Pro Ala Ser Tyr Arg Gly Asp
1825                1830                1835                1840

Ser Cys Gln Glu Cys Ala Pro Gly Phe Tyr Arg Asp Val Lys Gly Leu
                1845                1850                1855

Phe Leu Gly Arg Cys Val Pro Cys Gln Cys His Gly His Ser Asp Arg
            1860                1865                1870

Cys Leu Pro Gly Ser Gly Val Cys Val Asp Cys Gln His Asn Thr Glu
        1875                1880                1885

Gly Ala His Cys Glu Arg Cys Gln Ala Gly Phe Met Ser Ser Arg Asp
    1890                1895                1900

Asp Pro Ser Ala Pro Cys Val Ser Cys Pro Cys Pro Leu Ser Val Pro
1905                1910                1915                1920

Ser Asn Asn Phe Ala Glu Gly Cys Val Leu Arg Gly Gly Arg Thr Gln
                1925                1930                1935
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Cys Leu Cys Lys Pro Gly Tyr Ala Gly Ala Ser Cys Glu Arg Cys Ala
          1940                1945                1950

Pro Gly Phe Phe Gly Asn Pro Leu Val Leu Gly Ser Ser Cys Gln Pro
       1955                1960                1965

Cys Asp Cys Ser Gly Asn Gly Asp Pro Asn Leu Leu Phe Ser Asp Cys
   1970                1975                1980

Asp Pro Leu Thr Gly Ala Cys Arg Gly Cys Leu Arg His Thr Thr Gly
1985                1990                1995                2000

Pro Arg Cys Glu Ile Cys Ala Pro Gly Phe Tyr Gly Asn Ala Leu Leu
               2005                2010                2015

Pro Gly Asn Cys Thr Arg Cys Asp Cys Thr Pro Cys Gly Thr Glu Ala
          2020                2025                2030

Cys Asp Pro His Ser Gly His Cys Leu Cys Lys Ala Gly Val Thr Gly
       2035                2040                2045

Arg Arg Cys Asp Arg Cys Gln Glu Gly His Phe Gly Phe Asn Gly Cys
   2050                2055                2060

Gly Gly Cys Arg Pro Cys Ala Cys Gly Pro Ala Ala Glu Gly Ser Glu
2065                2070                2075                2080

Cys His Pro Gln Ser Gly Gln Cys His Cys Arg Pro Gly Thr Met Gly
               2085                2090                2095

Pro Gln Cys Arg Glu Cys Ala Pro Gly Tyr Trp Gly Leu Pro Glu Gln
          2100                2105                2110

Gly Cys Arg Arg Cys Gln Cys Pro Gly Gly Arg Cys Asp Pro His Thr
       2115                2120                2125

Gly Arg Cys Asn Cys Pro Pro Gly Leu Ser Gly Glu Arg Cys Asp Thr
   2130                2135                2140

Cys Ser Gln Gln His Gln Val Pro Val Pro Gly Gly Pro Val Gly His
2145                2150                2155                2160

Ser Ile His Cys Glu Val Cys Asp His Cys Val Val Leu Leu Leu Asp
               2165                2170                2175

Asp Leu Glu Arg Ala Gly Ala Leu Leu Pro Ala Ile His Glu Gln Leu
          2180                2185                2190

Arg Gly Ile Asn Ala Ser Ser Met Ala Trp Ala Arg Leu His Arg Leu
       2195                2200                2205

Asn Ala Ser Ile Ala Asp Leu Gln Ser Gln Leu Arg Ser Pro Leu Gly
   2210                2215                2220

Pro Arg His Glu Thr Ala Gln Gln Leu Glu Val Leu Glu Gln Gln Ser
2225                2230                2235                2240

Thr Ser Leu Gly Gln Asp Ala Arg Arg Leu Gly Gly Gln Ala Val Gly
               2245                2250                2255
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Thr Arg Asp Gln Ala Ser Gln Leu Leu Ala Gly Thr Glu Ala Thr Leu
2260 2265 2270

Gly His Ala Lys Thr Leu Leu Ala Ala Ile Arg Ala Val Asp Arg Thr
2275 2280 2285

Leu Ser Glu Leu Met Ser Gln Thr Gly His Leu Gly Leu Ala Asn Ala
2290 2295 2300

Ser Ala Pro Ser Gly Glu Gln Leu Leu Arg Thr Leu Ala Glu Val Glu
2305 2310 2315 2320

Arg Leu Leu Trp Glu Met Arg Ala Arg Asp Leu Gly Ala Pro Gln Ala
2325 2330 2335

Ala Ala Glu Ala Glu Leu Ala Ala Ala Gln Arg Leu Leu Ala Arg Val
2340 2345 2350

Gln Glu Gln Leu Ser Ser Leu Trp Glu Glu Asn Gln Ala Leu Ala Thr
2355 2360 2365

Gln Thr Arg Asp Arg Leu Ala Gln His Glu Ala Gly Leu Met Asp Leu
2370 2375 2380

Arg Glu Ala Leu Asn Arg Ala Val Asp Ala Thr Arg Glu Ala Gln Glu
2385 2390 2395 2400

Leu Asn Ser Arg Asn Gln Glu Arg Leu Glu Glu Ala Leu Gln Arg Lys
2405 2410 2415

Gln Glu Leu Ser Arg Asp Asn Ala Thr Leu Gln Ala Thr Leu His Ala
2420 2425 2430

Ala Arg Asp Thr Leu Ala Ser Val Phe Arg Leu Leu His Ser Leu Asp
2435 2440 2445

Gln Ala Lys Glu Glu Leu Glu Arg Leu Ala Ala Ser Leu Asp Gly Ala
2450 2455 2460

Arg Thr Pro Leu Leu Gln Arg Met Gln Thr Phe Ser Pro Ala Gly Ser
2465 2470 2475 2480

Lys Leu Arg Leu Val Glu Ala Ala Glu Ala His Ala Gln Gln Leu Gly
2485 2490 2495

Gln Leu Ala Leu Asn Leu Ser Ser Ile Ile Leu Asp Val Asn Gln Asp
2500 2505 2510

Arg Leu Thr Gln Arg Ala Ile Glu Ala Ser Asn Ala Tyr Ser Arg Ile
2515 2520 2525

Leu Gln Ala Val Gln Ala Ala Glu Asp Ala Ala Gly Gln Ala Leu Gln
2530 2535 2540

Gln Ala Asp His Thr Trp Ala Thr Val Val Arg Gln Gly Leu Val Asp
2545 2550 2555 2560

Arg Ala Gln Gln Leu Leu Ala Asn Ser Thr Ala Leu Glu Glu Ala Met
2565 2570 2575

Leu Gln Glu Gln Gln Arg Leu Gly Leu Val Trp Ala Ala Leu Gln Gly

2580 2585 2590

Ala Arg Thr Gln Leu Arg Asp Val Arg Ala Lys Lys Asp Gln Leu Glu
2595 2600 2605

Ala His Ile Gln Ala Ala Gln Ala Met Leu Ala Met Asp Thr Asp Glu
2610 2615 2620

Thr Ser Lys Lys Ile Ala His Ala Lys Ala Val Ala Ala Glu Ala Gln
2625 2630 2635 2640

Asp Thr Ala Thr Arg Val Gln Ser Gln Leu Gln Ala Met Gln Glu Asn
2645 2650 2655

Val Glu Arg Trp Gln Gly Gln Tyr Glu Gly Leu Arg Gly Gln Asp Leu
2660 2665 2670

Gly Gln Ala Val Leu Asp Ala Gly His Ser Val Ser Thr Leu Glu Lys
2675 2680 2685

Thr Leu Pro Gln Leu Leu Ala Lys Leu Ser Ile Leu Glu Asn Arg Gly
2690 2695 2700

Val His Asn Ala Ser Leu Ala Leu Ser Ala Ser Ile Gly Arg Val Arg
2705 2710 2715 2720

Glu Leu Ile Ala Gln Ala Arg Gly Ala Ala Ser Lys Val Lys Val Pro
2725 2730 2735

Met Lys Phe Asn Gly Arg Ser Gly Val Gln Leu Arg Thr Pro Arg Asp
2740 2745 2750

Leu Ala Asp Leu Ala Ala Tyr Thr Ala Leu Lys Phe Tyr Leu Gln Gly
2755 2760 2765

Pro Glu Pro Glu Pro Gly Gln Gly Thr Glu Asp Arg Phe Val Met Tyr
2770 2775 2780

Met Gly Ser Arg Gln Ala Thr Gly Asp Tyr Met Gly Val Ser Leu Arg
2785 2790 2795 2800

Asp Lys Lys Val His Trp Val Tyr Gln Leu Gly Glu Ala Gly Pro Ala
2805 2810 2815

Val Leu Ser Ile Asp Glu Asp Ile Gly Glu Gln Phe Ala Ala Val Ser
2820 2825 2830

Leu Asp Arg Thr Leu Gln Phe Gly His Met Ser Val Thr Val Glu Arg
2835 2840 2845

Gln Met Ile Gln Glu Thr Lys Gly Asp Thr Val Ala Pro Gly Ala Glu
2850 2855 2860

Gly Leu Leu Asn Leu Arg Pro Asp Asp Phe Val Phe Tyr Val Gly Gly
2865 2870 2875 2880

Tyr Pro Ser Thr Phe Thr Pro Pro Pro Leu Leu Arg Phe Pro Gly Tyr
2885 2890 2895

Arg Gly Cys Ile Glu Met Asp Thr Leu Asn Glu Glu Val Val Ser Leu
2900 2905 2910

```
Tyr Asn Phe Glu Arg Thr Phe Gln Leu Asp Thr Ala Val Asp Arg Pro
       2915                2920                2925

Cys Ala Arg Ser Lys Ser Thr Gly Asp Pro Trp Leu Thr Asp Gly Ser
   2930                2935                2940

Tyr Leu Asp Gly Thr Gly Phe Ala Arg Ile Ser Phe Asp Ser Gln Ile
2945                2950                2955                2960

Ser Thr Thr Lys Arg Phe Glu Gln Glu Leu Arg Leu Val Ser Tyr Ser
               2965                2970                2975

Gly Val Leu Phe Phe Leu Lys Gln Gln Ser Gln Phe Leu Cys Leu Ala
           2980                2985                2990

Val Gln Glu Gly Ser Leu Val Leu Leu Tyr Asp Phe Gly Ala Gly Leu
       2995                3000                3005

Lys Lys Ala Val Pro Leu Gln Pro Pro Pro Pro Leu Thr Ser Ala Ser
   3010                3015                3020

Lys Ala Ile Gln Val Phe Leu Leu Gly Gly Ser Arg Lys Arg Val Leu
3025                3030                3035                3040

Val Arg Val Glu Arg Ala Thr Val Tyr Ser Val Glu Gln Asp Asn Asp
               3045                3050                3055

Leu Glu Leu Ala Asp Ala Tyr Tyr Leu Gly Gly Val Pro Pro Asp Gln
           3060                3065                3070

Leu Pro Pro Ser Leu Arg Trp Leu Phe Pro Thr Gly Gly Ser Val Arg
       3075                3080                3085

Gly Cys Val Lys Gly Ile Lys Ala Leu Gly Lys Tyr Val Asp Leu Lys
   3090                3095                3100

Arg Leu Asn Thr Thr Gly Val Ser Ala Gly Cys Thr Ala Asp Leu Leu
3105                3110                3115                3120

Val Gly Arg Ala Met Thr Phe His Gly His Gly Phe Leu Arg Leu Ala
               3125                3130                3135

Leu Ser Asn Val Ala Pro Leu Thr Gly Asn Val Tyr Ser Gly Phe Gly
           3140                3145                3150

Phe His Ser Ala Gln Asp Ser Ala Leu Leu Tyr Tyr Arg Ala Ser Pro
       3155                3160                3165

Asp Gly Leu Cys Gln Val Ser Leu Gln Gln Gly Arg Val Ser Leu Gln
   3170                3175                3180

Leu Leu Arg Thr Glu Val Lys Thr Gln Ala Gly Phe Ala Asp Gly Ala
3185                3190                3195                3200

Pro His Tyr Val Ala Phe Tyr Ser Asn Ala Thr Gly Val Trp Leu Tyr
               3205                3210                3215

Val Asp Asp Gln Leu Gln Gln Met Lys Pro His Arg Gly Pro Pro Pro
           3220                3225                3230
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Glu Leu Gln Pro Gln Pro Glu Gly Pro Pro Arg Leu Leu Leu Gly Gly
3235 3240 3245

Leu Pro Glu Ser Gly Thr Ile Tyr Asn Phe Ser Gly Cys Ile Ser Asn
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Val Phe Val Gln Arg Leu Leu Gly Pro Gln Arg Val Phe Asp Leu Gln
3265 3270 3275 3280

Gln Asn Leu Gly Ser Val Asn Val Ser Thr Gly Cys Ala Pro Ala Leu
3285 3290 3295

Gln Ala Gln Thr Pro Gly Leu Gly Pro Arg Gly Leu Gln Ala Thr Ala
3300 3305 3310

Arg Lys Ala Ser Arg Arg Ser Arg Gln Pro Ala Arg His Pro Ala Cys
3315 3320 3325

Met Leu Pro Pro His Leu Arg Thr Thr Arg Asp Ser Tyr Gln Phe Gly
3330 3335 3340

Gly Ser Leu Ser Ser His Leu Glu Phe Val Gly Ile Leu Ala Arg His
3345 3350 3355 3360

Arg Asn Trp Pro Ser Leu Ser Met His Val Leu Pro Arg Ser Ser Arg
3365 3370 3375

Gly Leu Leu Leu Phe Thr Ala Arg Leu Arg Pro Gly Ser Pro Ser Leu
3380 3385 3390

Ala Leu Phe Leu Ser Asn Gly His Phe Val Ala Gln Met Glu Gly Leu
3395 3400 3405

Gly Thr Arg Leu Arg Ala Gln Ser Arg Gln Arg Ser Arg Pro Gly Arg
3410 3415 3420

Trp His Lys Val Ser Val Arg Trp Glu Lys Asn Arg Ile Leu Leu Val
3425 3430 3435 3440

Thr Asp Gly Ala Arg Ala Trp Ser Gln Glu Gly Pro His Arg Gln His
3445 3450 3455

Gln Gly Ala Glu His Pro Gln Pro His Thr Leu Phe Val Gly Gly Leu
3460 3465 3470

Pro Ala Ser Ser His Ser Ser Lys Leu Pro Val Thr Val Gly Phe Ser
3475 3480 3485

Gly Cys Val Lys Arg Leu Arg Leu His Gly Arg Pro Leu Gly Ala Pro
3490 3495 3500

Thr Arg Met Ala Gly Val Thr Pro Cys Ile Leu Gly Pro Leu Glu Ala
3505 3510 3515 3520

Gly Leu Phe Phe Pro Gly Ser Gly Gly Val Ile Thr Leu Asp Leu Pro
3525 3530 3535

Gly Ala Thr Leu Pro Asp Val Gly Leu Glu Leu Glu Val Arg Pro Leu
3540 3545 3550

Ala Val Thr Gly Leu Ile Phe His Leu Gly Gln Ala Arg Thr Pro Pro

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       3555                3560                3565

Tyr Leu Gln Leu Gln Val Thr Glu Lys Gln Val Leu Leu Arg Ala Asp
   3570                3575                3580

Asp Gly Ala Gly Glu Phe Ser Thr Ser Val Thr Arg Pro Ser Val Leu
3585                3590                3595                3600

Cys Asp Gly Gln Trp His Arg Leu Ala Val Met Lys Ser Gly Asn Val
               3605                3610                3615

Leu Arg Leu Glu Val Asp Ala Gln Ser Asn His Thr Val Gly Pro Leu
           3620                3625                3630

Leu Ala Ala Ala Ala Gly Ala Pro Ala Pro Leu Tyr Leu Gly Gly Leu
       3635                3640                3645

Pro Glu Pro Met Ala Val Gln Pro Trp Pro Pro Ala Tyr Cys Gly Cys
   3650                3655                3660

Met Arg Arg Leu Ala Val Asn Arg Ser Pro Val Ala Met Thr Arg Ser
3665                3670                3675                3680

Val Glu Val His Gly Ala Val Gly Ala Ser Gly Cys Pro Ala Ala
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Asp Leu Tyr Cys Lys Leu Val Gly Gly Pro Val Ala Gly Gly Asp Pro
  1               5                  10                  15

aat cag aca atc cag ggc cag tac tgt gac atc tgt aca gct gcc aac   96
Asn Gln Thr Ile Gln Gly Gln Tyr Cys Asp Ile Cys Thr Ala Ala Asn
             20                  25                  30

agc aac aag gca cac cct gtg agc aac gcc atc gat ggc acg gag cgc   144
Ser Asn Lys Ala His Pro Val Ser Asn Ala Ile Asp Gly Thr Glu Arg
         35                  40                  45

tgg tgg cag agc cca ccc ctg tcc cgt ggc ctg gag tac aat gag gtc   192
Trp Trp Gln Ser Pro Pro Leu Ser Arg Gly Leu Glu Tyr Asn Glu Val
     50                  55                  60

aac gtc aca ctg gac ctg ggc cag gtg ttc cat gtg gcc tat gtg ctc   240
Asn Val Thr Leu Asp Leu Gly Gln Val Phe His Val Ala Tyr Val Leu
 65                  70                  75                  80

atc aag ttt gcc aac tca cct cgg cct gac ctc tgg gtg ctg gag cgg   288
Ile Lys Phe Ala Asn Ser Pro Arg Pro Asp Leu Trp Val Leu Glu Arg
                 85                  90                  95
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tcc aca gac ttc ggt cac act tat cag ccg tgg cag ttc ttt gcc tcc   336
Ser Thr Asp Phe Gly His Thr Tyr Gln Pro Trp Gln Phe Phe Ala Ser
            100                 105                 110

tcc aag agg gat tgt ttg gag cgg ttt gga cct cgg act cta gag cgc   384
Ser Lys Arg Asp Cys Leu Glu Arg Phe Gly Pro Arg Thr Leu Glu Arg
        115                 120                 125

atc acg cag gac gac gac gtc atc tgc acc aca gaa tac tcg cga ata   432
Ile Thr Gln Asp Asp Asp Val Ile Cys Thr Thr Glu Tyr Ser Arg Ile
    130                 135                 140

gtg cct ttg gag aat ggc gag att gtg gtg tcc ttg gta aat ggg cgc   480
Val Pro Leu Glu Asn Gly Glu Ile Val Val Ser Leu Val Asn Gly Arg
145                 150                 155                 160

cct ggg gcc ttg aac ttc tcc tac tca ccg tta ctt cga gac ttc acc   528
Pro Gly Ala Leu Asn Phe Ser Tyr Ser Pro Leu Leu Arg Asp Phe Thr
                165                 170                 175

aaa gcc acc aac atc cgc ttg cgg ttt ctg cga acc aac acg cta ctg   576
Lys Ala Thr Asn Ile Arg Leu Arg Phe Leu Arg Thr Asn Thr Leu Leu
            180                 185                 190

ggc cac ctc atg ggc aag gcg ctg cgg gac ccc aca gtc acc cgc agg   624
Gly His Leu Met Gly Lys Ala Leu Arg Asp Pro Thr Val Thr Arg Arg
        195                 200                 205

tat tat tac agc atc aaa gac atc agc att ggt ggg cgc tgt gtc tgt   672
Tyr Tyr Tyr Ser Ile Lys Asp Ile Ser Ile Gly Gly Arg Cys Val Cys
    210                 215                 220

cat ggc cac gca gat gtc tgt gac gcc aag gac cca ttg gat cct ttc   720
His Gly His Ala Asp Val Cys Asp Ala Lys Asp Pro Leu Asp Pro Phe
225                 230                 235                 240

agg ctg cag tgt gcc tgc cag cac aat aca tgt gga ggc tct tgt gac   768
Arg Leu Gln Cys Ala Cys Gln His Asn Thr Cys Gly Gly Ser Cys Asp
                245                 250                 255

cga tgc tgt cca ggc ttc aac cag cag ccg tgg aag ccc gcc acc acg   816
Arg Cys Cys Pro Gly Phe Asn Gln Gln Pro Trp Lys Pro Ala Thr Thr
            260                 265                 270

gac agc gcc aat gag tgc cag tcc tgc aat tgc cac ggc cat gcc tac   864
Asp Ser Ala Asn Glu Cys Gln Ser Cys Asn Cys His Gly His Ala Tyr
        275                 280                 285

gac tgt tac tac gac cct gag gtg gat cgg cgc aat gcc agc cag aac   912
Asp Cys Tyr Tyr Asp Pro Glu Val Asp Arg Arg Asn Ala Ser Gln Asn
    290                 295                 300

cag gac aac gtg tac cag ggt gga ggt gtc tgc ctg gat tgc cag cat   960
Gln Asp Asn Val Tyr Gln Gly Gly Gly Val Cys Leu Asp Cys Gln His
305                 310                 315                 320

cac act acg ggt atc aac tgt gag cgt tgt ctg cct ggc ttc ttc cgt  1008
His Thr Thr Gly Ile Asn Cys Glu Arg Cys Leu Pro Gly Phe Phe Arg
                325                 330                 335

gcc cct gac cag cct ctc gac tca cct cat gtc tgt cgg ccc tgc gac  1056
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Ala Pro Asp Gln Pro Leu Asp Ser Pro His Val Cys Arg Pro Cys Asp
            340                 345                 350

tgt gag tca gac ttc acg gat ggg acc tgt gaa gac ttg acg ggc cgc   1104
Cys Glu Ser Asp Phe Thr Asp Gly Thr Cys Glu Asp Leu Thr Gly Arg
        355                 360                 365

tgt tac tgc agg ccg aac ttc aca gga gag cta tgt gct gcc tgc gct   1152
Cys Tyr Cys Arg Pro Asn Phe Thr Gly Glu Leu Cys Ala Ala Cys Ala
    370                 375                 380

gag ggc tac acg gac ttc cca cac tgc tac cct ctg cct tca ttt cct   1200
Glu Gly Tyr Thr Asp Phe Pro His Cys Tyr Pro Leu Pro Ser Phe Pro
385                 390                 395                 400

cac aat gac acg aga gaa cag gtg ctt ccc gct gga caa atc gtg aac   1248
His Asn Asp Thr Arg Glu Gln Val Leu Pro Ala Gly Gln Ile Val Asn
                405                 410                 415

tgt gat tgc aat gct gca ggg acc cag ggc aat gcc tgc cgg aag gac   1296
Cys Asp Cys Asn Ala Ala Gly Thr Gln Gly Asn Ala Cys Arg Lys Asp
            420                 425                 430

cca agg ttg gga cgg tgt gtc tgc aaa ccc aac ttc cgg ggt gcc cac   1344
Pro Arg Leu Gly Arg Cys Val Cys Lys Pro Asn Phe Arg Gly Ala His
        435                 440                 445

tgt gag ctc tgt gct cct gga ttc cac ggg cct agc tgc cac cca tgc   1392
Cys Glu Leu Cys Ala Pro Gly Phe His Gly Pro Ser Cys His Pro Cys
    450                 455                 460

cag tgt tcc agc cct ggg gta gcc aac agc ctc tgt gac cca gag tct   1440
Gln Cys Ser Ser Pro Gly Val Ala Asn Ser Leu Cys Asp Pro Glu Ser
465                 470                 475                 480

ggc cag tgc atg tgc cgc acc ggc ttt gag ggg gac agg tgt gac cac   1488
Gly Gln Cys Met Cys Arg Thr Gly Phe Glu Gly Asp Arg Cys Asp His
                485                 490                 495

tgt gcc ctt ggc tat ttc cac ttc cct ctc tgt cag ctg tgt ggc tgc   1536
Cys Ala Leu Gly Tyr Phe His Phe Pro Leu Cys Gln Leu Cys Gly Cys
            500                 505                 510

agc cca gca ggg acc ctg cct gaa ggc tgt gac gag gct ggc cgc tgc   1584
Ser Pro Ala Gly Thr Leu Pro Glu Gly Cys Asp Glu Ala Gly Arg Cys
        515                 520                 525

cag tgc cga cct ggc ttt gac ggt cct cac tgt gac cga tgc ctt cca   1632
Gln Cys Arg Pro Gly Phe Asp Gly Pro His Cys Asp Arg Cys Leu Pro
    530                 535                 540

gga tac cat ggg tat ccc gac tgt cac gct tgt gcc tgt gac cct cgg   1680
Gly Tyr His Gly Tyr Pro Asp Cys His Ala Cys Ala Cys Asp Pro Arg
545                 550                 555                 560

ggg gcc ctg gat caa cag tgt gga gtg ggc ggt ttg tgc cac tgc cgt   1728
Gly Ala Leu Asp Gln Gln Cys Gly Val Gly Gly Leu Cys His Cys Arg
                565                 570                 575

cct ggc aac aca ggt gcc act tgt cag gaa tgt agc ccc ggc ttc tac   1776
Pro Gly Asn Thr Gly Ala Thr Cys Gln Glu Cys Ser Pro Gly Phe Tyr
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            580                 585                 590

ggc ttc ccc agc tgc atc ccc tgc cac tgc tct gcc gat ggc tcc ttg   1824
Gly Phe Pro Ser Cys Ile Pro Cys His Cys Ser Ala Asp Gly Ser Leu
        595                 600                 605

cat aca acc tgt gac ccg aca acc ggc cag tgt agg tgt cga ccc cga   1872
His Thr Thr Cys Asp Pro Thr Thr Gly Gln Cys Arg Cys Arg Pro Arg
    610                 615                 620

gtg aca gga cta cat tgt gat atg tgt gta cca ggc gcc tat aac ttc   1920
Val Thr Gly Leu His Cys Asp Met Cys Val Pro Gly Ala Tyr Asn Phe
625                 630                 635                 640

ccc tac tgt gaa gct ggc tct tgt cat cct gct ggt ctg gcc cca gcc   1968
Pro Tyr Cys Glu Ala Gly Ser Cys His Pro Ala Gly Leu Ala Pro Ala
                645                 650                 655

aat cct gcc ctt cct gag aca cag gct ccc tgt atg tgc cgg gct cac   2016
Asn Pro Ala Leu Pro Glu Thr Gln Ala Pro Cys Met Cys Arg Ala His
            660                 665                 670

gtg gaa ggg cca agc tgt gat cgc tgt aaa cct ggg tac tgg ggg ctg   2064
Val Glu Gly Pro Ser Cys Asp Arg Cys Lys Pro Gly Tyr Trp Gly Leu
        675                 680                 685

agc gcc agc aac cct gaa ggc tgc aca cgc tgc agc tgt gac cca cga   2112
Ser Ala Ser Asn Pro Glu Gly Cys Thr Arg Cys Ser Cys Asp Pro Arg
    690                 695                 700

ggc acc ctg ggt gga gtt act gag tgc cag ggc aat ggg cag tgc ttc   2160
Gly Thr Leu Gly Gly Val Thr Glu Cys Gln Gly Asn Gly Gln Cys Phe
705                 710                 715                 720

tgc aag gct cac gtg tgt ggc aag acc tgt gca gcc tgc aag gat ggc   2208
Cys Lys Ala His Val Cys Gly Lys Thr Cys Ala Ala Cys Lys Asp Gly
                725                 730                 735

ttc ttt ggc ctg gat tat gct gac tac ttt ggc tgc cgt agc tgt agg   2256
Phe Phe Gly Leu Asp Tyr Ala Asp Tyr Phe Gly Cys Arg Ser Cys Arg
            740                 745                 750

tgt gat gtt ggt ggt gcc ctg ggt cag ggc tgt gaa cca aag aca ggt   2304
Cys Asp Val Gly Gly Ala Leu Gly Gln Gly Cys Glu Pro Lys Thr Gly
        755                 760                 765

gcc tgc agg tgc cgc cct aac acc caa gga ccc acc tgt agc gag cca   2352
Ala Cys Arg Cys Arg Pro Asn Thr Gln Gly Pro Thr Cys Ser Glu Pro
    770                 775                 780

gcg aag gac cac tac ttg cca gac ctg cac cac atg cgg ctg gaa cta   2400
Ala Lys Asp His Tyr Leu Pro Asp Leu His His Met Arg Leu Glu Leu
785                 790                 795                 800

gag gag gcg gcc act ccc gag ggc cac gct gta cgc ttt ggc ttc aac   2448
Glu Glu Ala Ala Thr Pro Glu Gly His Ala Val Arg Phe Gly Phe Asn
                805                 810                 815

ccc ctg gag ttt gag aac ttt agc tgg aga ggc tac gca cac atg atg   2496
Pro Leu Glu Phe Glu Asn Phe Ser Trp Arg Gly Tyr Ala His Met Met
            820                 825                 830
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gct atc cag ccc agg att gtg gcc agg ctg aac gtg acc tcc cct gac   2544
Ala Ile Gln Pro Arg Ile Val Ala Arg Leu Asn Val Thr Ser Pro Asp
        835                 840                 845

ctc ttt cga ctg gtt ttc cga tat gtc aac cgt gga tca acc agc gtg   2592
Leu Phe Arg Leu Val Phe Arg Tyr Val Asn Arg Gly Ser Thr Ser Val
    850                 855                 860

aat ggg cag atc tct gtt cgt gaa gag ggc aag ctt tcc agc tgt acc   2640
Asn Gly Gln Ile Ser Val Arg Glu Glu Gly Lys Leu Ser Ser Cys Thr
865                 870                 875                 880

aac tgc aca gag cag agc cag cca gtg gct ttc cca ccc agc act gag   2688
Asn Cys Thr Glu Gln Ser Gln Pro Val Ala Phe Pro Pro Ser Thr Glu
                885                 890                 895

cct gcc ttt gtc act gtg ccc cag agg ggc ttt ggg gaa ccc ttt gtg   2736
Pro Ala Phe Val Thr Val Pro Gln Arg Gly Phe Gly Glu Pro Phe Val
            900                 905                 910

ctg aac ccc ggc atc tgg gcc ttg ctg gtc gag gct gaa ggt gta ctc   2784
Leu Asn Pro Gly Ile Trp Ala Leu Leu Val Glu Ala Glu Gly Val Leu
        915                 920                 925

ttg gac tac gtg gtc cta ctg ccc agc acc tac tat gag gca gct ctc   2832
Leu Asp Tyr Val Val Leu Leu Pro Ser Thr Tyr Tyr Glu Ala Ala Leu
    930                 935                 940

cta cag cat cga gta acg gag gcc tgt acc tac cgt ccc tca gcc ctg   2880
Leu Gln His Arg Val Thr Glu Ala Cys Thr Tyr Arg Pro Ser Ala Leu
945                 950                 955                 960

cac tcc aca gag aac tgt ctt gtc tat gct cac cta ccc ctg gat ggc   2928
His Ser Thr Glu Asn Cys Leu Val Tyr Ala His Leu Pro Leu Asp Gly
                965                 970                 975

ttc cct tca gca gct gga act gag gcc ctg tgt cgc cat gac aac agc   2976
Phe Pro Ser Ala Ala Gly Thr Glu Ala Leu Cys Arg His Asp Asn Ser
            980                 985                 990

ctg ccc cgg ccc tgc ccc aca gag cag ctc agc ccc tca cac cca ccg   3024
Leu Pro Arg Pro Cys Pro Thr Glu Gln Leu Ser Pro Ser His Pro Pro
        995                1000                1005

ctg gcg acc tgc ttc ggc agt gat gtg gac atc cag ctc gag atg gcc   3072
Leu Ala Thr Cys Phe Gly Ser Asp Val Asp Ile Gln Leu Glu Met Ala
   1010                1015                1020

gtg cct cag cct ggc caa tat gtt ctc gtg gtg gaa tat gtc ggt gag   3120
Val Pro Gln Pro Gly Gln Tyr Val Leu Val Val Glu Tyr Val Gly Glu
1025                1030                1035                1040

gat tca cac caa gag atg gga gtg gct gtg cac acc cct cag aga gcc   3168
Asp Ser His Gln Glu Met Gly Val Ala Val His Thr Pro Gln Arg Ala
               1045                1050                1055

ccc cag caa ggg gtg ctc aac ctc cac ccc tgc cca tac agc tcc ctg   3216
Pro Gln Gln Gly Val Leu Asn Leu His Pro Cys Pro Tyr Ser Ser Leu
           1060                1065                1070
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tgc cgg agt ccg gct cgg gac acc cag cat cat cta gcc atc ttc cac   3264
Cys Arg Ser Pro Ala Arg Asp Thr Gln His His Leu Ala Ile Phe His
       1075                1080                1085

ctg gac tct gag gct agc atc cgg ctc aca gct gag caa gct cac ttc   3312
Leu Asp Ser Glu Ala Ser Ile Arg Leu Thr Ala Glu Gln Ala His Phe
   1090                1095                1100

ttc ctg cac agc gtc acc ctg gta cct gtg gag gag ttc agt act gag   3360
Phe Leu His Ser Val Thr Leu Val Pro Val Glu Glu Phe Ser Thr Glu
1105                1110                1115                1120

ttt gtg gag ccc cgg gtc ttc tgt gtg agc agt cat gga act ttc aac   3408
Phe Val Glu Pro Arg Val Phe Cys Val Ser Ser His Gly Thr Phe Asn
               1125                1130                1135

ccc agc agt gct gcc tgt cta gcc tcc cga ttc ccg aag cca ccg cag   3456
Pro Ser Ser Ala Ala Cys Leu Ala Ser Arg Phe Pro Lys Pro Pro Gln
           1140                1145                1150

ccc atc atc ctt aag gac tgc cag gtc ttg ccg ctg cct ccc gac ctg   3504
Pro Ile Ile Leu Lys Asp Cys Gln Val Leu Pro Leu Pro Pro Asp Leu
       1155                1160                1165

cct ctg act cag tct cag gag ctc tca cca ggt gca ccc ccc gag gga   3552
Pro Leu Thr Gln Ser Gln Glu Leu Ser Pro Gly Ala Pro Pro Glu Gly
   1170                1175                1180

cca cag cct cgg ccg cca act gcg gtg gat cct aat gca gaa ccc acc   3600
Pro Gln Pro Arg Pro Pro Thr Ala Val Asp Pro Asn Ala Glu Pro Thr
1185                1190                1195                1200

ttg ctg cgc cac ccc cag ggc acg gtg gtc ttc acc acc cag gtg ccc   3648
Leu Leu Arg His Pro Gln Gly Thr Val Val Phe Thr Thr Gln Val Pro
               1205                1210                1215

acc ctg ggc cgc tat gcc ttc ctg ctg cac ggc tac cag ccg gtc cac   3696
Thr Leu Gly Arg Tyr Ala Phe Leu Leu His Gly Tyr Gln Pro Val His
           1220                1225                1230

ccc tcc ttc cct gtg gag gta ctc att aat ggt ggc cgc atc tgg cag   3744
Pro Ser Phe Pro Val Glu Val Leu Ile Asn Gly Gly Arg Ile Trp Gln
       1235                1240                1245

ggc cac gcc aac gcc agc ttt tgt cct cat ggt tat ggc tgc cgt acc   3792
Gly His Ala Asn Ala Ser Phe Cys Pro His Gly Tyr Gly Cys Arg Thr
   1250                1255                1260

ctg gtg ttg tgt gag ggt cag acg atg ctg gat gtt aca gac aac gag   3840
Leu Val Leu Cys Glu Gly Gln Thr Met Leu Asp Val Thr Asp Asn Glu
1265                1270                1275                1280

ctc acc gtg act gtg cgt gtg cca gaa ggc cgg tgg ctc tgg ctg gac   3888
Leu Thr Val Thr Val Arg Val Pro Glu Gly Arg Trp Leu Trp Leu Asp
               1285                1290                1295

tac gta ctc att gtc cct gag gat gct tac agc tcc agt tac ctc caa   3936
Tyr Val Leu Ile Val Pro Glu Asp Ala Tyr Ser Ser Ser Tyr Leu Gln
           1300                1305                1310

gag gag cct ttg gac aaa tcc tat gac ttc atc agc cac tgt gcc acc   3984
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Glu Glu Pro Leu Asp Lys Ser Tyr Asp Phe Ile Ser His Cys Ala Thr
       1315                1320                1325

cag ggc tac cac att agc ccc agc agc tca tct cca ttc tgc cgg aat   4032
Gln Gly Tyr His Ile Ser Pro Ser Ser Ser Ser Pro Phe Cys Arg Asn
   1330                1335                1340

gcc gcc acc tcc ttg tct ctc ttc tac aac aac ggg gcc ctc cct tgt   4080
Ala Ala Thr Ser Leu Ser Leu Phe Tyr Asn Asn Gly Ala Leu Pro Cys
1345                1350                1355                1360

ggc tgc cac gag gtg ggt gcc gta agc ccc acg tgc gaa ccc ttc ggg   4128
Gly Cys His Glu Val Gly Ala Val Ser Pro Thr Cys Glu Pro Phe Gly
               1365                1370                1375

ggc cag tgt ccc tgc cgg ggc cac gtt att ggc cgt gac tgt tcc cgc   4176
Gly Gln Cys Pro Cys Arg Gly His Val Ile Gly Arg Asp Cys Ser Arg
           1380                1385                1390

tgt gcc acc ggc tac tgg ggt ttc ccc aac tgc agg ccc tgt gac tgt   4224
Cys Ala Thr Gly Tyr Trp Gly Phe Pro Asn Cys Arg Pro Cys Asp Cys
       1395                1400                1405

gga gcc cgc ctg tgt gac gag ctc acg ggc cag tgt atc tgt cca cca   4272
Gly Ala Arg Leu Cys Asp Glu Leu Thr Gly Gln Cys Ile Cys Pro Pro
   1410                1415                1420

cgc act gtt ccc cct gac tgc ttg gtc tgc cag cca cag agc ttt ggt   4320
Arg Thr Val Pro Pro Asp Cys Leu Val Cys Gln Pro Gln Ser Phe Gly
1425                1430                1435                1440

tgc cac ccc ttg gtg ggc tgt gag gag tgt aac tgc tca ggg ccc ggc   4368
Cys His Pro Leu Val Gly Cys Glu Glu Cys Asn Cys Ser Gly Pro Gly
               1445                1450                1455

gtc cag gag ctg acg gac cct acc tgt gac atg gac agc ggc cag tgc   4416
Val Gln Glu Leu Thr Asp Pro Thr Cys Asp Met Asp Ser Gly Gln Cys
           1460                1465                1470

aga tgc aga ccc aat gta gct gga cgt cgc tgt gat acc tgt gcc ccg   4464
Arg Cys Arg Pro Asn Val Ala Gly Arg Arg Cys Asp Thr Cys Ala Pro
       1475                1480                1485

ggc ttc tat ggc tat cct agc tgt cgc ccc tgt gac tgc cat gag gca   4512
Gly Phe Tyr Gly Tyr Pro Ser Cys Arg Pro Cys Asp Cys His Glu Ala
   1490                1495                1500

ggc acc atg gct agc gtg tgt gac ccc ctc aca ggc caa tgc cat tgc   4560
Gly Thr Met Ala Ser Val Cys Asp Pro Leu Thr Gly Gln Cys His Cys
1505                1510                1515                1520

aag gag aac gtg cag ggc tca aga tgt gac cag tgt cgc gtg ggg acc   4608
Lys Glu Asn Val Gln Gly Ser Arg Cys Asp Gln Cys Arg Val Gly Thr
               1525                1530                1535

ttc tcc ttg gat gct gct aac ccc aag ggc tgt acc cgc tgc ttc tgt   4656
Phe Ser Leu Asp Ala Ala Asn Pro Lys Gly Cys Thr Arg Cys Phe Cys
           1540                1545                1550

ttc ggg gcc aca gag cgc tgt ggg aac tct aac ctc gcc cgc cat gag   4704
Phe Gly Ala Thr Glu Arg Cys Gly Asn Ser Asn Leu Ala Arg His Glu
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      1555                1560                1565

ttc gtg gac atg gag ggc tgg gtg ctg ttg agc agt gac cgg cag gtg   4752
Phe Val Asp Met Glu Gly Trp Val Leu Leu Ser Ser Asp Arg Gln Val
   1570                1575                1580

gta ccc cac gag cat cgg cct gag ata gag ctg ctg cac gca gat ctg   4800
Val Pro His Glu His Arg Pro Glu Ile Glu Leu Leu His Ala Asp Leu
1585                1590                1595                1600

cgc tct gtg gct gac act ttc tca gag ctg tac tgg cag gct ccg ccc   4848
Arg Ser Val Ala Asp Thr Phe Ser Glu Leu Tyr Trp Gln Ala Pro Pro
               1605                1610                1615

tcc tat ctg gga gac agg gtg tca tcc tac ggt gga acc ctc cac tat   4896
Ser Tyr Leu Gly Asp Arg Val Ser Ser Tyr Gly Gly Thr Leu His Tyr
           1620                1625                1630

gag ctg cac tca gag acc cag cga ggt gat atc ttc att ccc tac gag   4944
Glu Leu His Ser Glu Thr Gln Arg Gly Asp Ile Phe Ile Pro Tyr Glu
       1635                1640                1645

agc cgg ccg gac gtc gtg ctg cag ggc aac caa atg agc atc gcc ttc   4992
Ser Arg Pro Asp Val Val Leu Gln Gly Asn Gln Met Ser Ile Ala Phe
   1650                1655                1660

ctg gaa ctg gcg tac cct ccg cct ggc cag gtt cac cga gga cag cta   5040
Leu Glu Leu Ala Tyr Pro Pro Pro Gly Gln Val His Arg Gly Gln Leu
1665                1670                1675                1680

cag ctg gta gag ggg aac ttc cgg cac ttg gag act cac aac ccc gtg   5088
Gln Leu Val Glu Gly Asn Phe Arg His Leu Glu Thr His Asn Pro Val
               1685                1690                1695

tcc cga gaa gaa ctc atg atg gtg ctg gcc ggc ctg gag cag ctg cag   5136
Ser Arg Glu Glu Leu Met Met Val Leu Ala Gly Leu Glu Gln Leu Gln
           1700                1705                1710

atc cgt gct ctc ttc tcg cag acc tct tcc agt gtc tcc ttg cgt aga   5184
Ile Arg Ala Leu Phe Ser Gln Thr Ser Ser Ser Val Ser Leu Arg Arg
       1715                1720                1725

gtg gta ctg gag gtg gct agc gag gct ggt agg ggg cct cca gcc agc   5232
Val Val Leu Glu Val Ala Ser Glu Ala Gly Arg Gly Pro Pro Ala Ser
   1730                1735                1740

aat gtg gaa ctg tgt atg tgc cct gcc aac tac cgt ggg gac tcg tgc   5280
Asn Val Glu Leu Cys Met Cys Pro Ala Asn Tyr Arg Gly Asp Ser Cys
1745                1750                1755                1760

cag gaa tgt gcc cct ggc tat tac cgg gac acc aag ggt ctc ttc cta   5328
Gln Glu Cys Ala Pro Gly Tyr Tyr Arg Asp Thr Lys Gly Leu Phe Leu
               1765                1770                1775

ggc cga tgt gtc ccc tgt cag tgc cat ggc cat tca gat cgc tgc ctt   5376
Gly Arg Cys Val Pro Cys Gln Cys His Gly His Ser Asp Arg Cys Leu
           1780                1785                1790

cct ggc tct ggc att tgt gtg ggc tgc cag cac aac aca gaa ggg gac   5424
Pro Gly Ser Gly Ile Cys Val Gly Cys Gln His Asn Thr Glu Gly Asp
       1795                1800                1805
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caa tgt gag cgc tgt agg cct ggc ttt gtc agc agt gat ccc agt aac   5472
Gln Cys Glu Arg Cys Arg Pro Gly Phe Val Ser Ser Asp Pro Ser Asn
   1810                1815                1820

cct gca tcc cca tgt gtg agc tgc cct tgc ccc ttg gca gtg ccc tcc   5520
Pro Ala Ser Pro Cys Val Ser Cys Pro Cys Pro Leu Ala Val Pro Ser
1825                1830                1835                1840

aat aat ttt gca gac ggt tgc gtc tta aga aat ggc cga acc cag tgc   5568
Asn Asn Phe Ala Asp Gly Cys Val Leu Arg Asn Gly Arg Thr Gln Cys
               1845                1850                1855

ctc tgc agg cca ggc tat gct ggt gcc tcc tgc gag cgg tgt gca cct   5616
Leu Cys Arg Pro Gly Tyr Ala Gly Ala Ser Cys Glu Arg Cys Ala Pro
          1860                1865                1870

ggc ttt ttt ggg aac ccc ctg gtg cta ggc agc tcc tgt cag ccc tgc   5664
Gly Phe Phe Gly Asn Pro Leu Val Leu Gly Ser Ser Cys Gln Pro Cys
       1875                1880                1885

gac tgc agc ggt aat gga gac ccc aac atg atc ttc agt gac tgc gac   5712
Asp Cys Ser Gly Asn Gly Asp Pro Asn Met Ile Phe Ser Asp Cys Asp
   1890                1895                1900

ccc ctg acg ggt gcc tgt cga ggc tgc ctc cgt cac acc act ggg ccc   5760
Pro Leu Thr Gly Ala Cys Arg Gly Cys Leu Arg His Thr Thr Gly Pro
1905                1910                1915                1920

cac tgt gaa cgc tgt gcc cca ggc ttc tat ggc aat gct ttg ttg cca   5808
His Cys Glu Arg Cys Ala Pro Gly Phe Tyr Gly Asn Ala Leu Leu Pro
               1925                1930                1935

ggc aac tgc acc cgg tgt gac tgt tcc cca tgt ggg aca gaa acc tgt   5856
Gly Asn Cys Thr Arg Cys Asp Cys Ser Pro Cys Gly Thr Glu Thr Cys
          1940                1945                1950

gat ccc cag agt gga cgc tgc ctg tgc aaa gca ggc gtg act gga caa   5904
Asp Pro Gln Ser Gly Arg Cys Leu Cys Lys Ala Gly Val Thr Gly Gln
       1955                1960                1965

cgt tgt gac cgc tgt ttg gaa gga tac ttc ggt ttt gag caa tgc cag   5952
Arg Cys Asp Arg Cys Leu Glu Gly Tyr Phe Gly Phe Glu Gln Cys Gln
   1970                1975                1980

ggc tgc cgc cct tgt gcc tgt gga cca gct gcc aag ggc tcc gag tgc   6000
Gly Cys Arg Pro Cys Ala Cys Gly Pro Ala Ala Lys Gly Ser Glu Cys
1985                1990                1995                2000

cac cct cag agc ggt cag tgt cac tgc cag cca ggg acc aca gga ccc   6048
His Pro Gln Ser Gly Gln Cys His Cys Gln Pro Gly Thr Thr Gly Pro
               2005                2010                2015

cag tgc ctc gag tgc gcc cct ggc tac tgg ggc ctc cca gag aag ggc   6096
Gln Cys Leu Glu Cys Ala Pro Gly Tyr Trp Gly Leu Pro Glu Lys Gly
          2020                2025                2030

tgc agg cgc tgc cag tgt ccc cga ggc cac tgt gac cca cac acg ggc   6144
Cys Arg Arg Cys Gln Cys Pro Arg Gly His Cys Asp Pro His Thr Gly
       2035                2040                2045
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cac tgc acc tgt ccc ccg ggg ctc agc ggg gaa cgc tgt gac acc tgc   6192
His Cys Thr Cys Pro Pro Gly Leu Ser Gly Glu Arg Cys Asp Thr Cys
   2050                2055                2060

agc cag cag cac cag gtg cct gta ccg ggc aag cct ggg ggc cat ggc   6240
Ser Gln Gln His Gln Val Pro Val Pro Gly Lys Pro Gly Gly His Gly
2065                2070                2075                2080

ata cac tgt gaa gtg tgt gac cac tgt gtg gtt ctc ctt ctg gat gac   6288
Ile His Cys Glu Val Cys Asp His Cys Val Val Leu Leu Leu Asp Asp
               2085                2090                2095

ctc gag cgg gct ggt gcc ctc ctc ccc gct atc cgt gag cag ctg cag   6336
Leu Glu Arg Ala Gly Ala Leu Leu Pro Ala Ile Arg Glu Gln Leu Gln
          2100                2105                2110

ggt atc aat gcc agc tcc gcg gcc tgg gcc agg ctg cac agg ctg aat   6384
Gly Ile Asn Ala Ser Ser Ala Ala Trp Ala Arg Leu His Arg Leu Asn
       2115                2120                2125

gcc tcc att gct gac ctg cag agt aaa ctc cgg agg cca ccg gga ccc   6432
Ala Ser Ile Ala Asp Leu Gln Ser Lys Leu Arg Arg Pro Pro Gly Pro
   2130                2135                2140

cgc tac cag gca gca cag cag cta cag act cta gag cag cag agt ata   6480
Arg Tyr Gln Ala Ala Gln Gln Leu Gln Thr Leu Glu Gln Gln Ser Ile
2145                2150                2155                2160

agc ctt caa cag gac acg gag agg ctg ggc agt cag gcc aca ggg gtc   6528
Ser Leu Gln Gln Asp Thr Glu Arg Leu Gly Ser Gln Ala Thr Gly Val
               2165                2170                2175

caa ggt cag gca ggc cag cta ctg gac acc aca gag tcc aca ctg ggc   6576
Gln Gly Gln Ala Gly Gln Leu Leu Asp Thr Thr Glu Ser Thr Leu Gly
          2180                2185                2190

cgg gca cag aag ttg ttg gag tct gtg cga gct gtg ggc cgt gcc ctg   6624
Arg Ala Gln Lys Leu Leu Glu Ser Val Arg Ala Val Gly Arg Ala Leu
       2195                2200                2205

aat gag ctg gca tct cgc atg ggc caa gga tct cca ggc gat gcc ttg   6672
Asn Glu Leu Ala Ser Arg Met Gly Gln Gly Ser Pro Gly Asp Ala Leu
   2210                2215                2220

gta ccg tct ggc gag cag ctg cgc tgg gct ctg gct gaa gtg gag cgg   6720
Val Pro Ser Gly Glu Gln Leu Arg Trp Ala Leu Ala Glu Val Glu Arg
2225                2230                2235                2240

ctg ctc tgg gat atg cgg acg cgt gac ctg ggg gcc cag ggg gca gtg   6768
Leu Leu Trp Asp Met Arg Thr Arg Asp Leu Gly Ala Gln Gly Ala Val
               2245                2250                2255

gca gag gcc gaa ctg gcc gaa gcc cag agg ctg atg gct cgt gtc cag   6816
Ala Glu Ala Glu Leu Ala Glu Ala Gln Arg Leu Met Ala Arg Val Gln
          2260                2265                2270

gag cag ctg acc agc ttc tgg gag gag aac cag tca ttg gcc aca cac   6864
Glu Gln Leu Thr Ser Phe Trp Glu Glu Asn Gln Ser Leu Ala Thr His
       2275                2280                2285

att cgg gac cag ctg gct cag tat gag tct ggc ctc atg gat ctt cgt   6912
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Ile Arg Asp Gln Leu Ala Gln Tyr Glu Ser Gly Leu Met Asp Leu Arg
   2290                2295                2300

gag gcc ctg aac cag gcc gtt aat acc acc cgg gag gct gag gaa ctc   6960
Glu Ala Leu Asn Gln Ala Val Asn Thr Thr Arg Glu Ala Glu Glu Leu
2305               2310                2315                2320

aac agc cgc aac cag gaa cgg gtg aag gaa gcc ctg caa tgg aaa cag   7008
Asn Ser Arg Asn Gln Glu Arg Val Lys Glu Ala Leu Gln Trp Lys Gln
               2325                2330                2335

gaa ctg tcc cag gac aat gcc acc ctg aag gcc act ctt caa gct gcc   7056
Glu Leu Ser Gln Asp Asn Ala Thr Leu Lys Ala Thr Leu Gln Ala Ala
           2340                2345                2350

agt ctc atc ttg ggc cat gtt tct gag ctt ctg cag ggc ata gac cag   7104
Ser Leu Ile Leu Gly His Val Ser Glu Leu Leu Gln Gly Ile Asp Gln
       2355                2360                2365

gct aag gag gac cta gag cac ctg gcg gcc agc ctg gat gga gcc tgg   7152
Ala Lys Glu Asp Leu Glu His Leu Ala Ala Ser Leu Asp Gly Ala Trp
   2370                2375                2380

aca ccc tta ctg aag agg atg cag gcc ttt tcc cct gcc agc agc aag   7200
Thr Pro Leu Leu Lys Arg Met Gln Ala Phe Ser Pro Ala Ser Ser Lys
2385               2390                2395                2400

gtg gac ttg gta gag gct gct gag gcc cac gct cag aag ctg aac cag   7248
Val Asp Leu Val Glu Ala Ala Glu Ala His Ala Gln Lys Leu Asn Gln
               2405                2410                2415

ctg gca atc aac ctg tct ggc atc atc ctt ggc atc aat cag gac cgc   7296
Leu Ala Ile Asn Leu Ser Gly Ile Ile Leu Gly Ile Asn Gln Asp Arg
           2420                2425                2430

ttc atc cag agg gct gtg gaa gcc tcc aat gcc tac agc agc atc ctt   7344
Phe Ile Gln Arg Ala Val Glu Ala Ser Asn Ala Tyr Ser Ser Ile Leu
       2435                2440                2445

cag gcc gtt cag gct gcc gag gat gcg gca ggc cag gca ctg agg cag   7392
Gln Ala Val Gln Ala Ala Glu Asp Ala Ala Gly Gln Ala Leu Arg Gln
   2450                2455                2460

gcc agc cgc aca tgg gag atg gtg gtg cag cgg ggc cta gca gct gga   7440
Ala Ser Arg Thr Trp Glu Met Val Val Gln Arg Gly Leu Ala Ala Gly
2465               2470                2475                2480

gcc cgg cag ctg tta gcc aac agc agt gcc ctg gag gag acc atc ctt   7488
Ala Arg Gln Leu Leu Ala Asn Ser Ser Ala Leu Glu Glu Thr Ile Leu
               2485                2490                2495

gga cac cag ggg agg ctg ggc ctt gct cag ggc cgt ctg cag gct gcg   7536
Gly His Gln Gly Arg Leu Gly Leu Ala Gln Gly Arg Leu Gln Ala Ala
           2500                2505                2510

ggg atc cag ctt cat aat gtc tgg gcc agg aag aac cag cta gca gcc   7584
Gly Ile Gln Leu His Asn Val Trp Ala Arg Lys Asn Gln Leu Ala Ala
       2515                2520                2525

cag atc cag gag gca caa gcc atg ctg gcc atg gac acg agc gag acc   7632
Gln Ile Gln Glu Ala Gln Ala Met Leu Ala Met Asp Thr Ser Glu Thr
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   2530                2535                2540

agt gag aag att gct cac gcc aag gct gtg gct gcc gaa gcc ctc agt   7680
Ser Glu Lys Ile Ala His Ala Lys Ala Val Ala Ala Glu Ala Leu Ser
2545              2550                2555                2560

acg gcc acc cac gtg cag tct cag ctt cag ggt atg cag aag aat gtg   7728
Thr Ala Thr His Val Gln Ser Gln Leu Gln Gly Met Gln Lys Asn Val
                2565                2570                2575

gag agg tgg cag agc cag ctg gga ggc ctg caa ggc cag gac ctg agc   7776
Glu Arg Trp Gln Ser Gln Leu Gly Gly Leu Gln Gly Gln Asp Leu Ser
           2580                2585                2590

cag gtg gaa cgg gat gca agc agt tca gtg tcc acc ctg gag aag aca   7824
Gln Val Glu Arg Asp Ala Ser Ser Ser Val Ser Thr Leu Glu Lys Thr
       2595                2600                2605

ttg cca cag ctg ctg gcc aaa ctg agc cgt cta gag aac cgt gga gtt   7872
Leu Pro Gln Leu Leu Ala Lys Leu Ser Arg Leu Glu Asn Arg Gly Val
   2610                2615                2620

cac aat gcc agc ctg gct ttg tct gcc aac att ggt cgt gtg cgc aag   7920
His Asn Ala Ser Leu Ala Leu Ser Ala Asn Ile Gly Arg Val Arg Lys
2625                2630                2635                2640

ctc att gcc caa gcc cgg agt gcc gcc agc aag gtc aag gtg tcc atg   7968
Leu Ile Ala Gln Ala Arg Ser Ala Ala Ser Lys Val Lys Val Ser Met
                2645                2650                2655

aag ttc aat ggg cgt tca ggg gta cga ctg cgt ccc cca cga gac ctt   8016
Lys Phe Asn Gly Arg Ser Gly Val Arg Leu Arg Pro Pro Arg Asp Leu
           2660                2665                2670

gcc gac ctt gct gcg tac act gcc ctc aag ttc cac atc cag agc cca   8064
Ala Asp Leu Ala Ala Tyr Thr Ala Leu Lys Phe His Ile Gln Ser Pro
       2675                2680                2685

gtg cca gcg ccc gaa cct ggc aag aac acg ggg gac cac ttt gtt ctg   8112
Val Pro Ala Pro Glu Pro Gly Lys Asn Thr Gly Asp His Phe Val Leu
   2690                2695                2700

tac atg ggc agc cgc cag gcc act ggg gac tac atg gga gtg tct ctg   8160
Tyr Met Gly Ser Arg Gln Ala Thr Gly Asp Tyr Met Gly Val Ser Leu
2705                2710                2715                2720

cgt aat cag aag gtg cac tgg gtg tac agg cta gga aag gct ggc ccc   8208
Arg Asn Gln Lys Val His Trp Val Tyr Arg Leu Gly Lys Ala Gly Pro
                2725                2730                2735

aca act ctc agc atc gac gag aac atc ggg gag cag ttt gca gcc gtc   8256
Thr Thr Leu Ser Ile Asp Glu Asn Ile Gly Glu Gln Phe Ala Ala Val
           2740                2745                2750

agc atc gac agg acc ctc cag ttt ggc cac atg tct gtc acc gtg gag   8304
Ser Ile Asp Arg Thr Leu Gln Phe Gly His Met Ser Val Thr Val Glu
       2755                2760                2765

aaa cag atg gtt cat gag atc aag gga gac acg gtg gcc cct ggg agc   8352
Lys Gln Met Val His Glu Ile Lys Gly Asp Thr Val Ala Pro Gly Ser
   2770                2775                2780
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gag gga cta ctc aac ctg cat cct gac gat ttt gtc ttc tac gtg gga   8400
Glu Gly Leu Leu Asn Leu His Pro Asp Asp Phe Val Phe Tyr Val Gly
2785                2790                2795                2800

gga tac ccc agc aac ttc acg ccc cct gaa ccc ctc cga ttc cct ggc   8448
Gly Tyr Pro Ser Asn Phe Thr Pro Pro Glu Pro Leu Arg Phe Pro Gly
                2805                2810                2815

tac ctg ggc tgc att gag atg gaa aca ctg aat gag gag gtg gtc agc   8496
Tyr Leu Gly Cys Ile Glu Met Glu Thr Leu Asn Glu Glu Val Val Ser
            2820                2825                2830

ctc tac aat ttt gag cag acc ttc atg ctg gac acg gca gta gat aaa   8544
Leu Tyr Asn Phe Glu Gln Thr Phe Met Leu Asp Thr Ala Val Asp Lys
        2835                2840                2845

cct tgt gct cgc tcc aag gcc acc ggt gac cca tgg ctc aca gat ggc   8592
Pro Cys Ala Arg Ser Lys Ala Thr Gly Asp Pro Trp Leu Thr Asp Gly
    2850                2855                2860

tcc tac ctg gat ggc agt ggc ttt gcc cgc atc agc ttt gag aag cag   8640
Ser Tyr Leu Asp Gly Ser Gly Phe Ala Arg Ile Ser Phe Glu Lys Gln
2865                2870                2875                2880

ttc agc aac aca aaa cgc ttt gac cag gag ctg cgg ctt gtg tcc tac   8688
Phe Ser Asn Thr Lys Arg Phe Asp Gln Glu Leu Arg Leu Val Ser Tyr
                2885                2890                2895

aat ggg atc atc ttt ttc ctc aag caa gag agc cag ttc ttg tgc ctg   8736
Asn Gly Ile Ile Phe Phe Leu Lys Gln Glu Ser Gln Phe Leu Cys Leu
            2900                2905                2910

gca gtg cag gaa ggc acc ctg gtg ctc ttc tat gac ttc ggc tct ggc   8784
Ala Val Gln Glu Gly Thr Leu Val Leu Phe Tyr Asp Phe Gly Ser Gly
        2915                2920                2925

ctg aag aag gcc gac cca ctg cag ccc cca caa gcc ttg acg gca gcc   8832
Leu Lys Lys Ala Asp Pro Leu Gln Pro Pro Gln Ala Leu Thr Ala Ala
    2930                2935                2940

agc aag gcg atc caa gtg ttt cta ttg gct ggc aat cgc aaa cgt gtg   8880
Ser Lys Ala Ile Gln Val Phe Leu Leu Ala Gly Asn Arg Lys Arg Val
2945                2950                2955                2960

ttg gtg cgt gtg gag cgg gcc act gtg ttc agc gta gac cag gat aac   8928
Leu Val Arg Val Glu Arg Ala Thr Val Phe Ser Val Asp Gln Asp Asn
                2965                2970                2975

atg ctg gag atg gct gat gcc tac tac ttg gga ggd gtg cca cct gaa   8976
Met Leu Glu Met Ala Asp Ala Tyr Tyr Leu Gly Gly Val Pro Pro Glu
            2980                2985                2990

cag ctg ccc ttg agc cta cgg cag ctc ttc ccc tcc gga ggc tct gtc   9024
Gln Leu Pro Leu Ser Leu Arg Gln Leu Phe Pro Ser Gly Gly Ser Val
        2995                3000                3005

cgt ggy tgc atc aag ggt att aag gct ctg ggc aag tac gtg gac ctc   9072
Arg Gly Cys Ile Lys Gly Ile Lys Ala Leu Gly Lys Tyr Val Asp Leu
    3010                3015                3020
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aaa cgg ttg aac acc acg ggc atc agt ttc ggc tgc acc gct gac ctg   9120
Lys Arg Leu Asn Thr Thr Gly Ile Ser Phe Gly Cys Thr Ala Asp Leu
3025              3030                3035                3040

cta gtg gga cgc acc atg act ttt cac ggc cac ggc ttc ctg ccc ctg   9168
Leu Val Gly Arg Thr Met Thr Phe His Gly His Gly Phe Leu Pro Leu
                3045                3050                3055

gca ctt cct gat gtg gca ccc atc acc gaa gtg gtc tat tct ggc ttt   9216
Ala Leu Pro Asp Val Ala Pro Ile Thr Glu Val Val Tyr Ser Gly Phe
           3060                3065                3070

ggc ttt cgt ggc acc cag gac aac aac ctg ctg tat tac cgt acc tcc   9264
Gly Phe Arg Gly Thr Gln Asp Asn Asn Leu Leu Tyr Tyr Arg Thr Ser
       3075                3080                3085

ccg gat ggg ccg tac cag gta tcc ctg agg gag ggc cac gtg aca ctc   9312
Pro Asp Gly Pro Tyr Gln Val Ser Leu Arg Glu Gly His Val Thr Leu
   3090                3095                3100

cgt ttt atg aac caa gag gtg gaa act caa agg gtc ttt gct gat ggt   9360
Arg Phe Met Asn Gln Glu Val Glu Thr Gln Arg Val Phe Ala Asp Gly
3105              3110                3115                3120

gct cct cac tat gtt gcc ttc tat agc aat gtc aca ggg gta tgg ctg   9408
Ala Pro His Tyr Val Ala Phe Tyr Ser Asn Val Thr Gly Val Trp Leu
                3125                3130                3135

tat gtg gat gac cag cta caa cta gta aag tct cat gag aga aca act   9456
Tyr Val Asp Asp Gln Leu Gln Leu Val Lys Ser His Glu Arg Thr Thr
           3140                3145                3150

ccc atg ctc caa cta cag ccc gag gaa ccc tca cgg ctt ctc ctg gga   9504
Pro Met Leu Gln Leu Gln Pro Glu Glu Pro Ser Arg Leu Leu Leu Gly
       3155                3160                3165

ggc ctg cct gtg tct ggt acc ttc cac aac ttc agt ggc tgc atc agc   9552
Gly Leu Pro Val Ser Gly Thr Phe His Asn Phe Ser Gly Cys Ile Ser
   3170                3175                3180

aat gtt ttt gta cag cga ctt cgg gga cca cag cgt gtg ttt gac cta   9600
Asn Val Phe Val Gln Arg Leu Arg Gly Pro Gln Arg Val Phe Asp Leu
3185              3190                3195                3200

cac cag aac atg ggg agt gtc aat gta agc gta ggc tgt aca cca gcc   9648
His Gln Asn Met Gly Ser Val Asn Val Ser Val Gly Cys Thr Pro Ala
                3205                3210                3215

caa ctc atc gag acc tca agg gcc acg gct cag aag gtt tcc cgc cgt   9696
Gln Leu Ile Glu Thr Ser Arg Ala Thr Ala Gln Lys Val Ser Arg Arg
           3220                3225                3230

agt cga caa ccc agc cag gac ctt gcc tgc acg aca ccc tgg ctc cct   9744
Ser Arg Gln Pro Ser Gln Asp Leu Ala Cys Thr Thr Pro Trp Leu Pro
       3235                3240                3245

ggg act att cag gat gca tac cag ttt ggg gga ccc ctg ccc agt tac   9792
Gly Thr Ile Gln Asp Ala Tyr Gln Phe Gly Gly Pro Leu Pro Ser Tyr
   3250                3255                3260

cta cag ttt gtg ggt atc tct ccg tcc cac agg aat agg ctc cac ctc   9840
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Leu Gln Phe Val Gly Ile Ser Pro Ser His Arg Asn Arg Leu His Leu
3265                3270                3275                3280

tcc atg ctt gtc cgt cca cat gcg gct tcc cag ggc ctc ctg ctc tct   9888
Ser Met Leu Val Arg Pro His Ala Ala Ser Gln Gly Leu Leu Leu Ser
                3285                3290                3295

aca gcc ccc atg tcg ggc cgc agc cct tcg ttg gta ctc ttt cta aac   9936
Thr Ala Pro Met Ser Gly Arg Ser Pro Ser Leu Val Leu Phe Leu Asn
            3300                3305                3310

cat gga cac ttt gtc gca cag act gag ggc cct ggg ccc cgg ctc cag   9984
His Gly His Phe Val Ala Gln Thr Glu Gly Pro Gly Pro Arg Leu Gln
        3315                3320                3325

gtc cag agt cgc cag cac tca cgg gct ggc cag tgg cac agg gtg tcc   10032
Val Gln Ser Arg Gln His Ser Arg Ala Gly Gln Trp His Arg Val Ser
    3330                3335                3340

gtc cgc tgg gga atg cag cag atc cag ctt gtg gtg gac ggc agc cag   10080
Val Arg Trp Gly Met Gln Gln Ile Gln Leu Val Val Asp Gly Ser Gln
3345                3350                3355                3360

acc tgg agc cag aag gct ctc cac cat cgg gtc ccc agg gca gag cga   10128
Thr Trp Ser Gln Lys Ala Leu His His Arg Val Pro Arg Ala Glu Arg
                3365                3370                3375

cca cag ccc tac acc ctc tct gta gga ggt ctt cct gcc agc agt tac   10176
Pro Gln Pro Tyr Thr Leu Ser Val Gly Gly Leu Pro Ala Ser Ser Tyr
            3380                3385                3390

agt tcc aag ctc cct gtg tct gtg ggg ttc agc ggc tgt ctg aag aaa   10224
Ser Ser Lys Leu Pro Val Ser Val Gly Phe Ser Gly Cys Leu Lys Lys
        3395                3400                3405

tta cag ctg gat aag cag cca ctg agg acc cca acg caa atg gtg ggg   10272
Leu Gln Leu Asp Lys Gln Pro Leu Arg Thr Pro Thr Gln Met Val Gly
    3410                3415                3420

gtc aca ccc tgt gtc tca ggc ccc ctg gaa gat ggc ctg ttc ttc cca   10320
Val Thr Pro Cys Val Ser Gly Pro Leu Glu Asp Gly Leu Phe Phe Pro
3425                3430                3435                3440

ggc agt gag gga gtt gtc aca tta gag ctc ccc aag gcc aag atg ccc   10368
Gly Ser Glu Gly Val Val Thr Leu Glu Leu Pro Lys Ala Lys Met Pro
                3445                3450                3455

tat gtg agc ctg gag cta gag atg cgg ccc ttg gca gct gct ggc ctc   10416
Tyr Val Ser Leu Glu Leu Glu Met Arg Pro Leu Ala Ala Ala Gly Leu
            3460                3465                3470

atc ttc cac ctg ggc cag gcc ctg gcc act ccc tac atg cag ctg aag   10464
Ile Phe His Leu Gly Gln Ala Leu Ala Thr Pro Tyr Met Gln Leu Lys
        3475                3480                3485

gtg ctg aca gaa cag gtc ctg ctg cag gca aat gat ggg gca ggg gag   10512
Val Leu Thr Glu Gln Val Leu Leu Gln Ala Asn Asp Gly Ala Gly Glu
    3490                3495                3500

ttt tcc acg tgg gtg acc tac ccc aag ctt tgt gat gga cgg tgg cac   10560
Phe Ser Thr Trp Val Thr Tyr Pro Lys Leu Cys Asp Gly Arg Trp His
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3505                3510                3515                3520

cga gtg gca gtg atc atg ggc agg gac aca ctc cgg ctg gag gta gac   10608
Arg Val Ala Val Ile Met Gly Arg Asp Thr Leu Arg Leu Glu Val Asp
                3525                3530                3535

aca cag agc aac cac acc aca ggc cgt ttg cca gag agc ttg gct ggt   10656
Thr Gln Ser Asn His Thr Thr Gly Arg Leu Pro Glu Ser Leu Ala Gly
            3540                3545                3550

tct cca gca ctt ctg cac ctc ggg agc ctg ccc aag tct tca act gct   10704
Ser Pro Ala Leu Leu His Leu Gly Ser Leu Pro Lys Ser Ser Thr Ala
        3555                3560                3565

cgg cca gag ctc cct gcc tac cga gga tgc ttg agg aag ctg ctg atc   10752
Arg Pro Glu Leu Pro Ala Tyr Arg Gly Cys Leu Arg Lys Leu Leu Ile
    3570                3575                3580

aat ggg gcc cct gtc aac gtg act gct tct gta caa atc cag ggg gca   10800
Asn Gly Ala Pro Val Asn Val Thr Ala Ser Val Gln Ile Gln Gly Ala
3585                3590                3595                3600

gtg ggg atg cgc gga tgc ccc tca gga acc cta gca ctt tcc aag cag   10848
Val Gly Met Arg Gly Cys Pro Ser Gly Thr Leu Ala Leu Ser Lys Gln
                3605                3610                3615

gga aag gca ctg acc cag agg cac gcc aag ccc agt gtc tcc ccg cta   10896
Gly Lys Ala Leu Thr Gln Arg His Ala Lys Pro Ser Val Ser Pro Leu
            3620                3625                3630

ctt tgg cat tgagggttcc cagaccttgg ggtttgccta cactttctat          10945
Leu Trp His
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gaataacaag tcatttctgg tttacactgt cttttagagg aaaaggactc tgtagaacag 11005

atat                                                              11009


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

Trp Trp Gln Ser Pro Pro Leu Ser Arg Gly Leu Glu Tyr Asn Glu Val
     50                  55                  60

Asn Val Thr Leu Asp Leu Gly Gln Val Phe His Val Ala Tyr Val Leu
 65                  70                  75                  80

Ile Lys Phe Ala Asn Ser Pro Arg Pro Asp Leu Trp Val Leu Glu Arg
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                85                  90                  95

Ser Thr Asp Phe Gly His Thr Tyr Gln Pro Trp Gln Phe Phe Ala Ser
            100                 105                 110

Ser Lys Arg Asp Cys Leu Glu Arg Phe Gly Pro Arg Thr Leu Glu Arg
        115                 120                 125

Ile Thr Gln Asp Asp Asp Val Ile Cys Thr Thr Glu Tyr Ser Arg Ile
    130                 135                 140

Val Pro Leu Glu Asn Gly Glu Ile Val Val Ser Leu Val Asn Gly Arg
145                 150                 155                 160

Pro Gly Ala Leu Asn Phe Ser Tyr Ser Pro Leu Leu Arg Asp Phe Thr
                165                 170                 175

Lys Ala Thr Asn Ile Arg Leu Arg Phe Leu Arg Thr Asn Thr Leu Leu
            180                 185                 190

Gly His Leu Met Gly Lys Ala Leu Arg Asp Pro Thr Val Thr Arg Arg
        195                 200                 205

Tyr Tyr Tyr Ser Ile Lys Asp Ile Ser Ile Gly Gly Arg Cys Val Cys
    210                 215                 220

His Gly His Ala Asp Val Cys Asp Ala Lys Asp Pro Leu Asp Pro Phe
225                 230                 235                 240

Arg Leu Gln Cys Ala Cys Gln His Asn Thr Cys Gly Gly Ser Cys Asp
                245                 250                 255

Arg Cys Cys Pro Gly Phe Asn Gln Gln Pro Trp Lys Pro Ala Thr Thr
            260                 265                 270

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

Asp Cys Tyr Tyr Asp Pro Glu Val Asp Arg Arg Asn Ala Ser Gln Asn
    290                 295                 300

Gln Asp Asn Val Tyr Gln Gly Gly Gly Val Cys Leu Asp Cys Gln His
305                 310                 315                 320

His Thr Thr Gly Ile Asn Cys Glu Arg Cys Leu Pro Gly Phe Phe Arg
                325                 330                 335

Ala Pro Asp Gln Pro Leu Asp Ser Pro His Val Cys Arg Pro Cys Asp
            340                 345                 350

Cys Glu Ser Asp Phe Thr Asp Gly Thr Cys Glu Asp Leu Thr Gly Arg
        355                 360                 365

Cys Tyr Cys Arg Pro Asn Phe Thr Gly Glu Leu Cys Ala Ala Cys Ala
    370                 375                 380

Glu Gly Tyr Thr Asp Phe Pro His Cys Tyr Pro Leu Pro Ser Phe Pro
385                 390                 395                 400

His Asn Asp Thr Arg Glu Gln Val Leu Pro Ala Gly Gln Ile Val Asn
                405                 410                 415
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Cys Asp Cys Asn Ala Ala Gly Thr Gln Gly Asn Ala Cys Arg Lys Asp
            420                 425                 430

Pro Arg Leu Gly Arg Cys Val Cys Lys Pro Asn Phe Arg Gly Ala His
        435                 440                 445

Cys Glu Leu Cys Ala Pro Gly Phe His Gly Pro Ser Cys His Pro Cys
    450                 455                 460

Gln Cys Ser Ser Pro Gly Val Ala Asn Ser Leu Cys Asp Pro Glu Ser
465                 470                 475                 480

Gly Gln Cys Met Cys Arg Thr Gly Phe Glu Gly Asp Arg Cys Asp His
                485                 490                 495

Cys Ala Leu Gly Tyr Phe His Phe Pro Leu Cys Gln Leu Cys Gly Cys
            500                 505                 510

Ser Pro Ala Gly Thr Leu Pro Glu Gly Cys Asp Glu Ala Gly Arg Cys
        515                 520                 525

Gln Cys Arg Pro Gly Phe Asp Gly Pro His Cys Asp Arg Cys Leu Pro
    530                 535                 540

Gly Tyr His Gly Tyr Pro Asp Cys His Ala Cys Ala Cys Asp Pro Arg
545                 550                 555                 560

Gly Ala Leu Asp Gln Gln Cys Gly Val Gly Gly Leu Cys His Cys Arg
                565                 570                 575

Pro Gly Asn Thr Gly Ala Thr Cys Gln Glu Cys Ser Pro Gly Phe Tyr
            580                 585                 590

Gly Phe Pro Ser Cys Ile Pro Cys His Cys Ser Ala Asp Gly Ser Leu
        595                 600                 605

His Thr Thr Cys Asp Pro Thr Thr Gly Gln Cys Arg Cys Arg Pro Arg
    610                 615                 620

Val Thr Gly Leu His Cys Asp Met Cys Val Pro Gly Ala Tyr Asn Phe
625                 630                 635                 640

Pro Tyr Cys Glu Ala Gly Ser Cys His Pro Ala Gly Leu Ala Pro Ala
                645                 650                 655

Asn Pro Ala Leu Pro Glu Thr Gln Ala Pro Cys Met Cys Arg Ala His
            660                 665                 670

Val Glu Gly Pro Ser Cys Asp Arg Cys Lys Pro Gly Tyr Trp Gly Leu
        675                 680                 685

Ser Ala Ser Asn Pro Glu Gly Cys Thr Arg Cys Ser Cys Asp Pro Arg
    690                 695                 700

Gly Thr Leu Gly Gly Val Thr Glu Cys Gln Gly Asn Gly Gln Cys Phe
705                 710                 715                 720

Cys Lys Ala His Val Cys Gly Lys Thr Cys Ala Ala Cys Lys Asp Gly
                725                 730                 735
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Phe Phe Gly Leu Asp Tyr Ala Asp Tyr Phe Gly Cys Arg Ser Cys Arg
            740                 745                 750

Cys Asp Val Gly Gly Ala Leu Gly Gln Gly Cys Glu Pro Lys Thr Gly
        755                 760                 765

Ala Cys Arg Cys Arg Pro Asn Thr Gln Gly Pro Thr Cys Ser Glu Pro
    770                 775                 780

Ala Lys Asp His Tyr Leu Pro Asp Leu His His Met Arg Leu Glu Leu
785                 790                 795                 800

Glu Glu Ala Ala Thr Pro Glu Gly His Ala Val Arg Phe Gly Phe Asn
                805                 810                 815

Pro Leu Glu Phe Glu Asn Phe Ser Trp Arg Gly Tyr Ala His Met Met
            820                 825                 830

Ala Ile Gln Pro Arg Ile Val Ala Arg Leu Asn Val Thr Ser Pro Asp
        835                 840                 845

Leu Phe Arg Leu Val Phe Arg Tyr Val Asn Arg Gly Ser Thr Ser Val
    850                 855                 860

Asn Gly Gln Ile Ser Val Arg Glu Glu Gly Lys Leu Ser Ser Cys Thr
865                 870                 875                 880

Asn Cys Thr Glu Gln Ser Gln Pro Val Ala Phe Pro Pro Ser Thr Glu
                885                 890                 895

Pro Ala Phe Val Thr Val Pro Gln Arg Gly Phe Gly Glu Pro Phe Val
            900                 905                 910

Leu Asn Pro Gly Ile Trp Ala Leu Leu Val Glu Ala Glu Gly Val Leu
        915                 920                 925

Leu Asp Tyr Val Val Leu Leu Pro Ser Thr Tyr Tyr Glu Ala Ala Leu
    930                 935                 940

Leu Gln His Arg Val Thr Glu Ala Cys Thr Tyr Arg Pro Ser Ala Leu
945                 950                 955                 960

His Ser Thr Glu Asn Cys Leu Val Tyr Ala His Leu Pro Leu Asp Gly
                965                 970                 975

Phe Pro Ser Ala Ala Gly Thr Glu Ala Leu Cys Arg His Asp Asn Ser
            980                 985                 990

Leu Pro Arg Pro Cys Pro Thr Glu Gln Leu Ser Pro Ser His Pro Pro
        995                1000                1005

Leu Ala Thr Cys Phe Gly Ser Asp Val Asp Ile Gln Leu Glu Met Ala
   1010                1015                1020

Val Pro Gln Pro Gly Gln Tyr Val Leu Val Val Glu Tyr Val Gly Glu
1025                1030                1035                1040

Asp Ser His Gln Glu Met Gly Val Ala Val His Thr Pro Gln Arg Ala
                1045                1050                1055

Pro Gln Gln Gly Val Leu Asn Leu His Pro Cys Pro Tyr Ser Ser Leu
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          1060                1065                1070

Cys Arg Ser Pro Ala Arg Asp Thr Gln His His Leu Ala Ile Phe His
       1075                1080                1085

Leu Asp Ser Glu Ala Ser Ile Arg Leu Thr Ala Glu Gln Ala His Phe
   1090                1095                1100

Phe Leu His Ser Val Thr Leu Val Pro Val Glu Glu Phe Ser Thr Glu
1105                1110                1115                1120

Phe Val Glu Pro Arg Val Phe Cys Val Ser Ser His Gly Thr Phe Asn
               1125                1130                1135

Pro Ser Ser Ala Ala Cys Leu Ala Ser Arg Phe Pro Lys Pro Pro Gln
           1140                1145                1150

Pro Ile Ile Leu Lys Asp Cys Gln Val Leu Pro Leu Pro Pro Asp Leu
       1155                1160                1165

Pro Leu Thr Gln Ser Gln Glu Leu Ser Pro Gly Ala Pro Pro Glu Gly
   1170                1175                1180

Pro Gln Pro Arg Pro Pro Thr Ala Val Asp Pro Asn Ala Glu Pro Thr
1185                1190                1195                1200

Leu Leu Arg His Pro Gln Gly Thr Val Val Phe Thr Thr Gln Val Pro
               1205                1210                1215

Thr Leu Gly Arg Tyr Ala Phe Leu Leu His Gly Tyr Gln Pro Val His
           1220                1225                1230

Pro Ser Phe Pro Val Glu Val Leu Ile Asn Gly Gly Arg Ile Trp Gln
       1235                1240                1245

Gly His Ala Asn Ala Ser Phe Cys Pro His Gly Tyr Gly Cys Arg Thr
   1250                1255                1260

Leu Val Leu Cys Glu Gly Gln Thr Met Leu Asp Val Thr Asp Asn Glu
1265                1270                1275                1280

Leu Thr Val Thr Val Arg Val Pro Glu Gly Arg Trp Leu Trp Leu Asp
               1285                1290                1295

Tyr Val Leu Ile Val Pro Glu Asp Ala Tyr Ser Ser Ser Tyr Leu Gln
           1300                1305                1310

Glu Glu Pro Leu Asp Lys Ser Tyr Asp Phe Ile Ser His Cys Ala Thr
       1315                1320                1325

Gln Gly Tyr His Ile Ser Pro Ser Ser Ser Ser Pro Phe Cys Arg Asn
   1330                1335                1340

Ala Ala Thr Ser Leu Ser Leu Phe Tyr Asn Asn Gly Ala Leu Pro Cys
1345                1350                1355                1360

Gly Cys His Glu Val Gly Ala Val Ser Pro Thr Cys Glu Pro Phe Gly
               1365                1370                1375

Gly Gln Cys Pro Cys Arg Gly His Val Ile Gly Arg Asp Cys Ser Arg
           1380                1385                1390
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Cys Ala Thr Gly Tyr Trp Gly Phe Pro Asn Cys Arg Pro Cys Asp Cys
       1395                1400                1405

Gly Ala Arg Leu Cys Asp Glu Leu Thr Gly Gln Cys Ile Cys Pro Pro
   1410                1415                1420

Arg Thr Val Pro Pro Asp Cys Leu Val Cys Gln Pro Gln Ser Phe Gly
1425                1430                1435                1440

Cys His Pro Leu Val Gly Cys Glu Glu Cys Asn Cys Ser Gly Pro Gly
               1445                1450                1455

Val Gln Glu Leu Thr Asp Pro Thr Cys Asp Met Asp Ser Gly Gln Cys
           1460                1465                1470

Arg Cys Arg Pro Asn Val Ala Gly Arg Arg Cys Asp Thr Cys Ala Pro
       1475                1480                1485

Gly Phe Tyr Gly Tyr Pro Ser Cys Arg Pro Cys Asp Cys His Glu Ala
   1490                1495                1500

Gly Thr Met Ala Ser Val Cys Asp Pro Leu Thr Gly Gln Cys His Cys
1505                1510                1515                1520

Lys Glu Asn Val Gln Gly Ser Arg Cys Asp Gln Cys Arg Val Gly Thr
               1525                1530                1535

Phe Ser Leu Asp Ala Ala Asn Pro Lys Gly Cys Thr Arg Cys Phe Cys
           1540                1545                1550

Phe Gly Ala Thr Glu Arg Cys Gly Asn Ser Asn Leu Ala Arg His Glu
       1555                1560                1565

Phe Val Asp Met Glu Gly Trp Val Leu Leu Ser Ser Asp Arg Gln Val
   1570                1575                1580

Val Pro His Glu His Arg Pro Glu Ile Glu Leu Leu His Ala Asp Leu
1585                1590                1595                1600

Arg Ser Val Ala Asp Thr Phe Ser Glu Leu Tyr Trp Gln Ala Pro Pro
               1605                1610                1615

Ser Tyr Leu Gly Asp Arg Val Ser Ser Tyr Gly Gly Thr Leu His Tyr
           1620                1625                1630

Glu Leu His Ser Glu Thr Gln Arg Gly Asp Ile Phe Ile Pro Tyr Glu
       1635                1640                1645

Ser Arg Pro Asp Val Val Leu Gln Gly Asn Gln Met Ser Ile Ala Phe
   1650                1655                1660

Leu Glu Leu Ala Tyr Pro Pro Pro Gly Gln Val His Arg Gly Gln Leu
1665                1670                1675                1680

Gln Leu Val Glu Gly Asn Phe Arg His Leu Glu Thr His Asn Pro Val
               1685                1690                1695

Ser Arg Glu Glu Leu Met Met Val Leu Ala Gly Leu Glu Gln Leu Gln
           1700                1705                1710
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Ile Arg Ala Leu Phe Ser Gln Thr Ser Ser Ser Val Ser Leu Arg Arg
1715 1720 1725

Val Val Leu Glu Val Ala Ser Glu Ala Gly Arg Gly Pro Pro Ala Ser
1730 1735 1740

Asn Val Glu Leu Cys Met Cys Pro Ala Asn Tyr Arg Gly Asp Ser Cys
1745 1750 1755 1760

Gln Glu Cys Ala Pro Gly Tyr Tyr Arg Asp Thr Lys Gly Leu Phe Leu
1765 1770 1775

Gly Arg Cys Val Pro Cys Gln Cys His Gly His Ser Asp Arg Cys Leu
1780 1785 1790

Pro Gly Ser Gly Ile Cys Val Gly Cys Gln His Asn Thr Glu Gly Asp
1795 1800 1805

Gln Cys Glu Arg Cys Arg Pro Gly Phe Val Ser Ser Asp Pro Ser Asn
1810 1815 1820

Pro Ala Ser Pro Cys Val Ser Cys Pro Cys Pro Leu Ala Val Pro Ser
1825 1830 1835 1840

Asn Asn Phe Ala Asp Gly Cys Val Leu Arg Asn Gly Arg Thr Gln Cys
1845 1850 1855

Leu Cys Arg Pro Gly Tyr Ala Gly Ala Ser Cys Glu Arg Cys Ala Pro
1860 1865 1870

Gly Phe Phe Gly Asn Pro Leu Val Leu Gly Ser Ser Cys Gln Pro Cys
1875 1880 1885

Asp Cys Ser Gly Asn Gly Asp Pro Asn Met Ile Phe Ser Asp Cys Asp
1890 1895 1900

Pro Leu Thr Gly Ala Cys Arg Gly Cys Leu Arg His Thr Thr Gly Pro
1905 1910 1915 1920

His Cys Glu Arg Cys Ala Pro Gly Phe Tyr Gly Asn Ala Leu Leu Pro
1925 1930 1935

Gly Asn Cys Thr Arg Cys Asp Cys Ser Pro Cys Gly Thr Glu Thr Cys
1940 1945 1950

Asp Pro Gln Ser Gly Arg Cys Leu Cys Lys Ala Gly Val Thr Gly Gln
1955 1960 1965

Arg Cys Asp Arg Cys Leu Glu Gly Tyr Phe Gly Phe Glu Gln Cys Gln
1970 1975 1980

Gly Cys Arg Pro Cys Ala Cys Gly Pro Ala Ala Lys Gly Ser Glu Cys
1985 1990 1995 2000

His Pro Gln Ser Gly Gln Cys His Cys Gln Pro Gly Thr Thr Gly Pro
2005 2010 2015

Gln Cys Leu Glu Cys Ala Pro Gly Tyr Trp Gly Leu Pro Glu Lys Gly
2020 2025 2030

Cys Arg Arg Cys Gln Cys Pro Arg Gly His Cys Asp Pro His Thr Gly

```
      2035                2040                2045

His Cys Thr Cys Pro Pro Gly Leu Ser Gly Glu Arg Cys Asp Thr Cys
   2050                2055                2060

Ser Gln Gln His Gln Val Pro Val Pro Gly Lys Pro Gly Gly His Gly
2065                2070                2075                2080

Ile His Cys Glu Val Cys Asp His Cys Val Val Leu Leu Leu Asp Asp
               2085                2090                2095

Leu Glu Arg Ala Gly Ala Leu Leu Pro Ala Ile Arg Glu Gln Leu Gln
           2100                2105                2110

Gly Ile Asn Ala Ser Ser Ala Ala Trp Ala Arg Leu His Arg Leu Asn
       2115                2120                2125

Ala Ser Ile Ala Asp Leu Gln Ser Lys Leu Arg Arg Pro Pro Gly Pro
   2130                2135                2140

Arg Tyr Gln Ala Ala Gln Gln Leu Gln Thr Leu Glu Gln Gln Ser Ile
2145                2150                2155                2160

Ser Leu Gln Gln Asp Thr Glu Arg Leu Gly Ser Gln Ala Thr Gly Val
               2165                2170                2175

Gln Gly Gln Ala Gly Gln Leu Leu Asp Thr Thr Glu Ser Thr Leu Gly
           2180                2185                2190

Arg Ala Gln Lys Leu Leu Glu Ser Val Arg Ala Val Gly Arg Ala Leu
       2195                2200                2205

Asn Glu Leu Ala Ser Arg Met Gly Gln Gly Ser Pro Gly Asp Ala Leu
   2210                2215                2220

Val Pro Ser Gly Glu Gln Leu Arg Trp Ala Leu Ala Glu Val Glu Arg
2225                2230                2235                2240

Leu Leu Trp Asp Met Arg Thr Arg Asp Leu Gly Ala Gln Gly Ala Val
               2245                2250                2255

Ala Glu Ala Glu Leu Ala Glu Ala Gln Arg Leu Met Ala Arg Val Gln
           2260                2265                2270

Glu Gln Leu Thr Ser Phe Trp Glu Glu Asn Gln Ser Leu Ala Thr His
       2275                2280                2285

Ile Arg Asp Gln Leu Ala Gln Tyr Glu Ser Gly Leu Met Asp Leu Arg
   2290                2295                2300

Glu Ala Leu Asn Gln Ala Val Asn Thr Thr Arg Glu Ala Glu Glu Leu
2305                2310                2315                2320

Asn Ser Arg Asn Gln Glu Arg Val Lys Glu Ala Leu Gln Trp Lys Gln
               2325                2330                2335

Glu Leu Ser Gln Asp Asn Ala Thr Leu Lys Ala Thr Leu Gln Ala Ala
           2340                2345                2350

Ser Leu Ile Leu Gly His Val Ser Glu Leu Leu Gln Gly Ile Asp Gln
       2355                2360                2365
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Ala Lys Glu Asp Leu Glu His Leu Ala Ala Ser Leu Asp Gly Ala Trp
   2370                2375                2380

Thr Pro Leu Leu Lys Arg Met Gln Ala Phe Ser Pro Ala Ser Ser Lys
2385                2390                2395                2400

Val Asp Leu Val Glu Ala Ala Glu Ala His Ala Gln Lys Leu Asn Gln
               2405                2410                2415

Leu Ala Ile Asn Leu Ser Gly Ile Ile Leu Gly Ile Asn Gln Asp Arg
           2420                2425                2430

Phe Ile Gln Arg Ala Val Glu Ala Ser Asn Ala Tyr Ser Ser Ile Leu
       2435                2440                2445

Gln Ala Val Gln Ala Ala Glu Asp Ala Ala Gly Gln Ala Leu Arg Gln
   2450                2455                2460

Ala Ser Arg Thr Trp Glu Met Val Val Gln Arg Gly Leu Ala Ala Gly
2465                2470                2475                2480

Ala Arg Gln Leu Leu Ala Asn Ser Ser Ala Leu Glu Glu Thr Ile Leu
               2485                2490                2495

Gly His Gln Gly Arg Leu Gly Leu Ala Gln Gly Arg Leu Gln Ala Ala
           2500                2505                2510

Gly Ile Gln Leu His Asn Val Trp Ala Arg Lys Asn Gln Leu Ala Ala
       2515                2520                2525

Gln Ile Gln Glu Ala Gln Ala Met Leu Ala Met Asp Thr Ser Glu Thr
   2530                2535                2540

Ser Glu Lys Ile Ala His Ala Lys Ala Val Ala Ala Glu Ala Leu Ser
2545                2550                2555                2560

Thr Ala Thr His Val Gln Ser Gln Leu Gln Gly Met Gln Lys Asn Val
               2565                2570                2575

Glu Arg Trp Gln Ser Gln Leu Gly Gly Leu Gln Gly Gln Asp Leu Ser
           2580                2585                2590

Gln Val Glu Arg Asp Ala Ser Ser Ser Val Ser Thr Leu Glu Lys Thr
       2595                2600                2605

Leu Pro Gln Leu Leu Ala Lys Leu Ser Arg Leu Glu Asn Arg Gly Val
   2610                2615                2620

His Asn Ala Ser Leu Ala Leu Ser Ala Asn Ile Gly Arg Val Arg Lys
2625                2630                2635                2640

Leu Ile Ala Gln Ala Arg Ser Ala Ala Ser Lys Val Lys Val Ser Met
               2645                2650                2655

Lys Phe Asn Gly Arg Ser Gly Val Arg Leu Arg Pro Pro Arg Asp Leu
           2660                2665                2670

Ala Asp Leu Ala Ala Tyr Thr Ala Leu Lys Phe His Ile Gln Ser Pro
       2675                2680                2685
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Val Pro Ala Pro Glu Pro Gly Lys Asn Thr Gly Asp His Phe Val Leu
   2690                2695                2700

Tyr Met Gly Ser Arg Gln Ala Thr Gly Asp Tyr Met Gly Val Ser Leu
2705                2710                2715                2720

Arg Asn Gln Lys Val His Trp Val Tyr Arg Leu Gly Lys Ala Gly Pro
                2725                2730                2735

Thr Thr Leu Ser Ile Asp Glu Asn Ile Gly Glu Gln Phe Ala Ala Val
            2740                2745                2750

Ser Ile Asp Arg Thr Leu Gln Phe Gly His Met Ser Val Thr Val Glu
        2755                2760                2765

Lys Gln Met Val His Glu Ile Lys Gly Asp Thr Val Ala Pro Gly Ser
   2770                2775                2780

Glu Gly Leu Leu Asn Leu His Pro Asp Asp Phe Val Phe Tyr Val Gly
2785                2790                2795                2800

Gly Tyr Pro Ser Asn Phe Thr Pro Pro Glu Pro Leu Arg Phe Pro Gly
                2805                2810                2815

Tyr Leu Gly Cys Ile Glu Met Glu Thr Leu Asn Glu Glu Val Val Ser
            2820                2825                2830

Leu Tyr Asn Phe Glu Gln Thr Phe Met Leu Asp Thr Ala Val Asp Lys
        2835                2840                2845

Pro Cys Ala Arg Ser Lys Ala Thr Gly Asp Pro Trp Leu Thr Asp Gly
   2850                2855                2860

Ser Tyr Leu Asp Gly Ser Gly Phe Ala Arg Ile Ser Phe Glu Lys Gln
2865                2870                2875                2880

Phe Ser Asn Thr Lys Arg Phe Asp Gln Glu Leu Arg Leu Val Ser Tyr
                2885                2890                2895

Asn Gly Ile Ile Phe Phe Leu Lys Gln Glu Ser Gln Phe Leu Cys Leu
            2900                2905                2910

Ala Val Gln Glu Gly Thr Leu Val Leu Phe Tyr Asp Phe Gly Ser Gly
        2915                2920                2925

Leu Lys Lys Ala Asp Pro Leu Gln Pro Pro Gln Ala Leu Thr Ala Ala
   2930                2935                2940

Ser Lys Ala Ile Gln Val Phe Leu Leu Ala Gly Asn Arg Lys Arg Val
2945                2950                2955                2960

Leu Val Arg Val Glu Arg Ala Thr Val Phe Ser Val Asp Gln Asp Asn
                2965                2970                2975

Met Leu Glu Met Ala Asp Ala Tyr Tyr Leu Gly Gly Val Pro Pro Glu
            2980                2985                2990

Gln Leu Pro Leu Ser Leu Arg Gln Leu Phe Pro Ser Gly Gly Ser Val
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Arg Gly Cys Ile Lys Gly Ile Lys Ala Leu Gly Lys Tyr Val Asp Leu
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Leu Val Gly Arg Thr Met Thr Phe His Gly His Gly Phe Leu Pro Leu
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Ala Leu Pro Asp Val Ala Pro Ile Thr Glu Val Val Tyr Ser Gly Phe
           3060                3065                3070

Gly Phe Arg Gly Thr Gln Asp Asn Asn Leu Leu Tyr Tyr Arg Thr Ser
       3075                3080                3085

Pro Asp Gly Pro Tyr Gln Val Ser Leu Arg Glu Gly His Val Thr Leu
   3090                3095                3100

Arg Phe Met Asn Gln Glu Val Glu Thr Gln Arg Val Phe Ala Asp Gly
3105                3110                3115                3120

Ala Pro His Tyr Val Ala Phe Tyr Ser Asn Val Thr Gly Val Trp Leu
               3125                3130                3135

Tyr Val Asp Asp Gln Leu Gln Leu Val Lys Ser His Glu Arg Thr Thr
           3140                3145                3150

Pro Met Leu Gln Leu Gln Pro Glu Glu Pro Ser Arg Leu Leu Leu Gly
       3155                3160                3165

Gly Leu Pro Val Ser Gly Thr Phe His Asn Phe Ser Gly Cys Ile Ser
   3170                3175                3180

Asn Val Phe Val Gln Arg Leu Arg Gly Pro Gln Arg Val Phe Asp Leu
3185                3190                3195                3200

His Gln Asn Met Gly Ser Val Asn Val Ser Val Gly Cys Thr Pro Ala
               3205                3210                3215

Gln Leu Ile Glu Thr Ser Arg Ala Thr Ala Gln Lys Val Ser Arg Arg
           3220                3225                3230

Ser Arg Gln Pro Ser Gln Asp Leu Ala Cys Thr Thr Pro Trp Leu Pro
       3235                3240                3245

Gly Thr Ile Gln Asp Ala Tyr Gln Phe Gly Gly Pro Leu Pro Ser Tyr
   3250                3255                3260

Leu Gln Phe Val Gly Ile Ser Pro Ser His Arg Asn Arg Leu His Leu
3265                3270                3275                3280

Ser Met Leu Val Arg Pro His Ala Ala Ser Gln Gly Leu Leu Leu Ser
               3285                3290                3295

Thr Ala Pro Met Ser Gly Arg Ser Pro Ser Leu Val Leu Phe Leu Asn
           3300                3305                3310

His Gly His Phe Val Ala Gln Thr Glu Gly Pro Gly Pro Arg Leu Gln
       3315                3320                3325

Val Gln Ser Arg Gln His Ser Arg Ala Gly Gln Trp His Arg Val Ser
   3330                3335                3340
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Val Arg Trp Gly Met Gln Gln Ile Gln Leu Val Val Asp Gly Ser Gln
3345                3350                3355                3360

Thr Trp Ser Gln Lys Ala Leu His His Arg Val Pro Arg Ala Glu Arg
                3365                3370                3375

Pro Gln Pro Tyr Thr Leu Ser Val Gly Gly Leu Pro Ala Ser Ser Tyr
            3380                3385                3390

Ser Ser Lys Leu Pro Val Ser Val Gly Phe Ser Gly Cys Leu Lys Lys
        3395                3400                3405

Leu Gln Leu Asp Lys Gln Pro Leu Arg Thr Pro Thr Gln Met Val Gly
    3410                3415                3420

Val Thr Pro Cys Val Ser Gly Pro Leu Glu Asp Gly Leu Phe Phe Pro
3425                3430                3435                3440

Gly Ser Glu Gly Val Val Thr Leu Glu Leu Pro Lys Ala Lys Met Pro
                3445                3450                3455

Tyr Val Ser Leu Glu Leu Glu Met Arg Pro Leu Ala Ala Ala Gly Leu
            3460                3465                3470

Ile Phe His Leu Gly Gln Ala Leu Ala Thr Pro Tyr Met Gln Leu Lys
        3475                3480                3485

Val Leu Thr Glu Gln Val Leu Leu Gln Ala Asn Asp Gly Ala Gly Glu
    3490                3495                3500

Phe Ser Thr Trp Val Thr Tyr Pro Lys Leu Cys Asp Gly Arg Trp His
3505                3510                3515                3520

Arg Val Ala Val Ile Met Gly Arg Asp Thr Leu Arg Leu Glu Val Asp
                3525                3530                3535

Thr Gln Ser Asn His Thr Thr Gly Arg Leu Pro Glu Ser Leu Ala Gly
            3540                3545                3550

Ser Pro Ala Leu Leu His Leu Gly Ser Leu Pro Lys Ser Ser Thr Ala
        3555                3560                3565

Arg Pro Glu Leu Pro Ala Tyr Arg Gly Cys Leu Arg Lys Leu Leu Ile
    3570                3575                3580

Asn Gly Ala Pro Val Asn Val Thr Ala Ser Val Gln Ile Gln Gly Ala
3585                3590                3595                3600

Val Gly Met Arg Gly Cys Pro Ser Gly Thr Leu Ala Leu Ser Lys Gln
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Gly Lys Ala Leu Thr Gln Arg His Ala Lys Pro Ser Val Ser Pro Leu
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Leu Trp His
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atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta gcc ctg tgc aga 165
Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg
1 5 10 15

gcc cga gtg cgc gct cag gaa ccc gag ttc agc tac ggc tgc gca gaa 213
Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
20 25 30

ggc agc tgc tat ccc gcc acg ggc gac ctt ctc atc ggc cga gca cag 261
Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
35 40 45

aag ctt tcg gtg acc tcg acg tgc ggg ctg cac aag ccc gaa ccc tac 309
Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
50 55 60

tgt atc gtc agc cac ttg cag gag gac aaa aaa tgc ttc ata tgc aat 357
Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn
65 70 75 80

tcc caa gat cct tat cat gag acc ctg aat cct gac agc cat ctc att 405
Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
85 90 95

gaa aat gtg gtc act aca ttt gct cca aac cgc ctt aag att tgg tgg 453
Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
100 105 110

caa tct gaa aat ggt gtg gaa aat gta act atc caa ctg gat ttg gaa 501
Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
115 120 125

gca gaa ttc cat ttt act cat ctc ata atg act ttc aag aca ttc cgt 549
Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
130 135 140

cca gct gct atg ctg ata gaa cga tcg tcc gac ttt ggg aaa acc tgg 597
Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145 150 155 160

ggt gtg tat aga tac ttc gcc tat gac tgt gag gcc tcg ttt cca ggc 645
Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly
165 170 175

att tca act ggc ccc atg aaa aaa gtc gat gac ata att tgt gat tct 693

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Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
            180                 185                 190

cga tat tct gac att gaa ccc tca act gaa gga gag gtg ata ttt cgt   741
Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
        195                 200                 205

gct tta gat cct gct ttc aaa ata gaa gat cct tat agc cca agg ata   789
Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
    210                 215                 220

cag aat tta tta aaa att acc aac ttg aga atc aag ttt gtg aaa ctg   837
Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
225                 230                 235                 240

cat act ttg gga gat aac ctt ctg gat tcc agg atg gaa atc aga gaa   885
His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
                245                 250                 255

aag tat tat tat gca gtt tat gat atg gtg gtt cga gga aat tgc ttc   933
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
            260                 265                 270

tgc tat ggt cat gcc agc gaa tgt gcc cct gtg gat gga ttc aat gaa   981
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu
        275                 280                 285

gaa gtg gaa gga atg gtt cac gga cac tgc atg tgc agg cat aac acc   1029
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
    290                 295                 300

aag ggc tta aac tgt gaa ctc tgc atg gat ttc tac cat gat tta cct   1077
Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
305                 310                 315                 320

tgg aga cct gct gaa ggc cga aac agc aac gcc tgt aaa aaa tgt aac   1125
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
                325                 330                 335

tgc aat gaa cat tcc atc tct tgt cac ttt gac atg gct gtt tac ctg   1173
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu
            340                 345                 350

gcc acg ggg aac gtc agc gga ggc gtg tgt gat gac tgt cag cac aac   1221
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn
        355                 360                 365

acc atg ggg cgc aac tgt gag cag tgc aag ccg ttt tac tac cag cac   1269
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His
    370                 375                 380

cca gag agg gac atc cga gat cct aat ttc tgt gaa cga tgt acg tgt   1317
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys
385                 390                 395                 400

gac cca gct ggc tct caa aat gag gga att tgt gac agc tat act gat   1365
Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp
                405                 410                 415

ttt tct act ggt ctc att gct ggc cag tgt cgg tgt aaa tta aat gtg   1413
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val
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            420                 425                 430

gaa gga gaa cat tgt gat gtt tgc aaa gaa ggc ttc tat gat tta agc   1461
Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser
        435                 440                 445

agt gaa gat cca ttt ggt tgt aaa tct tgt gct tgc aat cct ctg gga   1509
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly
    450                 455                 460

aca att cct gga ggg aat cct tgt gat tcc gag aca ggt cac tgc tac   1557
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr
465                 470                 475                 480

tgc aag cgt ctg gtg aca gga cag cat tgt gac cag tgc ctg cca gag   1605
Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu
                485                 490                 495

cac tgg ggc tta agc aat gat ttg gat gga tgt cga cca tgt gac tgt   1653
His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
            500                 505                 510

gac ctt ggg gga gcc tta aac aac agt tgc ttt gcg gag tca ggc cag   1701
Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln
        515                 520                 525

tgc tca tgc cgg cct cac atg att gga cgt cag tgc aac gaa gtg gaa   1749
Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
    530                 535                 540

cct ggt tac tac ttt gcc acc ctg gat cac tac ctc tat gaa gcg gag   1797
Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu
545                 550                 555                 560

gaa gcc aac ttg ggg cct ggg gtt agc ata gtg gag cgg caa tat atc   1845
Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile
                565                 570                 575

cag gac cgg att ccc tcc tgg act gga gcc ggc ttc gtc cga gtg cct   1893
Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro
            580                 585                 590

gaa ggg gct tat ttg gag ttt ttc att gac aac ata cca tat tcc atg   1941
Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
        595                 600                 605

gag tac gac atc cta att cgc tac gag cca cag cta ccc gac cac tgg   1989
Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
    610                 615                 620

gaa aaa gct gtc atc aca gtg cag cga cct gga agg att cca acc agc   2037
Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser
625                 630                 635                 640

agc cga tgt ggt aat acc atc ccc gat gat gac aac cag gtg gtg tca   2085
Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser
                645                 650                 655

tta tca cca ggc tca aga tat gtc gtc ctt cct cgg ccg gtg tgc ttt   2133
Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
            660                 665                 670
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gag aag gga aca aac tac acg gtg agg ttg gag ctg cct cag tac acc   2181
Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
        675                 680                 685

tcc tct gat agc gac gtg gag agc ccc tac acg ctg atc gat tct ctt   2229
Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu
    690                 695                 700

gtt ctc atg cca tac tgt aaa tca ctg gac atc ttc acc gtg gga ggt   2277
Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
705                 710                 715                 720

tca gga gat ggg gtg gtc acc aac agt gcc tgg gaa acc ttt cag aga   2325
Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
                725                 730                 735

tac cga tgt cta gag aac agc aga agc gtt gtg aaa aca ccg atg aca   2373
Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
            740                 745                 750

gat gtt tgc aga aac atc atc ttt agc att tct gcc ctg tta cac cag   2421
Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln
        755                 760                 765

aca ggc ctg gct tgt gaa tgc gac cct cag ggt tcg tta agt tcc gtg   2469
Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
    770                 775                 780

tgt gat ccc aac gga ggc cag tgc cag tgc cgg ccc aac gtg gtt gga   2517
Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
785                 790                 795                 800

aga acc tgc aac aga tgt gca cct gga act ttt ggc ttt ggc ccc agt   2565
Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser
                805                 810                 815

gga tgc aaa cct tgt gag tgc cat ctg caa gga tct gtc aat gcc ttc   2613
Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe
            820                 825                 830

tgc aat ccc gtc act ggc cag tgc cac tgt ttc cag gga gtg tat gct   2661
Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala
        835                 840                 845

cgg cag tgt gat cgg tgc tta cct ggg cac tgg ggc ttt cca agt tgc   2709
Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys
    850                 855                 860

cag ccc tgc cag tgc aat ggc cac gcc gat gac tgc gac cca gtg act   2757
Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr
865                 870                 875                 880

ggg gag tgc ttg aac tgc cag gac tac acc atg ggt cat aac tgt gaa   2805
Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu
                885                 890                 895

agg tgc ttg gct ggt tac tat ggc gac ccc atc att ggg tca ggt gat   2853
Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
            900                 905                 910
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cac tgc cgc cct tgc cct tgc cca gat ggt ccc gac agt gga cgc cag   2901
His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
        915                 920                 925

ttt gcc agg agc tgc tac caa gat cct gtt act tta cag ctt gcc tgt   2949
Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
    930                 935                 940

gtt tgt gat cct gga tac att ggt tcc aga tgt gac gac tgt gcc tca   2997
Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
945                 950                 955                 960

gga tac ttt ggc aat cca tca gaa gtt ggg ggg tcg tgt cag cct tgc   3045
Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys
                965                 970                 975

cag tgt cac aac aac att gac acg aca gac cca gaa gcc tgt gac aag   3093
Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
            980                 985                 990

gag act ggg agg tgt ctc aag tgc ctg tac cac acg gaa ggg gaa cac   3141
Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His
        995                1000                1005

tgt cag ttc tgc cgg ttt gga tac tat ggt gat gcc ctc cgg cag gac   3189
Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp
   1010                1015                1020

tgt cga aag tgt gtc tgt aat tac ctg ggc acc gtg caa gag cac tgt   3237
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys
1025                1030                1035                1040

aac ggc tct gac tgc cag tgc gac aaa gcc act ggt cag tgc ttg tgt   3285
Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys
                1045                1050                1055

ctt cct aat gtg atc ggg cag aac tgt gac cgc tgt gcg ccc aat acc   3333
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr
            1060                1065                1070

tgg cag ctg gcc agt ggc act ggc tgt gac cca tgc aac tgc aat gct   3381
Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala
        1075                1080                1085

gct cat tcc ttc ggg cca tct tgc aat gag ttc acg ggg cag tgc cag   3429
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln
   1090                1095                1100

tgc atg cct ggg ttt gga ggc cgc acc tgc agc gag tgc cag gaa ctc   3477
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu
1105                1110                1115                1120

ttc tgg gga gac ccc gac gtg gag tgc cga gcc tgt gac tgt gac ccc   3525
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro
                1125                1130                1135

agg ggc att gag acg cca cag tgt gac cag tcc acg ggc cag tgt gtc   3573
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val
            1140                1145                1150

tgc gtt gag ggt gtt gag ggt cca cgc tgt gac aag tgc acg cga ggg   3621
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Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly
       1155                1160                1165

tac tcg ggg gtc ttc cct gac tgc aca ccc tgc cac cag tgc ttt gct   3669
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala
   1170                1175                1180

ctc tgg gat gtg atc att gcc gag ctg acc aac agg aca cac aga ttc   3717
Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe
1185                1190                1195                1200

ctg gag aaa gcc aag gcc ttg aag atc agt ggt gtg atc ggg cct tac   3765
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr
               1205                1210                1215

cgt gag act gtg gac tcg gtg gag agg aaa gtc agc gag ata aaa gac   3813
Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp
           1220                1225                1230

atc ctg gcg cag agc ccc gca gca gag cca ctg aaa aac att ggg aat   3861
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn
       1235                1240                1245

ctc ttt gag gaa gca gag aaa ctg att aaa gat gtt aca gaa atg atg   3909
Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met
   1250                1255                1260

gct caa gta gaa gtg aaa tta tct gac aca act tcc caa agc aac agc   3957
Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser
1265                1270                1275                1280

aca gcc aaa gaa ctg gat tct cta cag aca gaa gcc gaa agc cta gac   4005
Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp
               1285                1290                1295

aac act gtg aaa gaa ctt gct gaa caa ctg gaa ttt atc aaa aac tca   4053
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser
           1300                1305                1310

gat att cgg ggt gcc ttg gat agc att acc aag tat ttc cag atg tct   4101
Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
       1315                1320                1325

ctt gag gca gag gag agg gtg aat gcc tcc acc aca gaa ccc aac agc   4149
Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser
   1330                1335                1340

act gtg gag cag tca gcc ctc atg aga gac aga gta gaa gac gtg atg   4197
Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met
1345                1350                1355                1360

atg gag cga gaa tcc cag ttc aag gaa aaa caa gag gag cag gct cgc   4245
Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg
               1365                1370                1375

ctc ctt gat gaa ctg gca ggc aag cta caa agc cta gac ctt tca gcc   4293
Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
           1380                1385                1390

gct gcc gaa atg acc tgt gga aca ccc cca ggg gcc tcc tgt tcc gag   4341
Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu
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      1395                1400                1405

act gaa tgt ggc ggg cca aac tgc aga act gac gaa gga gag agg aag   4389
Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys
   1410                1415                1420

tgt ggg ggg cct ggc tgt ggt ggt ctg gtt act gtt gca cac aac gcc   4437
Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala
1425                1430                1435                1440

tgg cag aaa gcc atg gac ttg gac caa gat gtc ctg agt gcc ctg gct   4485
Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala
               1445                1450                1455

gaa gtg gaa cag ctc tcc aag atg gtc tct gaa gca aaa ctg agg gca   4533
Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala
           1460                1465                1470

gat gag gca aaa caa agt gct gaa gac att ctg ttg aag aca aat gct   4581
Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala
       1475                1480                1485

acc aaa gaa aaa atg gac aag agc aat gag gag ctg aga aat cta atc   4629
Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile
   1490                1495                1500

aag caa atc aga aac ttt ttg acc cag gat agt gct gat ttg gac agc   4677
Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser
1505                1510                1515                1520

att gaa gca gtt gct aat gaa gta ttg aaa atg gag atg cct agc acc   4725
Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr
               1525                1530                1535

cca cag cag tta cag aac ttg aca gaa gat ata cgt gaa cga gtt gaa   4773
Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
           1540                1545                1550

agc ctt tct caa gta gag gtt att ctt cag cat agt gct gct gac att   4821
Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile
       1555                1560                1565

gcc aga gct gag atg ttg tta gaa gaa gct aaa aga gca agc aaa agt   4869
Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
   1570                1575                1580

gca aca gat gtt aaa gtc act gca gat atg gta aag gaa gct ctg gaa   4917
Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585                1590                1595                1600

gaa gca gaa aag gcc cag gtc gca gca gag aag gca att aaa caa gca   4965
Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
               1605                1610                1615

gat gaa gac att caa gga acc cag aac ctg tta act tcg att gag tct   5013
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
           1620                1625                1630

gaa aca gca gct tct gag gaa acc ttg ttc aac gcg tcc cag cgc atc   5061
Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile
       1635                1640                1645
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agc gag tta gag agg aat gtg gaa gaa ctt aag cgg aaa gct gcc caa   5109
Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
   1650                1655                1660

aac tcc ggg gag gca gaa tat att gaa aaa gta gta tat act gtg aag   5157
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys
1665               1670                1675                1680

caa agt gca gaa gat gtt aag aag act tta gat ggt gaa ctt gat gaa   5205
Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
               1685                1690                1695

aag tat aaa aaa gta gaa aat tta att gcc aaa aaa act gaa gag tca   5253
Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser
           1700                1705                1710

gct gat gcc aga agg aaa gcc gaa atg cta caa aat gaa gca aaa act   5301
Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr
       1715                1720                1725

ctt tta gct caa gca aat agc aag ctg caa ctg ctc aaa gat tta gaa   5349
Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu
   1730                1735                1740

aga aaa tat gaa gac aat caa aga tac tta gaa gat aaa gct caa gaa   5397
Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu
1745               1750                1755                1760

tta gca aga ctg gaa gga gaa gtc cgt tca ctc cta aag gat ata agc   5445
Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
               1765                1770                1775

cag aaa gtt gct gtg tat agc aca tgc ttg taacagagga gaataaaaaa     5495
Gln Lys Val Ala Val Tyr Ser Thr Cys Leu
           1780                1785

tggctgaggt gaacaaggta aaacaactac attttaaaaa ctgacttaat gctcttcaaa 5555

ataaaacatc acctatttaa tgtttttaat cacattttgt atgagttaaa taaagccc   5613
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<210> 6
<211> 1786
<212> PRT
<213> Homo sapiens

<400> 6

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

Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
             20                  25                  30

Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
         35                  40                  45

Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
     50                  55                  60

Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn
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 65                  70                  75                  80

Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
                 85                  90                  95

Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
            100                 105                 110

Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
        115                 120                 125

Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
    130                 135                 140

Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145                 150                 155                 160

Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly
                165                 170                 175

Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
            180                 185                 190

Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
        195                 200                 205

Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
    210                 215                 220

Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
225                 230                 235                 240

His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
                245                 250                 255

Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
            260                 265                 270

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

Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
    290                 295                 300

Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
305                 310                 315                 320

Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
                325                 330                 335

Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu
            340                 345                 350

Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn
        355                 360                 365

Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His
    370                 375                 380

Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys
385                 390                 395                 400
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Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp
                405                 410                 415

Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val
            420                 425                 430

Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser
        435                 440                 445

Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly
    450                 455                 460

Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr
465                 470                 475                 480

Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu
                485                 490                 495

His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
            500                 505                 510

Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln
        515                 520                 525

Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
    530                 535                 540

Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu
545                 550                 555                 560

Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile
                565                 570                 575

Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro
            580                 585                 590

Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
        595                 600                 605

Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
    610                 615                 620

Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser
625                 630                 635                 640

Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser
                645                 650                 655

Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
            660                 665                 670

Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
        675                 680                 685

Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu
    690                 695                 700

Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
705                 710                 715                 720
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Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
                725                 730                 735

Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
            740                 745                 750

Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln
        755                 760                 765

Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
    770                 775                 780

Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
785                 790                 795                 800

Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser
                805                 810                 815

Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe
            820                 825                 830

Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala
        835                 840                 845

Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys
    850                 855                 860

Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr
865                 870                 875                 880

Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu
                885                 890                 895

Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
            900                 905                 910

His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
        915                 920                 925

Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
    930                 935                 940

Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
945                 950                 955                 960

Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys
                965                 970                 975

Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
            980                 985                 990

Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His
        995                1000                1005

Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp
   1010                1015                1020

Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys
1025                1030                1035                1040

Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys
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                1045                1050                1055

Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr
            1060                1065                1070

Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala
        1075                1080                1085

Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln
    1090                1095                1100

Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu
1105                1110                1115                1120

Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro
                1125                1130                1135

Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val
            1140                1145                1150

Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly
        1155                1160                1165

Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala
    1170                1175                1180

Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe
1185                1190                1195                1200

Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr
                1205                1210                1215

Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp
            1220                1225                1230

Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn
        1235                1240                1245

Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met
    1250                1255                1260

Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser
1265                1270                1275                1280

Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp
                1285                1290                1295

Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser
            1300                1305                1310

Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
        1315                1320                1325

Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser
    1330                1335                1340

Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met
1345                1350                1355                1360

Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg
                1365                1370                1375
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Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
          1380                1385                1390

Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu
       1395                1400                1405

Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys
   1410                1415                1420

Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala
1425                1430                1435                1440

Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala
               1445                1450                1455

Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala
           1460                1465                1470

Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala
       1475                1480                1485

Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile
   1490                1495                1500

Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser
1505                1510                1515                1520

Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr
               1525                1530                1535

Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
           1540                1545                1550

Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile
       1555                1560                1565

Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
   1570                1575                1580

Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585                1590                1595                1600

Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
               1605                1610                1615

Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
           1620                1625                1630

Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile
       1635                1640                1645

Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
   1650                1655                1660

Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys
1665                1670                1675                1680

Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
               1685                1690                1695
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Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser
           1700                1705                1710

Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr
       1715                1720                1725

Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu
   1730                1735                1740

Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu
1745                1750                1755                1760

Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
               1765                1770                1775

Gln Lys Val Ala Val Tyr Ser Thr Cys Leu
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Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu Gly Ser Cys Tyr Pro
  1               5                  10                  15

gcc acg ggc gac ctt ctc atc ggc cga gca cag aag ctt tcg gtg acc   96
Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln Lys Leu Ser Val Thr
             20                  25                  30

tcg acg tgc ggg ctg cac aag ccc gaa ccc tac tgt atc gtc agc cac   144
Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr Cys Ile Val Ser His
         35                  40                  45

ttg cag gag gac aaa aaa tgc ttc ata tgc aat tcc caa gat cct tat   192
Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn Ser Gln Asp Pro Tyr
     50                  55                  60

cat gag acc ctg aat cct gac agc cat ctc att gaa aat gtg gtc act   240
His Glu Thr Leu Asn Pro Asp Ser His Leu Ile Glu Asn Val Val Thr
 65                  70                  75                  80

aca ttt gct cca aac cgc ctt aag att tgg tgg caa tct gaa aat ggt   288
Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp Gln Ser Glu Asn Gly
                 85                  90                  95

gtg gaa aat gta act atc caa ctg gat ttg gaa gca gaa ttc cat ttt   336
Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu Ala Glu Phe His Phe
            100                 105                 110

act cat ctc ata atg act ttc aag aca ttc cgt cca gct gct atg ctg   384
Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg Pro Ala Ala Met Leu
        115                 120                 125
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ata gaa cga tcg tcc gac ttt ggg aaa acc tgg ggt gtg tat aga tac   432
Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Gly Val Tyr Arg Tyr
    130                 135                 140

ttc gcc tat gac tgt gag gcc tcg ttt cca ggc att tca act ggc ccc   480
Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly Ile Ser Thr Gly Pro
145                 150                 155                 160

atg aaa aaa gtc gat gac ata att tgt gat tct cga tat tct gac att   528
Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser Arg Tyr Ser Asp Ile
                165                 170                 175

gaa ccc tca act gaa gga gag gtg ata ttt cgt gct tta gat cct gct   576
Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg Ala Leu Asp Pro Ala
            180                 185                 190

ttc aaa ata gaa gat cct tat agc cca agg ata cag aat tta tta aaa   624
Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile Gln Asn Leu Leu Lys
        195                 200                 205

att acc aac ttg aga atc aag ttt gtg aaa ctg cat act ttg gga gat   672
Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu His Thr Leu Gly Asp
    210                 215                 220

aac ctt ctg gat tcc agg atg gaa atc aga gaa aag tat tat tat gca   720
Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu Lys Tyr Tyr Tyr Ala
225                 230                 235                 240

gtt tat gat atg gtg gtt cga gga aat tgc ttc tgc tat ggt cat gcc   768
Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe Cys Tyr Gly His Ala
                245                 250                 255

agc gaa tgt gcc cct gtg gat gga ttc aat gaa gaa gtg gaa gga atg   816
Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu Glu Val Glu Gly Met
            260                 265                 270

gtt cac gga cac tgc atg tgc agg cat aac acc aag ggc tta aac tgt   864
Val His Gly His Cys Met Cys Arg His Asn Thr Lys Gly Leu Asn Cys
        275                 280                 285

gaa ctc tgc atg gat ttc tac cat gat tta cct tgg aga cct gct gaa   912
Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro Trp Arg Pro Ala Glu
    290                 295                 300

ggc cga aac agc aac gcc tgt aaa aaa tgt aac tgc aat gaa cat tcc   960
Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn Cys Asn Glu His Ser
305                 310                 315                 320

atc tct tgt cac ttt gac atg gct gtt tac ctg gcc acg ggg aac gtc  1008
Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu Ala Thr Gly Asn Val
                325                 330                 335

agc gga ggc gtg tgt gat gac tgt cag cac aac acc atg ggg cgc aac  1056
Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn Thr Met Gly Arg Asn
            340                 345                 350

tgt gag cag tgc aag ccg ttt tac tac cag cac cca gag agg gac atc  1104
Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His Pro Glu Arg Asp Ile
        355                 360                 365

cga gat cct aat ttc tgt gaa cga tgt acg tgt gac cca gct ggc tct  1152
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Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys Asp Pro Ala Gly Ser
    370                 375                 380

caa aat gag gga att tgt gac agc tat act gat ttt tct act ggt ctc   1200
Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp Phe Ser Thr Gly Leu
385                 390                 395                 400

att gct ggc cag tgt cgg tgt aaa tta aat gtg gaa gga gaa cat tgt   1248
Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val Glu Gly Glu His Cys
                405                 410                 415

gat gtt tgc aaa gaa ggc ttc tat gat tta agc agt gaa gat cca ttt   1296
Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser Ser Glu Asp Pro Phe
            420                 425                 430

ggt tgt aaa tct tgt gct tgc aat cct ctg gga aca att cct gga ggg   1344
Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly Thr Ile Pro Gly Gly
        435                 440                 445

aat cct tgt gat tcc gag aca ggt cac tgc tac tgc aag cgt ctg gtg   1392
Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr Cys Lys Arg Leu Val
    450                 455                 460

aca gga cag cat tgt gac cag tgc ctg cca gag cac tgg ggc tta agc   1440
Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu His Trp Gly Leu Ser
465                 470                 475                 480

aat gat ttg gat gga tgt cga cca tgt gac tgt gac ctt ggg gga gcc   1488
Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys Asp Leu Gly Gly Ala
                485                 490                 495

tta aac aac agt tgc ttt gcg gag tca ggc cag tgc tca tgc cgg cct   1536
Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln Cys Ser Cys Arg Pro
            500                 505                 510

cac atg att gga cgt cag tgc aac gaa gtg gaa cct ggt tac tac ttt   1584
His Met Ile Gly Arg Gln Cys Asn Glu Val Glu Pro Gly Tyr Tyr Phe
        515                 520                 525

gcc acc ctg gat cac tac ctc tat gaa gcg gag gaa gcc aac ttg ggg   1632
Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu Glu Ala Asn Leu Gly
    530                 535                 540

cct ggg gtt agc ata gtg gag cgg caa tat atc cag gac cgg att ccc   1680
Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile Gln Asp Arg Ile Pro
545                 550                 555                 560

tcc tgg act gga gcc ggc ttc gtc cga gtg cct gaa ggg gct tat ttg   1728
Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro Glu Gly Ala Tyr Leu
                565                 570                 575

gag ttt ttc att gac aac ata cca tat tcc atg gag tac gac atc cta   1776
Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met Glu Tyr Asp Ile Leu
            580                 585                 590

att cgc tac gag cca cag cta ccc gac cac tgg gaa aaa gct gtc atc   1824
Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp Glu Lys Ala Val Ile
        595                 600                 605

aca gtg cag cga cct gga agg att cca acc agc agc cga tgt ggt aat   1872
Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser Ser Arg Cys Gly Asn
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    610                 615                 620

acc atc ccc gat gat gac aac cag gtg gtg tca tta tca cca ggc tca   1920
Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser Leu Ser Pro Gly Ser
625                 630                 635                 640

aga tat gtc gtc ctt cct cgg ccg gtg tgc ttt gag aag gga aca aac   1968
Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe Glu Lys Gly Thr Asn
                645                 650                 655

tac acg gtg agg ttg gag ctg cct cag tac acc tcc tct gat agc gac   2016
Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr Ser Ser Asp Ser Asp
            660                 665                 670

gtg gag agc ccc tac acg ctg atc gat tct ctt gtt ctc atg cca tac   2064
Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu Val Leu Met Pro Tyr
        675                 680                 685

tgt aaa tca ctg gac atc ttc acc gtg gga ggt tca gga gat ggg gtg   2112
Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly Ser Gly Asp Gly Val
    690                 695                 700

gtc acc aac agt gcc tgg gaa acc ttt cag aga tac cga tgt cta gag   2160
Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg Tyr Arg Cys Leu Glu
705                 710                 715                 720

aac agc aga agc gtt gtg aaa aca ccg atg aca gat gtt tgc aga aac   2208
Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr Asp Val Cys Arg Asn
                725                 730                 735

atc atc ttt agc att tct gcc ctg tta cac cag aca ggc ctg gct tgt   2256
Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln Thr Gly Leu Ala Cys
            740                 745                 750

gaa tgc gac cct cag ggt tcg tta agt tcc gtg tgt gat ccc aac gga   2304
Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val Cys Asp Pro Asn Gly
        755                 760                 765

ggc cag tgc cag tgc cgg ccc aac gtg gtt gga aga acc tgc aac aga   2352
Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly Arg Thr Cys Asn Arg
    770                 775                 780

tgt gca cct gga act ttt ggc ttt ggc ccc agt gga tgc aaa cct tgt   2400
Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser Gly Cys Lys Pro Cys
785                 790                 795                 800

gag tgc cat ctg caa gga tct gtc aat gcc ttc tgc aat ccc gtc act   2448
Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe Cys Asn Pro Val Thr
                805                 810                 815

ggc cag tgc cac tgt ttc cag gga gtg tat gct cgg cag tgt gat cgg   2496
Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala Arg Gln Cys Asp Arg
            820                 825                 830

tgc tta cct ggg cac tgg ggc ttt cca agt tgc cag ccc tgc cag tgc   2544
Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys Gln Pro Cys Gln Cys
        835                 840                 845

aat ggc cac gcc gat gac tgc gac cca gtg act ggg gag tgc ttg aac   2592
Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr Gly Glu Cys Leu Asn
    850                 855                 860
```

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tgc cag gac tac acc atg ggt cat aac tgt gaa agg tgc ttg gct ggt   2640
Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu Arg Cys Leu Ala Gly
865                 870                 875                 880

tac tat ggc gac ccc atc att ggg tca ggt gat cac tgc cgc cct tgc   2688
Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp His Cys Arg Pro Cys
                885                 890                 895

cct tgc cca gat ggt ccc gac agt gga cgc cag ttt gcc agg agc tgc   2736
Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln Phe Ala Arg Ser Cys
            900                 905                 910

tac caa gat cct gtt act tta cag ctt gcc tgt gtt tgt gat cct gga   2784
Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys Val Cys Asp Pro Gly
        915                 920                 925

tac att ggt tcc aga tgt gac gac tgt gcc tca gga tac ttt ggc aat   2832
Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser Gly Tyr Phe Gly Asn
    930                 935                 940

cca tca gaa gtt ggg ggg tcg tgt cag cct tgc cag tgt cac aac aac   2880
Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys Gln Cys His Asn Asn
945                 950                 955                 960

att gac acg aca gac cca gaa gcc tgt gac aag gag act ggg agg tgt   2928
Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys Glu Thr Gly Arg Cys
                965                 970                 975

ctc aag tgc ctg tac cac acg gaa ggg gaa cac tgt cag ttc tgc cgg   2976
Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His Cys Gln Phe Cys Arg
            980                 985                 990

ttt gga tac tat ggt gat gcc ctc cgg cag gac tgt cga aag tgt gtc   3024
Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp Cys Arg Lys Cys Val
        995                1000                1005

tgt aat tac ctg ggc acc gtg caa gag cac tgt aac ggc tct gac tgc   3072
Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys Asn Gly Ser Asp Cys
   1010                1015                1020

cag tgc gac aaa gcc act ggt cag tgc ttg tgt ctt cct aat gtg atc   3120
Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys Leu Pro Asn Val Ile
1025                1030                1035                1040

ggg cag aac tgt gac cgc tgt gcg ccc aat acc tgg cag ctg gcc agt   3168
Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr Trp Gln Leu Ala Ser
               1045                1050                1055

ggc act ggc tgt gac cca tgc aac tgc aat gct gct cat tcc ttc ggg   3216
Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala Ala His Ser Phe Gly
           1060                1065                1070

cca tct tgc aat gag ttc acg ggg cag tgc cag tgc atg cct ggg ttt   3264
Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln Cys Met Pro Gly Phe
       1075                1080                1085

gga ggc cgc acc tgc agc gag tgc cag gaa ctc ttc tgg gga gac ccc   3312
Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu Phe Trp Gly Asp Pro
   1090                1095                1100
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gac gtg gag tgc cga gcc tgt gac tgt gac ccc agg ggc att gag acg   3360
Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro Arg Gly Ile Glu Thr
1105                1110                1115                1120

cca cag tgt gac cag tcc acg ggc cag tgt gtc tgc gtt gag ggt gtt   3408
Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val Cys Val Glu Gly Val
                1125                1130                1135

gag ggt cca cgc tgt gac aag tgc acg cga ggg tac tcg ggg gtc ttc   3456
Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly Tyr Ser Gly Val Phe
            1140                1145                1150

cct gac tgc aca ccc tgc cac cag tgc ttt gct ctc tgg gat gtg atc   3504
Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala Leu Trp Asp Val Ile
        1155                1160                1165

att gcc gag ctg acc aac agg aca cac aga ttc ctg gag aaa gcc aag   3552
Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe Leu Glu Lys Ala Lys
    1170                1175                1180

gcc ttg aag atc agt ggt gtg atc ggg cct tac cgt gag act gtg gac   3600
Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr Arg Glu Thr Val Asp
1185                1190                1195                1200

tcg gtg gag agg aaa gtc agc gag ata aaa gac atc ctg gcg cag agc   3648
Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp Ile Leu Ala Gln Ser
                1205                1210                1215

ccc gca gca gag cca ctg aaa aac att ggg aat ctc ttt gag gaa gca   3696
Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn Leu Phe Glu Glu Ala
            1220                1225                1230

gag aaa ctg att aaa gat gtt aca gaa atg atg gct caa gta gaa gtg   3744
Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met Ala Gln Val Glu Val
        1235                1240                1245

aaa tta tct gac aca act tcc caa agc aac agc aca gcc aaa gaa ctg   3792
Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser Thr Ala Lys Glu Leu
    1250                1255                1260

gat tct cta cag aca gaa gcc gaa agc cta gac aac act gtg aaa gaa   3840
Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp Asn Thr Val Lys Glu
1265                1270                1275                1280

ctt gct gaa caa ctg gaa ttt atc aaa aac tca gat att cgg ggt gcc   3888
Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser Asp Ile Arg Gly Ala
                1285                1290                1295

ttg gat agc att acc aag tat ttc cag atg tct ctt gag gca gag gag   3936
Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser Leu Glu Ala Glu Glu
            1300                1305                1310

agg gtg aat gcc tcc acc aca gaa ccc aac agc act gtg gag cag tca   3984
Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser Thr Val Glu Gln Ser
        1315                1320                1325

gcc ctc atg aga gac aga gta gaa gac gtg atg atg gag cga gaa tcc   4032
Ala Leu Met Arg Asp Arg Val Glu Asp Val Met Met Glu Arg Glu Ser
    1330                1335                1340

cag ttc aag gaa aaa caa gag gag cag gct cgc ctc ctt gat gaa ctg   4080
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Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg Leu Leu Asp Glu Leu
1345                1350                1355                1360

gca ggc aag cta caa agc cta gac ctt tca gcc gct gcc gaa atg acc   4128
Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala Ala Ala Glu Met Thr
                1365                1370                1375

tgt gga aca ccc cca ggg gcc tcc tgt tcc gag act gaa tgt ggc ggg   4176
Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu Thr Glu Cys Gly Gly
            1380                1385                1390

cca aac tgc aga act gac gaa gga gag agg aag tgt ggg ggg cct ggc   4224
Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys Cys Gly Gly Pro Gly
        1395                1400                1405

tgt ggt ggt ctg gtt act gtt gca cac aac gcc tgg cag aaa gcc atg   4272
Cys Gly Gly Leu Val Thr Val Ala His Asn Ala Trp Gln Lys Ala Met
    1410                1415                1420

gac ttg gac caa gat gtc ctg agt gcc ctg gct gaa gtg gaa cag ctc   4320
Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala Glu Val Glu Gln Leu
1425                1430                1435                1440

tcc aag atg gtc tct gaa gca aaa ctg agg gca gat gag gca aaa caa   4368
Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala Asp Glu Ala Lys Gln
                1445                1450                1455

agt gct gaa gac att ctg ttg aag aca aat gct acc aaa gaa aaa atg   4416
Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala Thr Lys Glu Lys Met
            1460                1465                1470

gac aag agc aat gag gag ctg aga aat cta atc aag caa atc aga aac   4464
Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile Lys Gln Ile Arg Asn
        1475                1480                1485

ttt ttg acc cag gat agt gct gat ttg gac agc att gaa gca gtt gct   4512
Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser Ile Glu Ala Val Ala
    1490                1495                1500

aat gaa gta ttg aaa atg gag atg cct agc acc cca cag cag tta cag   4560
Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr Pro Gln Gln Leu Gln
1505                1510                1515                1520

aac ttg aca gaa gat ata cgt gaa cga gtt gaa agc ctt tct caa gta   4608
Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu Ser Leu Ser Gln Val
                1525                1530                1535

gag gtt att ctt cag cat agt gct gct gac att gcc aga gct gag atg   4656
Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile Ala Arg Ala Glu Met
            1540                1545                1550

ttg tta gaa gaa gct aaa aga gca agc aaa agt gca aca gat gtt aaa   4704
Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser Ala Thr Asp Val Lys
        1555                1560                1565

gtc act gca gat atg gta aag gaa gct ctg gaa gaa gca gaa aag gcc   4752
Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu Glu Ala Glu Lys Ala
    1570                1575                1580

cag gtc gca gca gag aag gca att aaa caa gca gat gaa gac att caa   4800
Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala Asp Glu Asp Ile Gln
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1585                1590                1595                1600

gga acc cag aac ctg tta act tcg att gag tct gaa aca gca gct tct   4848
Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser Glu Thr Ala Ala Ser
                1605                1610                1615

gag gaa acc ttg ttc aac gcg tcc cag cgc atc agc gag tta gag agg   4896
Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile Ser Glu Leu Glu Arg
            1620                1625                1630

aat gtg gaa gaa ctt aag cgg aaa gct gcc caa aac tcc ggg gag gca   4944
Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln Asn Ser Gly Glu Ala
        1635                1640                1645

gaa tat att gaa aaa gta gta tat act gtg aag caa agt gca gaa gat   4992
Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys Gln Ser Ala Glu Asp
    1650                1655                1660

gtt aag aag act tta gat ggt gaa ctt gat gaa aag tat aaa aaa gta   5040
Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu Lys Tyr Lys Lys Val
1665                1670                1675                1680

gaa aat tta att gcc aaa aaa act gaa gag tca gct gat gcc aga agg   5088
Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser Ala Asp Ala Arg Arg
                1685                1690                1695

aaa gcc gaa atg cta caa aat gaa gca aaa act ctt tta gct caa gca   5136
Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr Leu Leu Ala Gln Ala
            1700                1705                1710

aat agc aag ctg caa ctg ctc aaa gat tta gaa aga aaa tat gaa gac   5184
Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu Arg Lys Tyr Glu Asp
        1715                1720                1725

aat caa aga tac tta gaa gat aaa gct caa gaa tta gca aga ctg gaa   5232
Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu Leu Ala Arg Leu Glu
    1730                1735                1740

gga gaa gtc cgt tca ctc cta aag gat ata agc cag aaa gtt gct gtg   5280
Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser Gln Lys Val Ala Val
1745                1750                1755                1760

tat agc aca tgc ttg taacagagga gaataaaaaa tggctgaggt gaacaaggta   5335
Tyr Ser Thr Cys Leu
                1765

aaacaactac attttaaaaa ctgacttaat gctcttcaaa ataaaacatc acctatttaa 5395

tgtttttaat cacattttgt atgagttaaa taaagccc                         5433


<210> 8
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<212> PRT
<213> Homo sapiens

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Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu Gly Ser Cys Tyr Pro
  1               5                  10                  15

Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln Lys Leu Ser Val Thr
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            20                  25                  30

Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr Cys Ile Val Ser His
         35                  40                  45

Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn Ser Gln Asp Pro Tyr
     50                  55                  60

His Glu Thr Leu Asn Pro Asp Ser His Leu Ile Glu Asn Val Val Thr
 65                  70                  75                  80

Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp Gln Ser Glu Asn Gly
                 85                  90                  95

Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu Ala Glu Phe His Phe
            100                 105                 110

Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg Pro Ala Ala Met Leu
        115                 120                 125

Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Gly Val Tyr Arg Tyr
    130                 135                 140

Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly Ile Ser Thr Gly Pro
145                 150                 155                 160

Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser Arg Tyr Ser Asp Ile
                165                 170                 175

Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg Ala Leu Asp Pro Ala
            180                 185                 190

Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile Gln Asn Leu Leu Lys
        195                 200                 205

Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu His Thr Leu Gly Asp
    210                 215                 220

Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu Lys Tyr Tyr Tyr Ala
225                 230                 235                 240

Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe Cys Tyr Gly His Ala
                245                 250                 255

Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu Glu Val Glu Gly Met
            260                 265                 270

Val His Gly His Cys Met Cys Arg His Asn Thr Lys Gly Leu Asn Cys
        275                 280                 285

Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro Trp Arg Pro Ala Glu
    290                 295                 300

Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn Cys Asn Glu His Ser
305                 310                 315                 320

Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu Ala Thr Gly Asn Val
                325                 330                 335

Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn Thr Met Gly Arg Asn
            340                 345                 350
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Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His Pro Glu Arg Asp Ile
        355                 360                 365

Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys Asp Pro Ala Gly Ser
    370                 375                 380

Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp Phe Ser Thr Gly Leu
385                 390                 395                 400

Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val Glu Gly Glu His Cys
                405                 410                 415

Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser Ser Glu Asp Pro Phe
            420                 425                 430

Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly Thr Ile Pro Gly Gly
        435                 440                 445

Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr Cys Lys Arg Leu Val
    450                 455                 460

Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu His Trp Gly Leu Ser
465                 470                 475                 480

Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys Asp Leu Gly Gly Ala
                485                 490                 495

Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln Cys Ser Cys Arg Pro
            500                 505                 510

His Met Ile Gly Arg Gln Cys Asn Glu Val Glu Pro Gly Tyr Tyr Phe
        515                 520                 525

Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu Glu Ala Asn Leu Gly
    530                 535                 540

Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile Gln Asp Arg Ile Pro
545                 550                 555                 560

Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro Glu Gly Ala Tyr Leu
                565                 570                 575

Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met Glu Tyr Asp Ile Leu
            580                 585                 590

Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp Glu Lys Ala Val Ile
        595                 600                 605

Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser Ser Arg Cys Gly Asn
    610                 615                 620

Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser Leu Ser Pro Gly Ser
625                 630                 635                 640

Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe Glu Lys Gly Thr Asn
                645                 650                 655

Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr Ser Ser Asp Ser Asp
            660                 665                 670
```

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Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu Val Leu Met Pro Tyr
        675                 680                 685

Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly Ser Gly Asp Gly Val
    690                 695                 700

Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg Tyr Arg Cys Leu Glu
705                 710                 715                 720

Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr Asp Val Cys Arg Asn
                725                 730                 735

Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln Thr Gly Leu Ala Cys
            740                 745                 750

Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val Cys Asp Pro Asn Gly
        755                 760                 765

Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly Arg Thr Cys Asn Arg
    770                 775                 780

Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser Gly Cys Lys Pro Cys
785                 790                 795                 800

Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe Cys Asn Pro Val Thr
                805                 810                 815

Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala Arg Gln Cys Asp Arg
            820                 825                 830

Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys Gln Pro Cys Gln Cys
        835                 840                 845

Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr Gly Glu Cys Leu Asn
    850                 855                 860

Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu Arg Cys Leu Ala Gly
865                 870                 875                 880

Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp His Cys Arg Pro Cys
                885                 890                 895

Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln Phe Ala Arg Ser Cys
            900                 905                 910

Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys Val Cys Asp Pro Gly
        915                 920                 925

Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser Gly Tyr Phe Gly Asn
    930                 935                 940

Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys Gln Cys His Asn Asn
945                 950                 955                 960

Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys Glu Thr Gly Arg Cys
                965                 970                 975

Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His Cys Gln Phe Cys Arg
            980                 985                 990

Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp Cys Arg Lys Cys Val
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995 1000 1005

Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys Asn Gly Ser Asp Cys
1010 1015 1020

Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys Leu Pro Asn Val Ile
1025 1030 1035 1040

Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr Trp Gln Leu Ala Ser
1045 1050 1055

Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala Ala His Ser Phe Gly
1060 1065 1070

Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln Cys Met Pro Gly Phe
1075 1080 1085

Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu Phe Trp Gly Asp Pro
1090 1095 1100

Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro Arg Gly Ile Glu Thr
1105 1110 1115 1120

Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val Cys Val Glu Gly Val
1125 1130 1135

Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly Tyr Ser Gly Val Phe
1140 1145 1150

Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala Leu Trp Asp Val Ile
1155 1160 1165

Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe Leu Glu Lys Ala Lys
1170 1175 1180

Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr Arg Glu Thr Val Asp
1185 1190 1195 1200

Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp Ile Leu Ala Gln Ser
1205 1210 1215

Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn Leu Phe Glu Glu Ala
1220 1225 1230

Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met Ala Gln Val Glu Val
1235 1240 1245

Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser Thr Ala Lys Glu Leu
1250 1255 1260

Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp Asn Thr Val Lys Glu
1265 1270 1275 1280

Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser Asp Ile Arg Gly Ala
1285 1290 1295

Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser Leu Glu Ala Glu Glu
1300 1305 1310

Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser Thr Val Glu Gln Ser
1315 1320 1325

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Ala Leu Met Arg Asp Arg Val Glu Asp Val Met Met Glu Arg Glu Ser
   1330                1335                1340

Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg Leu Leu Asp Glu Leu
1345                1350                1355                1360

Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala Ala Ala Glu Met Thr
               1365                1370                1375

Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu Thr Glu Cys Gly Gly
           1380                1385                1390

Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys Cys Gly Gly Pro Gly
       1395                1400                1405

Cys Gly Gly Leu Val Thr Val Ala His Asn Ala Trp Gln Lys Ala Met
   1410                1415                1420

Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala Glu Val Glu Gln Leu
1425                1430                1435                1440

Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala Asp Glu Ala Lys Gln
               1445                1450                1455

Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala Thr Lys Glu Lys Met
           1460                1465                1470

Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile Lys Gln Ile Arg Asn
       1475                1480                1485

Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser Ile Glu Ala Val Ala
   1490                1495                1500

Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr Pro Gln Gln Leu Gln
1505                1510                1515                1520

Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu Ser Leu Ser Gln Val
               1525                1530                1535

Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile Ala Arg Ala Glu Met
           1540                1545                1550

Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser Ala Thr Asp Val Lys
       1555                1560                1565

Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu Glu Ala Glu Lys Ala
   1570                1575                1580

Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala Asp Glu Asp Ile Gln
1585                1590                1595                1600

Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser Glu Thr Ala Ala Ser
               1605                1610                1615

Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile Ser Glu Leu Glu Arg
           1620                1625                1630

Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln Asn Ser Gly Glu Ala
       1635                1640                1645
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Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys Gln Ser Ala Glu Asp
   1650                1655                1660

Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu Lys Tyr Lys Lys Val
1665                1670                1675                1680

Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser Ala Asp Ala Arg Arg
               1685                1690                1695

Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr Leu Leu Ala Gln Ala
           1700                1705                1710

Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu Arg Lys Tyr Glu Asp
       1715                1720                1725

Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu Leu Ala Arg Leu Glu
   1730                1735                1740

Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser Gln Lys Val Ala Val
1745                1750                1755                1760

Tyr Ser Thr Cys Leu
               1765
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acatttgcct tttctccccg ctacctctcc agaaaggaag acccgaagaa aagacaggca 120

gcttgcctgc tgcgtcctcc ttcccgtgcc gcgtcccctc gtctgcgagg actggac    177

atg ggg ctg ctc cag gtg ttc gcc ttt ggt gtc cta gcc cta tgg ggc   225
Met Gly Leu Leu Gln Val Phe Ala Phe Gly Val Leu Ala Leu Trp Gly
  1               5                  10                  15

acc cga gtg tgc gct cag gaa ccg gag ttc agc tat ggc tgc gca gaa   273
Thr Arg Val Cys Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
             20                  25                  30

ggc agc tgc tac cct gcc act ggc gac ctt ctc atc ggc cga gcg caa   321
Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
         35                  40                  45

aag ctc tcc gtg act tcg aca tgt gga ctg cac aaa cca gag ccc tac   369
Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
     50                  55                  60
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tgt att gtt agc cac ctg cag gag gac aag aaa tgc ttc ata tgt gac   417
Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asp
 65                  70                  75                  80

tcc cga gac cct tat cac gag acc ctc aac ccc gac agc cat ctc att   465
Ser Arg Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
                 85                  90                  95

gag aac gtg gtc acc aca ttt gct cca aac cgc ctt aag atc tgg tgg   513
Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
            100                 105                 110

caa tcg gaa aat ggt gtg gag aac gtg acc atc caa ctg gac ctg gaa   561
Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
        115                 120                 125

gca gaa ttc cat ttc act cat ctc atc atg acc ttc aag aca ttc cgc   609
Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
    130                 135                 140

cca gcc gcc atg ctg atc gag cgg tct tct gac ttt ggg aag act tgg   657
Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145                 150                 155                 160

ggc gtg tac aga tac ttc gcc tac gac tgt gag agc tcg ttc cca ggc   705
Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ser Ser Phe Pro Gly
                165                 170                 175

att tca act gga ccc atg aag aaa gtg gat gac atc atc tgt gac tct   753
Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
            180                 185                 190

cga tat tct gac att gag ccc tcg aca gaa gga gag gta ata ttt cgt   801
Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
        195                 200                 205

gct tta gat cct gct ttc aaa att gaa gac cct tat agt cca agg ata   849
Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
    210                 215                 220

cag aat cta tta aaa atc acc aac ttg aga atc aag ttt gtg aaa ctg   897
Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
225                 230                 235                 240

cac acc ttg ggg gat aac ctt ttg gac tcc aga atg gaa atc cga gag   945
His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
                245                 250                 255

aag tac tat tac gct gtt tat gat atg gtg gtt cga ggg aac tgc ttc   993
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
            260                 265                 270

tgc tat ggc cac gcc agt gaa tgc gcc cct gtg gat gga gtc aat gaa   1041
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Val Asn Glu
        275                 280                 285

gaa gtg gaa gga atg gtt cac ggg cac tgc atg tgc aga cac aac acc   1089
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
    290                 295                 300

aaa ggc ctg aac tgt gag ctg tgc atg gat ttc tac cac gat ttg ccg   1137
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Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
305                 310                 315                 320

tgg aga cct gct gaa ggc cgg aac agc aac gcc tgc aaa aaa tgt aac   1185
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
                325                 330                 335

tgc aat gaa cat tcc agc tcg tgt cac ttt gac atg gca gtc ttc ctg   1233
Cys Asn Glu His Ser Ser Ser Cys His Phe Asp Met Ala Val Phe Leu
            340                 345                 350

gct act ggc aac gtc agc ggg gga gtg tgt gat aac tgt cag cac aac   1281
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asn Cys Gln His Asn
        355                 360                 365

acc atg ggg cgc aac tgt gaa cag tgc aaa ccg ttc tac ttc cag cac   1329
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Phe Gln His
    370                 375                 380

cct gag agg gac atc cgg gac ccc aat ctc tgt gaa cca tgt acc tgt   1377
Pro Glu Arg Asp Ile Arg Asp Pro Asn Leu Cys Glu Pro Cys Thr Cys
385                 390                 395                 400

gac cca gct ggt tct gag aat ggc ggg atc tgt gat ggg tac act gat   1425
Asp Pro Ala Gly Ser Glu Asn Gly Gly Ile Cys Asp Gly Tyr Thr Asp
                405                 410                 415

ttt tct gtg ggt ctc att gct ggt cag tgt cgg tgc aaa ttg cac gtg   1473
Phe Ser Val Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu His Val
            420                 425                 430

gag gga gag cgc tgt gat gtt tgt aaa gaa ggc ttc tac gac tta agt   1521
Glu Gly Glu Arg Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser
        435                 440                 445

gct gaa gac ccg tat ggt tgt aaa tca tgt gct tgc aat cct ctg gga   1569
Ala Glu Asp Pro Tyr Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly
    450                 455                 460

aca att cct ggt ggg aat cct tgt gat tct gag act ggc tac tgc tac   1617
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly Tyr Cys Tyr
465                 470                 475                 480

tgt aag cgc ctg gtg aca gga cag cgc tgt gac cag tgc ctg ccg cag   1665
Cys Lys Arg Leu Val Thr Gly Gln Arg Cys Asp Gln Cys Leu Pro Gln
                485                 490                 495

cac tgg ggt tta agc aat gat ttg gat ggg tgt cga cct tgt gac tgt   1713
His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
            500                 505                 510

gac ctt gga ggg gcg ctg aac aat agc tgc tcc gag gac tcc ggc cag   1761
Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Ser Glu Asp Ser Gly Gln
        515                 520                 525

tgc tcc tgc ctg ccc cac atg att ggg cgg cag tgt aac gag gtg gag   1809
Cys Ser Cys Leu Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
    530                 535                 540

tcc ggt tac tac ttc acc acc ctg gac cac tac atc tac gaa gcc gag   1857
Ser Gly Tyr Tyr Phe Thr Thr Leu Asp His Tyr Ile Tyr Glu Ala Glu
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545                 550                 555                 560

gaa gcc aat ctg ggg cct gga gtc gtt gtg gtg gaa agg cag tac att   1905
Glu Ala Asn Leu Gly Pro Gly Val Val Val Val Glu Arg Gln Tyr Ile
                565                 570                 575

cag gac cgc att cct tcc tgg aca gga cct ggc ttc gtc cgg gtg cct   1953
Gln Asp Arg Ile Pro Ser Trp Thr Gly Pro Gly Phe Val Arg Val Pro
            580                 585                 590

gaa ggg gct tat ttg gag ttt ttc att gac aac ata cca tat tcc atg   2001
Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
        595                 600                 605

gag tat gaa atc ctg att cgc tat gag cca cag ctg ccg gac cac tgg   2049
Glu Tyr Glu Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
    610                 615                 620

gag aaa gct gtc atc act gta cag cgg ccg ggg aag att cca gcc agc   2097
Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Lys Ile Pro Ala Ser
625                 630                 635                 640

agc cga tgt ggt aac acc gtt ccc gat gat gac aac cag gtg gtg tcc   2145
Ser Arg Cys Gly Asn Thr Val Pro Asp Asp Asp Asn Gln Val Val Ser
                645                 650                 655

ttg tca ccg ggc tca aga tac gtt gtc ctc cct cgc ccc gtg tgc ttt   2193
Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
            660                 665                 670

gag aag gga atg aac tac acg gtg agg ttg gag ctg ccc cag tat acg   2241
Glu Lys Gly Met Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
        675                 680                 685

gca tcg ggc agt gac gtg gag agc cct tac acg ttc atc gac tcg ctt   2289
Ala Ser Gly Ser Asp Val Glu Ser Pro Tyr Thr Phe Ile Asp Ser Leu
    690                 695                 700

gtt ctc atg ccc tac tgt aaa tcg ctg gac atc ttc act gtt ggc ggc   2337
Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
705                 710                 715                 720

tca ggc gat ggg gag gtc acc aat agt gcc tgg gaa acc ttc cag cgc   2385
Ser Gly Asp Gly Glu Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
                725                 730                 735

tac agg tgt ctg gag aac agc agg agt gtg gta aaa aca ccc atg aca   2433
Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
            740                 745                 750

gat gtc tgc aga aac att atc ttc agc att tct gcc ttg att cac cag   2481
Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Ile His Gln
        755                 760                 765

acg ggc ctt gct tgt gaa tgt gac ccc cag gga tct ctg agt tct gtg   2529
Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
    770                 775                 780

tgt gac ccc aat ggt ggc cag tgc cag tgc cgt cct aat gtg gtt gga   2577
Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
785                 790                 795                 800
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aga acc tgc aac agg tgt gcc ccg ggc acc ttt ggc ttt ggc ccc aac   2625
Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Asn
                805                 810                 815

gga tgc aaa cct tgt gac tgc cat ctg caa ggg tct gcc agt gcc ttc   2673
Gly Cys Lys Pro Cys Asp Cys His Leu Gln Gly Ser Ala Ser Ala Phe
            820                 825                 830

tgc gat gcg atc act ggc cag tgc cac tgt ttc cag ggc atc tat gct   2721
Cys Asp Ala Ile Thr Gly Gln Cys His Cys Phe Gln Gly Ile Tyr Ala
        835                 840                 845

cgg cag tgt gac cga tgt ctc cct ggg tat tgg ggc ttt ccc agc tgc   2769
Arg Gln Cys Asp Arg Cys Leu Pro Gly Tyr Trp Gly Phe Pro Ser Cys
    850                 855                 860

cag ccc tgc cag tgt aat ggt cat gct cta gac tgt gac aca gtg aca   2817
Gln Pro Cys Gln Cys Asn Gly His Ala Leu Asp Cys Asp Thr Val Thr
865                 870                 875                 880

ggg gag tgt ctg agc tgt cag gac tac acc acg ggc cac aac tgc gaa   2865
Gly Glu Cys Leu Ser Cys Gln Asp Tyr Thr Thr Gly His Asn Cys Glu
                885                 890                 895

agg tgc ctg gct ggc tac tac ggt gat ccc atc att ggg tca gga gac   2913
Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
            900                 905                 910

cac tgt cgc cct tgc cct tgt cct gat ggt cct gac agt gga cga cag   2961
His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
        915                 920                 925

ttt gcc agg agc tgt tat caa gac ccc gtc act ctc cag ctt gcg tgt   3009
Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
    930                 935                 940

gtt tgt gat cct ggg tac att ggc tcc aga tgt gat gac tgt gcc tct   3057
Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
945                 950                 955                 960

gga ttt ttt ggc aat ccc tca gac ttt ggg ggt tca tgt caa ccg tgt   3105
Gly Phe Phe Gly Asn Pro Ser Asp Phe Gly Gly Ser Cys Gln Pro Cys
                965                 970                 975

cag tgc cac cac aac att gac act acc gat cca gaa gcc tgt gac aag   3153
Gln Cys His His Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
            980                 985                 990

gac acg gga cga tgc ctc aag tgc ctg tac cac acg gaa ggg gac cat   3201
Asp Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Asp His
        995                1000                1005

tgc cag ctc tgc cag tat ggg tac tac ggc gat gct ctt cgg caa gac   3249
Cys Gln Leu Cys Gln Tyr Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp
   1010                1015                1020

tgt aga aag tgt gtc tgc aat tac ctg ggc acg gtg aag gaa cat tgt   3297
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Lys Glu His Cys
1025                1030                1035                1040
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aat ggc tct gac tgc cac tgt gac aaa gcc act ggt cag tgc tcg tgc   3345
Asn Gly Ser Asp Cys His Cys Asp Lys Ala Thr Gly Gln Cys Ser Cys
               1045                1050                1055

ctt ccc aat gtg atc ggg cag aac tgt gac cgg tgt gcg ccc aac acc   3393
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr
           1060                1065                1070

tgg cag ctg gct agc ggg act ggc tgc ggg ccc tgc aat tgc aat gct   3441
Trp Gln Leu Ala Ser Gly Thr Gly Cys Gly Pro Cys Asn Cys Asn Ala
       1075                1080                1085

gcg cat tcc ttt ggg cca tcc tgc aac gag ttc aca ggg cag tgc cag   3489
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln
   1090                1095                1100

tgc atg ccg ggc ttt gga ggc cga acc tgc agc gag tgc cag gag ctc   3537
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu
1105                1110                1115                1120

ttc tgg gga gac cct gat gtg gaa tgc cga gcc tgt gac tgt gat ccc   3585
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro
               1125                1130                1135

agg ggc att gag aca cct cag tgt gac cag tcc acg ggc cag tgt gtc   3633
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val
           1140                1145                1150

tgt gtg gag ggt gta gag ggt cct cgc tgc gac aag tgc acc aga ggt   3681
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly
       1155                1160                1165

tac tcg ggg gtc ttt cct gac tgc aca ccc tgc cac cag tgc ttt gct   3729
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala
   1170                1175                1180

ctc tgg gat gct atc att ggt gag ctg acc aac agg acc cac aaa ttc   3777
Leu Trp Asp Ala Ile Ile Gly Glu Leu Thr Asn Arg Thr His Lys Phe
1185                1190                1195                1200

ctg gag aaa gcc aag gct ctg aaa atc agt ggt gtg att ggt ccc tac   3825
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr
               1205                1210                1215

cga gag acc gtg gac tct gta gag aag aaa gtc aat gag ata aaa gac   3873
Arg Glu Thr Val Asp Ser Val Glu Lys Lys Val Asn Glu Ile Lys Asp
           1220                1225                1230

atc ctg gcc cag agc cca gca gcg gaa cca ctg aaa aac att ggc att   3921
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Ile
       1235                1240                1245

ctc ttc gag gag gca gag aaa cta acc aaa gat gtc aca gaa aag atg   3969
Leu Phe Glu Glu Ala Glu Lys Leu Thr Lys Asp Val Thr Glu Lys Met
   1250                1255                1260

gcg cag gta gaa gtg aaa tta act gat aca gct tca cag agt aac agc   4017
Ala Gln Val Glu Val Lys Leu Thr Asp Thr Ala Ser Gln Ser Asn Ser
1265                1270                1275                1280

aca gct gga gag ctc ggc gca ctg cag gca gaa gca gag agc ctt gac   4065
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Thr Ala Gly Glu Leu Gly Ala Leu Gln Ala Glu Ala Glu Ser Leu Asp
                1285                1290                1295

aag acc gtg aag gag ctg gca gaa cag ctg gag ttt atc aaa aac tcc   4113
Lys Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser
            1300                1305                1310

gat att cag ggc gcc ttg gat agc atc acc aag tat ttc cag atg tct   4161
Asp Ile Gln Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
        1315                1320                1325

ctt gag gca gag aag cgg gtg aat gcc tcc acc aca gac ccc aac agc   4209
Leu Glu Ala Glu Lys Arg Val Asn Ala Ser Thr Thr Asp Pro Asn Ser
    1330                1335                1340

act gtg gag cag tct gcc ctc acg cga gac aga gta gaa gat ctg atg   4257
Thr Val Glu Gln Ser Ala Leu Thr Arg Asp Arg Val Glu Asp Leu Met
1345                1350                1355                1360

ttg gag cga gag tct ccg ttc aag gag cag cag gag gaa cag gca cgc   4305
Leu Glu Arg Glu Ser Pro Phe Lys Glu Gln Gln Glu Glu Gln Ala Arg
                1365                1370                1375

ctc ctg gac gaa ctg gcc ggc aaa ctg caa agt ctc gac ctg tcg gct   4353
Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
            1380                1385                1390

gct gca cag atg acc tgt gga aca cct cca ggg gct gac tgt tct gaa   4401
Ala Ala Gln Met Thr Cys Gly Thr Pro Pro Gly Ala Asp Cys Ser Glu
        1395                1400                1405

agt gaa tgt ggt ggc ccc aac tgc aga act gac gaa gga gag aag aag   4449
Ser Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Lys Lys
    1410                1415                1420

tgt ggg ggg cct ggc tgt ggt ggt ctg gtc act gtg gcc cac agt gct   4497
Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Ser Ala
1425                1430                1435                1440

tgg cag aaa gcc atg gat ttt gac cgt gat gtc ctg agt gcc ctg gct   4545
Trp Gln Lys Ala Met Asp Phe Asp Arg Asp Val Leu Ser Ala Leu Ala
                1445                1450                1455

gaa gtc gaa cag ctc tcc aag atg gtc tct gaa gca aaa gtg aga gca   4593
Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Val Arg Ala
            1460                1465                1470

gat gag gcg aag cag aat gcg cag gat gtc ctg tta aaa aca aat gct   4641
Asp Glu Ala Lys Gln Asn Ala Gln Asp Val Leu Leu Lys Thr Asn Ala
        1475                1480                1485

acc aaa gaa aaa gtg gac aag agc aac gag gac ctg cgg aac ctc atc   4689
Thr Lys Glu Lys Val Asp Lys Ser Asn Glu Asp Leu Arg Asn Leu Ile
    1490                1495                1500

aag cag atc aga aac ttc ctg act gag gat agt gct gat cta gac agt   4737
Lys Gln Ile Arg Asn Phe Leu Thr Glu Asp Ser Ala Asp Leu Asp Ser
1505                1510                1515                1520

att gaa gca gtt gct aat gaa gta ctg aaa agt gga aat gct agc acg   4785
Ile Glu Ala Val Ala Asn Glu Val Leu Lys Ser Gly Asn Ala Ser Thr
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                1525                1530                1535

cca cag cag tta cag aac cta aca gaa gac att cgg gag cga gtt gaa   4833
Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
          1540                1545                1550

acc ctc tct caa gta gag gtt att ttg cag cag agt gca gct gac att   4881
Thr Leu Ser Gln Val Glu Val Ile Leu Gln Gln Ser Ala Ala Asp Ile
       1555                1560                1565

gcc aga gct gag ctg ttg ctt gag gaa gct aag aga gca agc aaa agt   4929
Ala Arg Ala Glu Leu Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
   1570                1575                1580

gca aca gat gtt aaa gtc act gca gac atg gtg aag gaa gca tta gaa   4977
Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585                1590                1595                1600

gaa gca gaa aag gcc cag gtt gca gca gag aag gcg att aaa caa gct   5025
Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
               1605                1610                1615

gat gag gat atc caa gga acc caa aac ctg cta aca tcg att gaa tct   5073
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
          1620                1625                1630

gaa acg gca gct tct gag gaa acc ctg acc aac gcc tcc cag cgc atc   5121
Glu Thr Ala Ala Ser Glu Glu Thr Leu Thr Asn Ala Ser Gln Arg Ile
       1635                1640                1645

agc aag ctt gag agg aac gtg gaa gag ctt aag cgt aaa gct gcc cag   5169
Ser Lys Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
   1650                1655                1660

aac tct ggg gag gca gaa tat atc gaa aaa gta gta tat tct gta aaa   5217
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Ser Val Lys
1665                1670                1675                1680

cag aat gca gac gat gtt aaa aag act cta gat ggc gaa ctt gat gaa   5265
Gln Asn Ala Asp Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
               1685                1690                1695

aag tat aag aag gta gaa agt tta att gcc caa aaa act gaa gag tca   5313
Lys Tyr Lys Lys Val Glu Ser Leu Ile Ala Gln Lys Thr Glu Glu Ser
          1700                1705                1710

gca gat gcc agg agg aaa gct gag ctg cta caa aat gaa gca aaa aca   5361
Ala Asp Ala Arg Arg Lys Ala Glu Leu Leu Gln Asn Glu Ala Lys Thr
       1715                1720                1725

ctc ttg gct caa gct aac agc aag ctc cag ctg ttg gaa gac tta gaa   5409
Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Glu Asp Leu Glu
   1730                1735                1740

aga aaa tat gag gac aat caa aaa tac tta gaa gat aaa gct caa gaa   5457
Arg Lys Tyr Glu Asp Asn Gln Lys Tyr Leu Glu Asp Lys Ala Gln Glu
1745                1750                1755                1760

ttg gtg cga ctg gaa gga gag gtt cgc tcc ctc ctt aag gac ata agt   5505
Leu Val Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
               1765                1770                1775
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gag aaa gtt gcg gtt tac agc acc tgc tta taacaggaag gggctgtaga     5555
Glu Lys Val Ala Val Tyr Ser Thr Cys Leu
          1780                1785

ggggctcggt gaccaaggta aaccacacgc gcaaaccgag gcagtcatct acaaataacc 5615

catcatctat ttaatgtttt taaccaccta cttttgtatg gagttaaata aaagacattg 5675

gttttgtata aaca                                                   5689


<210> 10
<211> 1786
<212> PRT
<213> Mus musculus

<400> 10
Met Gly Leu Leu Gln Val Phe Ala Phe Gly Val Leu Ala Leu Trp Gly
  1               5                  10                  15

Thr Arg Val Cys Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
             20                  25                  30

Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
         35                  40                  45

Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
     50                  55                  60

Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asp
 65                  70                  75                  80

Ser Arg Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
                85                  90                  95

Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
            100                 105                 110

Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
        115                 120                 125

Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
    130                 135                 140

Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145                 150                 155                 160

Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ser Ser Phe Pro Gly
                165                 170                 175

Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
            180                 185                 190

Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
        195                 200                 205

Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
    210                 215                 220

Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
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225                 230                 235                 240

His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
                245                 250                 255

Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
            260                 265                 270

Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Val Asn Glu
        275                 280                 285

Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
    290                 295                 300

Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
305                 310                 315                 320

Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
                325                 330                 335

Cys Asn Glu His Ser Ser Ser Cys His Phe Asp Met Ala Val Phe Leu
            340                 345                 350

Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asn Cys Gln His Asn
        355                 360                 365

Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Phe Gln His
    370                 375                 380

Pro Glu Arg Asp Ile Arg Asp Pro Asn Leu Cys Glu Pro Cys Thr Cys
385                 390                 395                 400

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

Phe Ser Val Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu His Val
            420                 425                 430

Glu Gly Glu Arg Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser
        435                 440                 445

Ala Glu Asp Pro Tyr Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly
    450                 455                 460

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

Cys Lys Arg Leu Val Thr Gly Gln Arg Cys Asp Gln Cys Leu Pro Gln
                485                 490                 495

His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
            500                 505                 510

Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Ser Glu Asp Ser Gly Gln
        515                 520                 525

Cys Ser Cys Leu Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
    530                 535                 540

Ser Gly Tyr Tyr Phe Thr Thr Leu Asp His Tyr Ile Tyr Glu Ala Glu
545                 550                 555                 560
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Glu Ala Asn Leu Gly Pro Gly Val Val Val Val Glu Arg Gln Tyr Ile
                565                 570                 575

Gln Asp Arg Ile Pro Ser Trp Thr Gly Pro Gly Phe Val Arg Val Pro
            580                 585                 590

Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
        595                 600                 605

Glu Tyr Glu Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
    610                 615                 620

Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Lys Ile Pro Ala Ser
625                 630                 635                 640

Ser Arg Cys Gly Asn Thr Val Pro Asp Asp Asp Asn Gln Val Val Ser
                645                 650                 655

Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
            660                 665                 670

Glu Lys Gly Met Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
        675                 680                 685

Ala Ser Gly Ser Asp Val Glu Ser Pro Tyr Thr Phe Ile Asp Ser Leu
    690                 695                 700

Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
705                 710                 715                 720

Ser Gly Asp Gly Glu Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
                725                 730                 735

Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
            740                 745                 750

Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Ile His Gln
        755                 760                 765

Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
    770                 775                 780

Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
785                 790                 795                 800

Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Asn
                805                 810                 815

Gly Cys Lys Pro Cys Asp Cys His Leu Gln Gly Ser Ala Ser Ala Phe
            820                 825                 830

Cys Asp Ala Ile Thr Gly Gln Cys His Cys Phe Gln Gly Ile Tyr Ala
        835                 840                 845

Arg Gln Cys Asp Arg Cys Leu Pro Gly Tyr Trp Gly Phe Pro Ser Cys
    850                 855                 860

Gln Pro Cys Gln Cys Asn Gly His Ala Leu Asp Cys Asp Thr Val Thr
865                 870                 875                 880
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Gly Glu Cys Leu Ser Cys Gln Asp Tyr Thr Thr Gly His Asn Cys Glu
                885                 890                 895

Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
            900                 905                 910

His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
        915                 920                 925

Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
    930                 935                 940

Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
945                 950                 955                 960

Gly Phe Phe Gly Asn Pro Ser Asp Phe Gly Gly Ser Cys Gln Pro Cys
                965                 970                 975

Gln Cys His His Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
            980                 985                 990

Asp Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Asp His
        995                1000                1005

Cys Gln Leu Cys Gln Tyr Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp
   1010                1015                1020

Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Lys Glu His Cys
1025                1030                1035                1040

Asn Gly Ser Asp Cys His Cys Asp Lys Ala Thr Gly Gln Cys Ser Cys
                1045                1050                1055

Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr
            1060                1065                1070

Trp Gln Leu Ala Ser Gly Thr Gly Cys Gly Pro Cys Asn Cys Asn Ala
       1075                1080                1085

Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln
   1090                1095                1100

Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu
1105                1110                1115                1120

Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro
                1125                1130                1135

Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val
            1140                1145                1150

Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly
       1155                1160                1165

Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala
   1170                1175                1180

Leu Trp Asp Ala Ile Ile Gly Glu Leu Thr Asn Arg Thr His Lys Phe
1185                1190                1195                1200

Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr
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                1205                1210                1215

Arg Glu Thr Val Asp Ser Val Glu Lys Lys Val Asn Glu Ile Lys Asp
            1220                1225                1230

Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Ile
        1235                1240                1245

Leu Phe Glu Glu Ala Glu Lys Leu Thr Lys Asp Val Thr Glu Lys Met
    1250                1255                1260

Ala Gln Val Glu Val Lys Leu Thr Asp Thr Ala Ser Gln Ser Asn Ser
1265                1270                1275                1280

Thr Ala Gly Glu Leu Gly Ala Leu Gln Ala Glu Ala Glu Ser Leu Asp
                1285                1290                1295

Lys Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser
            1300                1305                1310

Asp Ile Gln Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
        1315                1320                1325

Leu Glu Ala Glu Lys Arg Val Asn Ala Ser Thr Thr Asp Pro Asn Ser
    1330                1335                1340

Thr Val Glu Gln Ser Ala Leu Thr Arg Asp Arg Val Glu Asp Leu Met
1345                1350                1355                1360

Leu Glu Arg Glu Ser Pro Phe Lys Glu Gln Gln Glu Glu Gln Ala Arg
                1365                1370                1375

Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
            1380                1385                1390

Ala Ala Gln Met Thr Cys Gly Thr Pro Pro Gly Ala Asp Cys Ser Glu
        1395                1400                1405

Ser Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Lys Lys
    1410                1415                1420

Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Ser Ala
1425                1430                1435                1440

Trp Gln Lys Ala Met Asp Phe Asp Arg Asp Val Leu Ser Ala Leu Ala
                1445                1450                1455

Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Val Arg Ala
            1460                1465                1470

Asp Glu Ala Lys Gln Asn Ala Gln Asp Val Leu Leu Lys Thr Asn Ala
        1475                1480                1485

Thr Lys Glu Lys Val Asp Lys Ser Asn Glu Asp Leu Arg Asn Leu Ile
    1490                1495                1500

Lys Gln Ile Arg Asn Phe Leu Thr Glu Asp Ser Ala Asp Leu Asp Ser
1505                1510                1515                1520

Ile Glu Ala Val Ala Asn Glu Val Leu Lys Ser Gly Asn Ala Ser Thr
                1525                1530                1535
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Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
          1540                1545                1550

Thr Leu Ser Gln Val Glu Val Ile Leu Gln Gln Ser Ala Ala Asp Ile
       1555                1560                1565

Ala Arg Ala Glu Leu Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
   1570                1575                1580

Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585                1590                1595                1600

Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
               1605                1610                1615

Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
          1620                1625                1630

Glu Thr Ala Ala Ser Glu Glu Thr Leu Thr Asn Ala Ser Gln Arg Ile
       1635                1640                1645

Ser Lys Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
   1650                1655                1660

Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Ser Val Lys
1665                1670                1675                1680

Gln Asn Ala Asp Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
               1685                1690                1695

Lys Tyr Lys Lys Val Glu Ser Leu Ile Ala Gln Lys Thr Glu Glu Ser
          1700                1705                1710

Ala Asp Ala Arg Arg Lys Ala Glu Leu Leu Gln Asn Glu Ala Lys Thr
       1715                1720                1725

Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Glu Asp Leu Glu
   1730                1735                1740

Arg Lys Tyr Glu Asp Asn Gln Lys Tyr Leu Glu Asp Lys Ala Gln Glu
1745                1750                1755                1760

Leu Val Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
               1765                1770                1775

Glu Lys Val Ala Val Tyr Ser Thr Cys Leu
          1780                1785


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  1               5                  10                  15

ata tgt gac tcc cga gac cct tat cac gag acc ctc aac ccc gac agc   96
Ile Cys Asp Ser Arg Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser
             20                  25                  30

cat ctc att gag aac gtg gtc acc aca ttt gct cca aac cgc ctt aag   144
His Leu Ile Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys
         35                  40                  45

atc tgg tgg caa tcg gaa aat ggt gtg gag aac gtg acc atc caa ctg   192
Ile Trp Trp Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu
     50                  55                  60

gac ctg gaa gca gaa ttc cat ttc act cat ctc atc atg acc ttc aag   240
Asp Leu Glu Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys
 65                  70                  75                  80

aca ttc cgc cca gcc gcc atg ctg atc gag cgg tct tct gac ttt ggg   288
Thr Phe Arg Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly
                 85                  90                  95

aag act tgg ggc gtg tac aga tac ttc gcc tac gac tgt gag agc tcg   336
Lys Thr Trp Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ser Ser
            100                 105                 110

ttc cca ggc att tca act gga ccc atg aag aaa gtg gat gac atc atc   384
Phe Pro Gly Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile
        115                 120                 125

tgt gac tct cga tat tct gac att gag ccc tcg aca gaa gga gag gta   432
Cys Asp Ser Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val
    130                 135                 140

ata ttt cgt gct tta gat cct gct ttc aaa att gaa gac cct tat agt   480
Ile Phe Arg Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser
145                 150                 155                 160

cca agg ata cag aat cta tta aaa atc acc aac ttg aga atc aag ttt   528
Pro Arg Ile Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe
                165                 170                 175

gtg aaa ctg cac acc ttg ggg gat aac ctt ttg gac tcc aga atg gaa   576
Val Lys Leu His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu
            180                 185                 190

atc cga gag aag tac tat tac gct gtt tat gat atg gtg gtt cga ggg   624
Ile Arg Glu Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly
        195                 200                 205

aac tgc ttc tgc tat ggc cac gcc agt gaa tgc gcc cct gtg gat gga   672
Asn Cys Phe Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly
    210                 215                 220

gtc aat gaa gaa gtg gaa gga atg gtt cac ggg cac tgc atg tgc aga   720
Val Asn Glu Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg
225                 230                 235                 240

cac aac acc aaa ggc ctg aac tgt gag ctg tgc atg gat ttc tac cac   768
His Asn Thr Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His
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                245                 250                 255

gat ttg ccg tgg aga cct gct gaa ggc cgg aac agc aac gcc tgc aaa   816
Asp Leu Pro Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys
            260                 265                 270

aaa tgt aac tgc aat gaa cat tcc agc tcg tgt cac ttt gac atg gca   864
Lys Cys Asn Cys Asn Glu His Ser Ser Ser Cys His Phe Asp Met Ala
        275                 280                 285

gtc ttc ctg gct act ggc aac gtc agc ggg gga gtg tgt gat aac tgt   912
Val Phe Leu Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asn Cys
    290                 295                 300

cag cac aac acc atg ggg cgc aac tgt gaa cag tgc aaa ccg ttc tac   960
Gln His Asn Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr
305                 310                 315                 320

ttc cag cac cct gag agg gac atc cgg gac ccc aat ctc tgt gaa cca   1008
Phe Gln His Pro Glu Arg Asp Ile Arg Asp Pro Asn Leu Cys Glu Pro
                325                 330                 335

tgt acc tgt gac cca gct ggt tct gag aat ggc ggg atc tgt gat ggg   1056
Cys Thr Cys Asp Pro Ala Gly Ser Glu Asn Gly Gly Ile Cys Asp Gly
            340                 345                 350

tac act gat ttt tct gtg ggt ctc att gct ggt cag tgt cgg tgc aaa   1104
Tyr Thr Asp Phe Ser Val Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys
        355                 360                 365

ttg cac gtg gag gga gag cgc tgt gat gtt tgt aaa gaa ggc ttc tac   1152
Leu His Val Glu Gly Glu Arg Cys Asp Val Cys Lys Glu Gly Phe Tyr
    370                 375                 380

gac tta agt gct gaa gac ccg tat ggt tgt aaa tca tgt gct tgc aat   1200
Asp Leu Ser Ala Glu Asp Pro Tyr Gly Cys Lys Ser Cys Ala Cys Asn
385                 390                 395                 400

cct ctg gga aca att cct ggt ggg aat cct tgt gat tct gag act ggc   1248
Pro Leu Gly Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly
                405                 410                 415

tac tgc tac tgt aag cgc ctg gtg aca gga cag cgc tgt gac cag tgc   1296
Tyr Cys Tyr Cys Lys Arg Leu Val Thr Gly Gln Arg Cys Asp Gln Cys
            420                 425                 430

ctg ccg cag cac tgg ggt tta agc aat gat ttg gat ggg tgt cga cct   1344
Leu Pro Gln His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro
        435                 440                 445

tgt gac tgt gac ctt gga ggg gcg ctg aac aat agc tgc tcc gag gac   1392
Cys Asp Cys Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Ser Glu Asp
    450                 455                 460

tcc ggc cag tgc tcc tgc ctg ccc cac atg att ggg cgg cag tgt aac   1440
Ser Gly Gln Cys Ser Cys Leu Pro His Met Ile Gly Arg Gln Cys Asn
465                 470                 475                 480

gag gtg gag tcc ggt tac tac ttc acc acc ctg gac cac tac atc tac   1488
Glu Val Glu Ser Gly Tyr Tyr Phe Thr Thr Leu Asp His Tyr Ile Tyr
                485                 490                 495
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gaa gcc gag gaa gcc aat ctg ggg cct gga gtc gtt gtg gtg gaa agg   1536
Glu Ala Glu Glu Ala Asn Leu Gly Pro Gly Val Val Val Val Glu Arg
            500                 505                 510

cag tac att cag gac cgc att cct tcc tgg aca gga cct ggc ttc gtc   1584
Gln Tyr Ile Gln Asp Arg Ile Pro Ser Trp Thr Gly Pro Gly Phe Val
        515                 520                 525

cgg gtg cct gaa ggg gct tat ttg gag ttt ttc att gac aac ata cca   1632
Arg Val Pro Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro
    530                 535                 540

tat tcc atg gag tat gaa atc ctg att cgc tat gag cca cag ctg ccg   1680
Tyr Ser Met Glu Tyr Glu Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro
545                 550                 555                 560

gac cac tgg gag aaa gct gtc atc act gta cag cgg ccg ggg aag att   1728
Asp His Trp Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Lys Ile
                565                 570                 575

cca gcc agc agc cga tgt ggt aac acc gtt ccc gat gat gac aac cag   1776
Pro Ala Ser Ser Arg Cys Gly Asn Thr Val Pro Asp Asp Asp Asn Gln
            580                 585                 590

gtg gtg tcc ttg tca ccg ggc tca aga tac gtt gtc ctc cct cgc ccc   1824
Val Val Ser Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro
        595                 600                 605

gtg tgc ttt gag aag gga atg aac tac acg gtg agg ttg gag ctg ccc   1872
Val Cys Phe Glu Lys Gly Met Asn Tyr Thr Val Arg Leu Glu Leu Pro
    610                 615                 620

cag tat acg gca tcg ggc agt gac gtg gag agc cct tac acg ttc atc   1920
Gln Tyr Thr Ala Ser Gly Ser Asp Val Glu Ser Pro Tyr Thr Phe Ile
625                 630                 635                 640

gac tcg ctt gtt ctc atg ccc tac tgt aaa tcg ctg gac atc ttc act   1968
Asp Ser Leu Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr
                645                 650                 655

gtt ggc ggc tca ggc gat ggg gag gtc acc aat agt gcc tgg gaa acc   2016
Val Gly Gly Ser Gly Asp Gly Glu Val Thr Asn Ser Ala Trp Glu Thr
            660                 665                 670

ttc cag cgc tac agg tgt ctg gag aac agc agg agt gtg gta aaa aca   2064
Phe Gln Arg Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr
        675                 680                 685

ccc atg aca gat gtc tgc aga aac att atc ttc agc att tct gcc ttg   2112
Pro Met Thr Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu
    690                 695                 700

att cac cag acg ggc ctt gct tgt gaa tgt gac ccc cag gga tct ctg   2160
Ile His Gln Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu
705                 710                 715                 720

agt tct gtg tgt gac ccc aat ggt ggc cag tgc cag tgc cgt cct aat   2208
Ser Ser Val Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn
                725                 730                 735
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gtg gtt gga aga acc tgc aac agg tgt gcc ccg ggc acc ttt ggc ttt   2256
Val Val Gly Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe
            740                 745                 750

ggc ccc aac gga tgc aaa cct tgt gac tgc cat ctg caa ggg tct gcc   2304
Gly Pro Asn Gly Cys Lys Pro Cys Asp Cys His Leu Gln Gly Ser Ala
        755                 760                 765

agt gcc ttc tgc gat gcg atc act ggc cag tgc cac tgt ttc cag ggc   2352
Ser Ala Phe Cys Asp Ala Ile Thr Gly Gln Cys His Cys Phe Gln Gly
    770                 775                 780

atc tat gct cgg cag tgt gac cga tgt ctc cct ggg tat tgg ggc ttt   2400
Ile Tyr Ala Arg Gln Cys Asp Arg Cys Leu Pro Gly Tyr Trp Gly Phe
785                 790                 795                 800

ccc agc tgc cag ccc tgc cag tgt aat ggt cat gct cta gac tgt gac   2448
Pro Ser Cys Gln Pro Cys Gln Cys Asn Gly His Ala Leu Asp Cys Asp
                805                 810                 815

aca gtg aca ggg gag tgt ctg agc tgt cag gac tac acc acg ggc cac   2496
Thr Val Thr Gly Glu Cys Leu Ser Cys Gln Asp Tyr Thr Thr Gly His
            820                 825                 830

aac tgc gaa agg tgc ctg gct ggc tac tac ggt gat ccc atc att ggg   2544
Asn Cys Glu Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly
        835                 840                 845

tca gga gac cac tgt cgc cct tgc cct tgt cct gat ggt cct gac agt   2592
Ser Gly Asp His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser
    850                 855                 860

gga cga cag ttt gcc agg agc tgt tat caa gac ccc gtc act ctc cag   2640
Gly Arg Gln Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln
865                 870                 875                 880

ctt gcg tgt gtt tgt gat cct ggg tac att ggc tcc aga tgt gat gac   2688
Leu Ala Cys Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp
                885                 890                 895

tgt gcc tct gga ttt ttt ggc aat ccc tca gac ttt ggg ggt tca tgt   2736
Cys Ala Ser Gly Phe Phe Gly Asn Pro Ser Asp Phe Gly Gly Ser Cys
            900                 905                 910

caa ccg tgt cag tgc cac cac aac att gac act acc gat cca gaa gcc   2784
Gln Pro Cys Gln Cys His His Asn Ile Asp Thr Thr Asp Pro Glu Ala
        915                 920                 925

tgt gac aag gac acg gga cga tgc ctc aag tgc ctg tac cac acg gaa   2832
Cys Asp Lys Asp Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu
    930                 935                 940

ggg gac cat tgc cag ctc tgc cag tat ggg tac tac ggc gat gct ctt   2880
Gly Asp His Cys Gln Leu Cys Gln Tyr Gly Tyr Tyr Gly Asp Ala Leu
945                 950                 955                 960

cgg caa gac tgt aga aag tgt gtc tgc aat tac ctg ggc acg gtg aag   2928
Arg Gln Asp Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Lys
                965                 970                 975

gaa cat tgt aat ggc tct gac tgc cac tgt gac aaa gcc act ggt cag   2976
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Glu His Cys Asn Gly Ser Asp Cys His Cys Asp Lys Ala Thr Gly Gln
            980                 985                 990

tgc tcg tgc ctt ccc aat gtg atc ggg cag aac tgt gac cgg tgt gcg   3024
Cys Ser Cys Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala
        995                1000                1005

ccc aac acc tgg cag ctg gct agc ggg act ggc tgc ggg ccc tgc aat   3072
Pro Asn Thr Trp Gln Leu Ala Ser Gly Thr Gly Cys Gly Pro Cys Asn
   1010                1015                1020

tgc aat gct gcg cat tcc ttt ggg cca tcc tgc aac gag ttc aca ggg   3120
Cys Asn Ala Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly
1025                1030                1035                1040

cag tgc cag tgc atg ccg ggc ttt gga ggc cga acc tgc agc gag tgc   3168
Gln Cys Gln Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys
               1045                1050                1055

cag gag ctc ttc tgg gga gac cct gat gtg gaa tgc cga gcc tgt gac   3216
Gln Glu Leu Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp
           1060                1065                1070

tgt gat ccc agg ggc att gag aca cct cag tgt gac cag tcc acg ggc   3264
Cys Asp Pro Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly
       1075                1080                1085

cag tgt gtc tgt gtg gag ggt gta gag ggt cct cgc tgc gac aag tgc   3312
Gln Cys Val Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys
   1090                1095                1100

acc aga ggt tac tcg ggg gtc ttt cct gac tgc aca ccc tgc cac cag   3360
Thr Arg Gly Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln
1105                1110                1115                1120

tgc ttt gct ctc tgg gat gct atc att ggt gag ctg acc aac agg acc   3408
Cys Phe Ala Leu Trp Asp Ala Ile Ile Gly Glu Leu Thr Asn Arg Thr
               1125                1130                1135

cac aaa ttc ctg gag aaa gcc aag gct ctg aaa atc agt ggt gtg att   3456
His Lys Phe Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile
           1140                1145                1150

ggt ccc tac cga gag acc gtg gac tct gta gag aag aaa gtc aat gag   3504
Gly Pro Tyr Arg Glu Thr Val Asp Ser Val Glu Lys Lys Val Asn Glu
       1155                1160                1165

ata aaa gac atc ctg gcc cag agc cca gca gcg gaa cca ctg aaa aac   3552
Ile Lys Asp Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn
   1170                1175                1180

att ggc att ctc ttc gag gag gca gag aaa cta acc aaa gat gtc aca   3600
Ile Gly Ile Leu Phe Glu Glu Ala Glu Lys Leu Thr Lys Asp Val Thr
1185                1190                1195                1200

gaa aag atg gcg cag gta gaa gtg aaa tta act gat aca gct tca cag   3648
Glu Lys Met Ala Gln Val Glu Val Lys Leu Thr Asp Thr Ala Ser Gln
               1205                1210                1215

agt aac agc aca gct gga gag ctc ggc gca ctg cag gca gaa gca gag   3696
Ser Asn Ser Thr Ala Gly Glu Leu Gly Ala Leu Gln Ala Glu Ala Glu
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          1220                1225                1230

agc ctt gac aag acc gtg aag gag ctg gca gaa cag ctg gag ttt atc   3744
Ser Leu Asp Lys Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile
       1235                1240                1245

aaa aac tcc gat att cag ggc gcc ttg gat agc atc acc aag tat ttc   3792
Lys Asn Ser Asp Ile Gln Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe
   1250                1255                1260

cag atg tct ctt gag gca gag aag cgg gtg aat gcc tcc acc aca gac   3840
Gln Met Ser Leu Glu Ala Glu Lys Arg Val Asn Ala Ser Thr Thr Asp
1265                1270                1275                1280

ccc aac agc act gtg gag cag tct gcc ctc acg cga gac aga gta gaa   3888
Pro Asn Ser Thr Val Glu Gln Ser Ala Leu Thr Arg Asp Arg Val Glu
               1285                1290                1295

gat ctg atg ttg gag cga gag tct ccg ttc aag gag cag cag gag gaa   3936
Asp Leu Met Leu Glu Arg Glu Ser Pro Phe Lys Glu Gln Gln Glu Glu
           1300                1305                1310

cag gca cgc ctc ctg gac gaa ctg gcc ggc aaa ctg caa agt ctc gac   3984
Gln Ala Arg Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp
       1315                1320                1325

ctg tcg gct gct gca cag atg acc tgt gga aca cct cca ggg gct gac   4032
Leu Ser Ala Ala Ala Gln Met Thr Cys Gly Thr Pro Pro Gly Ala Asp
   1330                1335                1340

tgt tct gaa agt gaa tgt ggt ggc ccc aac tgc aga act gac gaa gga   4080
Cys Ser Glu Ser Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly
1345                1350                1355                1360

gag aag aag tgt ggg ggg cct ggc tgt ggt ggt ctg gtc act gtg gcc   4128
Glu Lys Lys Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala
               1365                1370                1375

cac agt gct tgg cag aaa gcc atg gat ttt gac cgt gat gtc ctg agt   4176
His Ser Ala Trp Gln Lys Ala Met Asp Phe Asp Arg Asp Val Leu Ser
           1380                1385                1390

gcc ctg gct gaa gtc gaa cag ctc tcc aag atg gtc tct gaa gca aaa   4224
Ala Leu Ala Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys
       1395                1400                1405

gtg aga gca gat gag gcg aag cag aat gcg cag gat gtc ctg tta aaa   4272
Val Arg Ala Asp Glu Ala Lys Gln Asn Ala Gln Asp Val Leu Leu Lys
   1410                1415                1420

aca aat gct acc aaa gaa aaa gtg gac aag agc aac gag gac ctg cgg   4320
Thr Asn Ala Thr Lys Glu Lys Val Asp Lys Ser Asn Glu Asp Leu Arg
1425                1430                1435                1440

aac ctc atc aag cag atc aga aac ttc ctg act gag gat agt gct gat   4368
Asn Leu Ile Lys Gln Ile Arg Asn Phe Leu Thr Glu Asp Ser Ala Asp
               1445                1450                1455

cta gac agt att gaa gca gtt gct aat gaa gta ctg aaa agt gga aat   4416
Leu Asp Ser Ile Glu Ala Val Ala Asn Glu Val Leu Lys Ser Gly Asn
           1460                1465                1470
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gct agc acg cca cag cag tta cag aac cta aca gaa gac att cgg gag   4464
Ala Ser Thr Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu
       1475                1480                1485

cga gtt gaa acc ctc tct caa gta gag gtt att ttg cag cag agt gca   4512
Arg Val Glu Thr Leu Ser Gln Val Glu Val Ile Leu Gln Gln Ser Ala
   1490                1495                1500

gct gac att gcc aga gct gag ctg ttg ctt gag gaa gct aag aga gca   4560
Ala Asp Ile Ala Arg Ala Glu Leu Leu Leu Glu Glu Ala Lys Arg Ala
1505                1510                1515                1520

agc aaa agt gca aca gat gtt aaa gtc act gca gac atg gtg aag gaa   4608
Ser Lys Ser Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu
               1525                1530                1535

gca tta gaa gaa gca gaa aag gcc cag gtt gca gca gag aag gcg att   4656
Ala Leu Glu Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile
           1540                1545                1550

aaa caa gct gat gag gat atc caa gga acc caa aac ctg cta aca tcg   4704
Lys Gln Ala Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser
       1555                1560                1565

att gaa tct gaa acg gca gct tct gag gaa acc ctg acc aac gcc tcc   4752
Ile Glu Ser Glu Thr Ala Ala Ser Glu Glu Thr Leu Thr Asn Ala Ser
   1570                1575                1580

cag cgc atc agc aag ctt gag agg aac gtg gaa gag ctt aag cgt aaa   4800
Gln Arg Ile Ser Lys Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys
1585                1590                1595                1600

gct gcc cag aac tct ggg gag gca gaa tat atc gaa aaa gta gta tat   4848
Ala Ala Gln Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr
               1605                1610                1615

tct gta aaa cag aat gca gac gat gtt aaa aag act cta gat ggc gaa   4896
Ser Val Lys Gln Asn Ala Asp Asp Val Lys Lys Thr Leu Asp Gly Glu
           1620                1625                1630

ctt gat gaa aag tat aag aag gta gaa agt tta att gcc caa aaa act   4944
Leu Asp Glu Lys Tyr Lys Lys Val Glu Ser Leu Ile Ala Gln Lys Thr
       1635                1640                1645

gaa gag tca gca gat gcc agg agg aaa gct gag ctg cta caa aat gaa   4992
Glu Glu Ser Ala Asp Ala Arg Arg Lys Ala Glu Leu Leu Gln Asn Glu
   1650                1655                1660

gca aaa aca ctc ttg gct caa gct aac agc aag ctc cag ctg ttg gaa   5040
Ala Lys Thr Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Glu
1665                1670                1675                1680

gac tta gaa aga aaa tat gag gac aat caa aaa tac tta gaa gat aaa   5088
Asp Leu Glu Arg Lys Tyr Glu Asp Asn Gln Lys Tyr Leu Glu Asp Lys
               1685                1690                1695

gct caa gaa ttg gtg cga ctg gaa gga gag gtt cgc tcc ctc ctt aag   5136
Ala Gln Glu Leu Val Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys
           1700                1705                1710
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gac ata agt gag aaa gtt gcg gtt tac agc acc tgc tta taacaggaag    5185
Asp Ile Ser Glu Lys Val Ala Val Tyr Ser Thr Cys Leu
       1715                1720                1725

gggctgtaga ggggctcggt gaccaaggta aaccacacgc gcaaaccgag gcagtcatct 5245

acaaataacc catcatctat ttaatgtttt taaccaccta cttttgtatg gagttaaata 5305

aaagacattg gttttgtata aaca                                        5329


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Ile Cys Asp Ser Arg Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser
             20                  25                  30

His Leu Ile Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys
         35                  40                  45

Ile Trp Trp Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu
     50                  55                  60

Asp Leu Glu Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys
 65                  70                  75                  80

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

Lys Thr Trp Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ser Ser
            100                 105                 110

Phe Pro Gly Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile
        115                 120                 125

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

Ile Phe Arg Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser
145                 150                 155                 160

Pro Arg Ile Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe
                165                 170                 175

Val Lys Leu His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu
            180                 185                 190

Ile Arg Glu Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly
        195                 200                 205

Asn Cys Phe Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly
    210                 215                 220

Val Asn Glu Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg
225                 230                 235                 240
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His Asn Thr Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His
                245                 250                 255

Asp Leu Pro Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys
            260                 265                 270

Lys Cys Asn Cys Asn Glu His Ser Ser Ser Cys His Phe Asp Met Ala
        275                 280                 285

Val Phe Leu Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asn Cys
    290                 295                 300

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

Phe Gln His Pro Glu Arg Asp Ile Arg Asp Pro Asn Leu Cys Glu Pro
                325                 330                 335

Cys Thr Cys Asp Pro Ala Gly Ser Glu Asn Gly Gly Ile Cys Asp Gly
            340                 345                 350

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

Leu His Val Glu Gly Glu Arg Cys Asp Val Cys Lys Glu Gly Phe Tyr
    370                 375                 380

Asp Leu Ser Ala Glu Asp Pro Tyr Gly Cys Lys Ser Cys Ala Cys Asn
385                 390                 395                 400

Pro Leu Gly Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly
                405                 410                 415

Tyr Cys Tyr Cys Lys Arg Leu Val Thr Gly Gln Arg Cys Asp Gln Cys
            420                 425                 430

Leu Pro Gln His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro
        435                 440                 445

Cys Asp Cys Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Ser Glu Asp
    450                 455                 460

Ser Gly Gln Cys Ser Cys Leu Pro His Met Ile Gly Arg Gln Cys Asn
465                 470                 475                 480

Glu Val Glu Ser Gly Tyr Tyr Phe Thr Thr Leu Asp His Tyr Ile Tyr
                485                 490                 495

Glu Ala Glu Glu Ala Asn Leu Gly Pro Gly Val Val Val Val Glu Arg
            500                 505                 510

Gln Tyr Ile Gln Asp Arg Ile Pro Ser Trp Thr Gly Pro Gly Phe Val
        515                 520                 525

Arg Val Pro Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro
    530                 535                 540

Tyr Ser Met Glu Tyr Glu Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro
545                 550                 555                 560
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Asp His Trp Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Lys Ile
                565                 570                 575

Pro Ala Ser Ser Arg Cys Gly Asn Thr Val Pro Asp Asp Asp Asn Gln
            580                 585                 590

Val Val Ser Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro
        595                 600                 605

Val Cys Phe Glu Lys Gly Met Asn Tyr Thr Val Arg Leu Glu Leu Pro
    610                 615                 620

Gln Tyr Thr Ala Ser Gly Ser Asp Val Glu Ser Pro Tyr Thr Phe Ile
625                 630                 635                 640

Asp Ser Leu Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr
                645                 650                 655

Val Gly Gly Ser Gly Asp Gly Glu Val Thr Asn Ser Ala Trp Glu Thr
            660                 665                 670

Phe Gln Arg Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr
        675                 680                 685

Pro Met Thr Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu
    690                 695                 700

Ile His Gln Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu
705                 710                 715                 720

Ser Ser Val Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn
                725                 730                 735

Val Val Gly Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe
            740                 745                 750

Gly Pro Asn Gly Cys Lys Pro Cys Asp Cys His Leu Gln Gly Ser Ala
        755                 760                 765

Ser Ala Phe Cys Asp Ala Ile Thr Gly Gln Cys His Cys Phe Gln Gly
    770                 775                 780

Ile Tyr Ala Arg Gln Cys Asp Arg Cys Leu Pro Gly Tyr Trp Gly Phe
785                 790                 795                 800

Pro Ser Cys Gln Pro Cys Gln Cys Asn Gly His Ala Leu Asp Cys Asp
                805                 810                 815

Thr Val Thr Gly Glu Cys Leu Ser Cys Gln Asp Tyr Thr Thr Gly His
            820                 825                 830

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

Ser Gly Asp His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser
    850                 855                 860

Gly Arg Gln Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln
865                 870                 875                 880

Leu Ala Cys Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp
```

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                885                 890                 895

Cys Ala Ser Gly Phe Phe Gly Asn Pro Ser Asp Phe Gly Gly Ser Cys
            900                 905                 910

Gln Pro Cys Gln Cys His His Asn Ile Asp Thr Thr Asp Pro Glu Ala
        915                 920                 925

Cys Asp Lys Asp Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu
    930                 935                 940

Gly Asp His Cys Gln Leu Cys Gln Tyr Gly Tyr Tyr Gly Asp Ala Leu
945                 950                 955                 960

Arg Gln Asp Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Lys
                965                 970                 975

Glu His Cys Asn Gly Ser Asp Cys His Cys Asp Lys Ala Thr Gly Gln
            980                 985                 990

Cys Ser Cys Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala
        995                1000                1005

Pro Asn Thr Trp Gln Leu Ala Ser Gly Thr Gly Cys Gly Pro Cys Asn
   1010                1015                1020

Cys Asn Ala Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly
1025                1030                1035                1040

Gln Cys Gln Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys
                1045                1050                1055

Gln Glu Leu Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp
            1060                1065                1070

Cys Asp Pro Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly
        1075                1080                1085

Gln Cys Val Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys
   1090                1095                1100

Thr Arg Gly Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln
1105                1110                1115                1120

Cys Phe Ala Leu Trp Asp Ala Ile Ile Gly Glu Leu Thr Asn Arg Thr
                1125                1130                1135

His Lys Phe Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile
            1140                1145                1150

Gly Pro Tyr Arg Glu Thr Val Asp Ser Val Glu Lys Lys Val Asn Glu
        1155                1160                1165

Ile Lys Asp Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn
   1170                1175                1180

Ile Gly Ile Leu Phe Glu Glu Ala Glu Lys Leu Thr Lys Asp Val Thr
1185                1190                1195                1200

Glu Lys Met Ala Gln Val Glu Val Lys Leu Thr Asp Thr Ala Ser Gln
                1205                1210                1215
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Ser Asn Ser Thr Ala Gly Glu Leu Gly Ala Leu Gln Ala Glu Ala Glu
          1220                1225                1230

Ser Leu Asp Lys Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile
      1235                1240                1245

Lys Asn Ser Asp Ile Gln Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe
  1250                1255                1260

Gln Met Ser Leu Glu Ala Glu Lys Arg Val Asn Ala Ser Thr Thr Asp
1265                1270                1275                1280

Pro Asn Ser Thr Val Glu Gln Ser Ala Leu Thr Arg Asp Arg Val Glu
              1285                1290                1295

Asp Leu Met Leu Glu Arg Glu Ser Pro Phe Lys Glu Gln Gln Glu Glu
          1300                1305                1310

Gln Ala Arg Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp
      1315                1320                1325

Leu Ser Ala Ala Ala Gln Met Thr Cys Gly Thr Pro Pro Gly Ala Asp
  1330                1335                1340

Cys Ser Glu Ser Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly
1345                1350                1355                1360

Glu Lys Lys Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala
              1365                1370                1375

His Ser Ala Trp Gln Lys Ala Met Asp Phe Asp Arg Asp Val Leu Ser
          1380                1385                1390

Ala Leu Ala Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys
      1395                1400                1405

Val Arg Ala Asp Glu Ala Lys Gln Asn Ala Gln Asp Val Leu Leu Lys
  1410                1415                1420

Thr Asn Ala Thr Lys Glu Lys Val Asp Lys Ser Asn Glu Asp Leu Arg
1425                1430                1435                1440

Asn Leu Ile Lys Gln Ile Arg Asn Phe Leu Thr Glu Asp Ser Ala Asp
              1445                1450                1455

Leu Asp Ser Ile Glu Ala Val Ala Asn Glu Val Leu Lys Ser Gly Asn
          1460                1465                1470

Ala Ser Thr Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu
      1475                1480                1485

Arg Val Glu Thr Leu Ser Gln Val Glu Val Ile Leu Gln Gln Ser Ala
  1490                1495                1500

Ala Asp Ile Ala Arg Ala Glu Leu Leu Leu Glu Glu Ala Lys Arg Ala
1505                1510                1515                1520

Ser Lys Ser Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu
              1525                1530                1535
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Ala Leu Glu Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile
          1540                1545                1550

Lys Gln Ala Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser
       1555                1560                1565

Ile Glu Ser Glu Thr Ala Ala Ser Glu Glu Thr Leu Thr Asn Ala Ser
   1570                1575                1580

Gln Arg Ile Ser Lys Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys
1585                1590                1595                1600

Ala Ala Gln Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr
               1605                1610                1615

Ser Val Lys Gln Asn Ala Asp Asp Val Lys Lys Thr Leu Asp Gly Glu
          1620                1625                1630

Leu Asp Glu Lys Tyr Lys Lys Val Glu Ser Leu Ile Ala Gln Lys Thr
       1635                1640                1645

Glu Glu Ser Ala Asp Ala Arg Arg Lys Ala Glu Leu Leu Gln Asn Glu
   1650                1655                1660

Ala Lys Thr Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Glu
1665                1670                1675                1680

Asp Leu Glu Arg Lys Tyr Glu Asp Asn Gln Lys Tyr Leu Glu Asp Lys
               1685                1690                1695

Ala Gln Glu Leu Val Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys
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Asp Ile Ser Glu Lys Val Ala Val Tyr Ser Thr Cys Leu
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cgccgccacc gcccgcgccg gagtcaggcc cctgggcccc caggctcaag cagcgaagcg 180

gcctccgggg gacgccgcta ggcgagagga acgcgccggt gcccttgcct tcgccgtgac 240

ccagcgtgcg ggcggcggg atg aga ggg agc cat cgg gcc gcg ccg gcc ctg  292
                    Met Arg Gly Ser His Arg Ala Ala Pro Ala Leu
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                        1               5                  10

cgg ccc cgg ggg cgg ctc tgg ccc gtg ctg gcc gtg ctg gcg gcg gcc   340
Arg Pro Arg Gly Arg Leu Trp Pro Val Leu Ala Val Leu Ala Ala Ala
            15                  20                  25

gcc gcg gcg ggc tgt gcc cag gca gcc atg gac gag tgc acg gac gag   388
Ala Ala Ala Gly Cys Ala Gln Ala Ala Met Asp Glu Cys Thr Asp Glu
        30                  35                  40

ggc ggg cgg ccg cag cgc tgc atg ccc gag ttc gtc aac gcc gct ttc   436
Gly Gly Arg Pro Gln Arg Cys Met Pro Glu Phe Val Asn Ala Ala Phe
    45                  50                  55

aac gtg act gtg gtg gcc acc aac acg tgt ggg act ccg ccc gag gaa   484
Asn Val Thr Val Val Ala Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu
60                  65                  70                  75

tac tgt gtg cag acc ggg gtg acc ggg gtc acc aag tcc tgt cac ctg   532
Tyr Cys Val Gln Thr Gly Val Thr Gly Val Thr Lys Ser Cys His Leu
                80                  85                  90

tgc gac gcc ggg cag ccc cac ctg cag cac ggg gca gcc ttc ctg acc   580
Cys Asp Ala Gly Gln Pro His Leu Gln His Gly Ala Ala Phe Leu Thr
            95                  100                 105

gac tac aac aac cag gcc gac acc acc tgg tgg caa agc cag acc atg   628
Asp Tyr Asn Asn Gln Ala Asp Thr Thr Trp Trp Gln Ser Gln Thr Met
        110                 115                 120

ctg gcc ggg gtg cag tac ccc agc tcc atc aac ctc acg ctg cac ctg   676
Leu Ala Gly Val Gln Tyr Pro Ser Ser Ile Asn Leu Thr Leu His Leu
    125                 130                 135

gga aaa gct ttt gac atc acc tat gtg cgt ctc aag ttc cac acc agc   724
Gly Lys Ala Phe Asp Ile Thr Tyr Val Arg Leu Lys Phe His Thr Ser
140                 145                 150                 155

cgc ccg gag agc ttt gcc att tac aag cgc aca cgg gaa gac ggg ccc   772
Arg Pro Glu Ser Phe Ala Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro
                160                 165                 170

tgg att cct tac cag tac tac agt ggt tcc tgc gag aac acc tac tcc   820
Trp Ile Pro Tyr Gln Tyr Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser
            175                 180                 185

aag gca aac cgc ggc ttc atc agg aca gga ggg gac gag cag cag gcc   868
Lys Ala Asn Arg Gly Phe Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala
        190                 195                 200

ttg tgt act gat gaa ttc agt gac att tct ccc ctc act ggg ggc aac   916
Leu Cys Thr Asp Glu Phe Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn
    205                 210                 215

gtg gcc ttt tct acc ctg gaa gga agg ccc agc gcc tat aac ttt gac   964
Val Ala Phe Ser Thr Leu Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp
220                 225                 230                 235

aat agc cct gtg ctg cag gaa tgg gta act gcc act gac atc aga gta   1012
Asn Ser Pro Val Leu Gln Glu Trp Val Thr Ala Thr Asp Ile Arg Val
                240                 245                 250
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act ctt aat cgc ctg aac act ttt gga gat gaa gtg ttt aac gat ccc   1060
Thr Leu Asn Arg Leu Asn Thr Phe Gly Asp Glu Val Phe Asn Asp Pro
            255                 260                 265

aaa gtt ctc aag tcc tat tat tat gcc atc tct gat ttt gct gta ggt   1108
Lys Val Leu Lys Ser Tyr Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly
        270                 275                 280

ggc aga tgt aaa tgt aat gga cac gca agc gag tgt atg aag aac gaa   1156
Gly Arg Cys Lys Cys Asn Gly His Ala Ser Glu Cys Met Lys Asn Glu
    285                 290                 295

ttt gat aag ctg gtg tgt aat tgc aaa cat aac aca tat gga gta gac   1204
Phe Asp Lys Leu Val Cys Asn Cys Lys His Asn Thr Tyr Gly Val Asp
300                 305                 310                 315

tgt gaa aag tgt ctt cct ttc ttc aat gac cgg ccg tgg agg agg gca   1252
Cys Glu Lys Cys Leu Pro Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala
                320                 325                 330

act gcg gaa agt gcc agt gaa tgc ctg ccc tgt gat tgc aat ggt cga   1300
Thr Ala Glu Ser Ala Ser Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg
            335                 340                 345

tcc cag gaa tgc tac ttc gac cct gaa ctc tat cgt tcc act ggc cat   1348
Ser Gln Glu Cys Tyr Phe Asp Pro Glu Leu Tyr Arg Ser Thr Gly His
        350                 355                 360

ggg ggc cac tgt acc aac tgc cag gat aac aca gat ggc gcc cac tgt   1396
Gly Gly His Cys Thr Asn Cys Gln Asp Asn Thr Asp Gly Ala His Cys
    365                 370                 375

gag agg tgc cga gag aac ttc ttc cgc ctt ggc aac aat gaa gcc tgc   1444
Glu Arg Cys Arg Glu Asn Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys
380                 385                 390                 395

tct tca tgc cac tgt agt cct gtg ggc tct cta agc aca cag tgt gat   1492
Ser Ser Cys His Cys Ser Pro Val Gly Ser Leu Ser Thr Gln Cys Asp
                400                 405                 410

agt tac ggc aga tgc agc tgt aag cca gga gtg atg ggg gac aaa tgt   1540
Ser Tyr Gly Arg Cys Ser Cys Lys Pro Gly Val Met Gly Asp Lys Cys
            415                 420                 425

gac cgt tgc cag cct gga ttc cat tct ctc act gaa gca gga tgc agg   1588
Asp Arg Cys Gln Pro Gly Phe His Ser Leu Thr Glu Ala Gly Cys Arg
        430                 435                 440

cca tgc tct tgt gat ccc tct ggc agc ata gat gaa tgt aat gtt gaa   1636
Pro Cys Ser Cys Asp Pro Ser Gly Ser Ile Asp Glu Cys Asn Val Glu
    445                 450                 455

aca gga aga tgt gtt tgc aaa gac aat gtc gaa ggc ttc aat tgt gaa   1684
Thr Gly Arg Cys Val Cys Lys Asp Asn Val Glu Gly Phe Asn Cys Glu
460                 465                 470                 475

aga tgc aaa cct gga ttt ttt aat ctg gaa tca tct aat cct cgg ggt   1732
Arg Cys Lys Pro Gly Phe Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly
                480                 485                 490
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tgc aca ccc tgc ttc tgc ttt ggg cat tct tct gtc tgt aca aac gct   1780
Cys Thr Pro Cys Phe Cys Phe Gly His Ser Ser Val Cys Thr Asn Ala
            495                 500                 505

gtt ggc tac agt gtt tat tct atc tcc tct acc ttt cag att gat gag   1828
Val Gly Tyr Ser Val Tyr Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu
        510                 515                 520

gat ggg tgg cgt gcg gaa cag aga gat ggc tct gaa gca tct ctc gag   1876
Asp Gly Trp Arg Ala Glu Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu
    525                 530                 535

tgg tcc tct gag agg caa gat atc gcc gtg atc tca gac agc tac ttt   1924
Trp Ser Ser Glu Arg Gln Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe
540                 545                 550                 555

cct cgg tac ttc att gct cct gca aag ttc ttg ggc aag cag gtg ttg   1972
Pro Arg Tyr Phe Ile Ala Pro Ala Lys Phe Leu Gly Lys Gln Val Leu
                560                 565                 570

agt tat ggt cag aac ctc tcc ttc tcc ttt cga gtg gac agg cga gat   2020
Ser Tyr Gly Gln Asn Leu Ser Phe Ser Phe Arg Val Asp Arg Arg Asp
            575                 580                 585

act cgc ctc tct gcc gaa gac ctt gtg ctt gag gga gct ggc tta aga   2068
Thr Arg Leu Ser Ala Glu Asp Leu Val Leu Glu Gly Ala Gly Leu Arg
        590                 595                 600

gta tct gta ccc ttg atc gct cag ggc aat tcc tat cca agt gag acc   2116
Val Ser Val Pro Leu Ile Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr
    605                 610                 615

act gtg aag tat gtc ttc agg ctc cat gaa gca aca gat tac cct tgg   2164
Thr Val Lys Tyr Val Phe Arg Leu His Glu Ala Thr Asp Tyr Pro Trp
620                 625                 630                 635

agg cct gct ctt acc cct ttt gaa ttt cag aag ctc cta aac aac ttg   2212
Arg Pro Ala Leu Thr Pro Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu
                640                 645                 650

acc tct atc aag ata cgt ggg aca tac agt gag aga agt gct gga tat   2260
Thr Ser Ile Lys Ile Arg Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr
            655                 660                 665

ttg gat gat gtc acc ctg gca agt gct cgt cct ggg cct gga gtc cct   2308
Leu Asp Asp Val Thr Leu Ala Ser Ala Arg Pro Gly Pro Gly Val Pro
        670                 675                 680

gca act tgg gtg gag tcc tgc acc tgt cct gtg gga tat gga ggg cag   2356
Ala Thr Trp Val Glu Ser Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln
    685                 690                 695

ttt tgt gag atg tgc ctc tca ggt tac aga aga gaa act cct aat ctt   2404
Phe Cys Glu Met Cys Leu Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu
700                 705                 710                 715

gga cca tac agt cca tgt gtg ctt tgc gcc tgc aat gga cac agc gag   2452
Gly Pro Tyr Ser Pro Cys Val Leu Cys Ala Cys Asn Gly His Ser Glu
                720                 725                 730

acc tgt gat cct gag aca ggt gtt tgt aac tgc aga gac aat acg gct   2500
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Thr Cys Asp Pro Glu Thr Gly Val Cys Asn Cys Arg Asp Asn Thr Ala
            735                 740                 745

ggc ccg cac tgt gag aag tgc agt gat ggg tac tat gga gat tca act   2548
Gly Pro His Cys Glu Lys Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr
        750                 755                 760

gca ggc acc tcc tcc gat tgc caa ccc tgt ccg tgt cct gga ggt tca   2596
Ala Gly Thr Ser Ser Asp Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser
    765                 770                 775

agt tgt gct gtt gtt ccc aag aca aag gag gtg gtg tgc acc aac tgt   2644
Ser Cys Ala Val Val Pro Lys Thr Lys Glu Val Val Cys Thr Asn Cys
780                 785                 790                 795

cct act ggc acc act ggt aag aga tgt gag ctc tgt gat gat ggc tac   2692
Pro Thr Gly Thr Thr Gly Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr
                800                 805                 810

ttt gga gac ccc ctg ggt aga aac ggc cct gtg aga ctt tgc cgc ctg   2740
Phe Gly Asp Pro Leu Gly Arg Asn Gly Pro Val Arg Leu Cys Arg Leu
            815                 820                 825

tgc cag tgc agt gac aac atc gat ccc aac gca gtt gga aat tgc aat   2788
Cys Gln Cys Ser Asp Asn Ile Asp Pro Asn Ala Val Gly Asn Cys Asn
        830                 835                 840

cgc ttg acg gga gaa tgc ctg aag tgc atc tat aac act gct ggc ttc   2836
Arg Leu Thr Gly Glu Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe
    845                 850                 855

tat tgt gac cgg tgc aaa gac gga ttt ttt gga aat ccc ctg gct ccc   2884
Tyr Cys Asp Arg Cys Lys Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro
860                 865                 870                 875

aat cca gca gac aaa tgc aaa gcc tgc aat tgc aat ccg tat ggg acc   2932
Asn Pro Ala Asp Lys Cys Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr
                880                 885                 890

atg aag cag cag agc agc tgt aac ccc gtg acg ggg cag tgt gaa tgt   2980
Met Lys Gln Gln Ser Ser Cys Asn Pro Val Thr Gly Gln Cys Glu Cys
            895                 900                 905

ttg cct cac gtg act ggc cag gac tgt ggt gct tgt gac cct gga ttc   3028
Leu Pro His Val Thr Gly Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe
        910                 915                 920

tac aat ctg cag agt ggg caa ggc tgt gag agg tgt gac tgc cat gcc   3076
Tyr Asn Leu Gln Ser Gly Gln Gly Cys Glu Arg Cys Asp Cys His Ala
    925                 930                 935

ttg ggc tcc acc aat ggg cag tgt gac atc cgc acc ggc cag tgt gag   3124
Leu Gly Ser Thr Asn Gly Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu
940                 945                 950                 955

tgc cag ccc ggc atc act ggt cag cac tgt gag cgc tgt gag gtc aac   3172
Cys Gln Pro Gly Ile Thr Gly Gln His Cys Glu Arg Cys Glu Val Asn
                960                 965                 970

cac ttt ggg ttt gga cct gaa ggc tgc aaa ccc tgt gac tgt cat cct   3220
His Phe Gly Phe Gly Pro Glu Gly Cys Lys Pro Cys Asp Cys His Pro
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           975                 980                 985

gag gga tct ctt tca ctt cag tgc aaa gat gat ggt cgc tgt gaa tgc   3268
Glu Gly Ser Leu Ser Leu Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys
        990                 995                1000

aga gaa ggc ttt gtg gga aat cgc tgt gac cag tgt gaa gaa aac tat   3316
Arg Glu Gly Phe Val Gly Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr
   1005                1010                1015

ttc tac aat cgg tct tgg cct ggc tgc cag gaa tgt cca gct tgt tac   3364
Phe Tyr Asn Arg Ser Trp Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr
1020                1025                1030                1035

cgg ctg gta aag gat aag gtt gct gat cat aga gtg aag ctc cag gaa   3412
Arg Leu Val Lys Asp Lys Val Ala Asp His Arg Val Lys Leu Gln Glu
               1040                1045                1050

tta gag agt ctc ata gca aac ctt gga act ggg gat gag atg gtg aca   3460
Leu Glu Ser Leu Ile Ala Asn Leu Gly Thr Gly Asp Glu Met Val Thr
           1055                1060                1065

gat caa gcc ttc gag gat aga cta aag gaa gca gag agg gaa gtt atg   3508
Asp Gln Ala Phe Glu Asp Arg Leu Lys Glu Ala Glu Arg Glu Val Met
       1070                1075                1080

gac ctc ctt cgt gag gcc cag gat gtc aaa gat gtt gac cag aat ttg   3556
Asp Leu Leu Arg Glu Ala Gln Asp Val Lys Asp Val Asp Gln Asn Leu
   1085                1090                1095

atg gat cgc cta cag aga gtg aat aac act ctg tcc agc caa att agc   3604
Met Asp Arg Leu Gln Arg Val Asn Asn Thr Leu Ser Ser Gln Ile Ser
1100                1105                1110                1115

cgt tta cag aat atc cgg aat acc att gaa gag act gga aac ttg gct   3652
Arg Leu Gln Asn Ile Arg Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala
               1120                1125                1130

gaa caa gcg cgt gcc cat gta gag aac aca gag cgg ttg att gaa atc   3700
Glu Gln Ala Arg Ala His Val Glu Asn Thr Glu Arg Leu Ile Glu Ile
           1135                1140                1145

gca tcc aga gaa ctt gag aaa gca aaa gtc gct gct gcc aat gtg tca   3748
Ala Ser Arg Glu Leu Glu Lys Ala Lys Val Ala Ala Ala Asn Val Ser
       1150                1155                1160

gtc act cag cca gaa tct aca ggg gac cca aac aac atg act ctt ttg   3796
Val Thr Gln Pro Glu Ser Thr Gly Asp Pro Asn Asn Met Thr Leu Leu
   1165                1170                1175

gca gaa gag gct cga aag ctt gct gaa cgt cat aaa cag gaa gct gat   3844
Ala Glu Glu Ala Arg Lys Leu Ala Glu Arg His Lys Gln Glu Ala Asp
1180                1185                1190                1195

gac att gtt cga gtg gca aag aca gcc aat gat acg tca act gag gca   3892
Asp Ile Val Arg Val Ala Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala
               1200                1205                1210

tac aac ctg ctt ctg agg aca ctg gca gga gaa aat caa aca gca ttt   3940
Tyr Asn Leu Leu Leu Arg Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe
           1215                1220                1225
```

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gag att gaa gag ctt aat agg aag tat gaa caa gcg aag aac atc tca   3988
Glu Ile Glu Glu Leu Asn Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser
       1230                1235                1240

cag gat ctg gaa aaa caa gct gcc cga gta cat gag gag gcc aaa agg   4036
Gln Asp Leu Glu Lys Gln Ala Ala Arg Val His Glu Glu Ala Lys Arg
   1245                1250                1255

gcc ggt gac aaa gct gtg gag atc tat gcc agc gtg gct cag ctg agc   4084
Ala Gly Asp Lys Ala Val Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser
1260                1265                1270                1275

cct ttg gac tct gag aca ctg gag aat gaa gca aat aac ata aag atg   4132
Pro Leu Asp Ser Glu Thr Leu Glu Asn Glu Ala Asn Asn Ile Lys Met
               1280                1285                1290

gaa gct gag aat ctg gaa caa ctg att gac cag aaa tta aaa gat tat   4180
Glu Ala Glu Asn Leu Glu Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr
           1295                1300                1305

gag gac ctc aga gaa gat atg aga ggg aag gaa ctt gaa gtc aag aac   4228
Glu Asp Leu Arg Glu Asp Met Arg Gly Lys Glu Leu Glu Val Lys Asn
       1310                1315                1320

ctt ctg gag aaa ggc aag act gaa cag cag acc gca gac caa ctc cta   4276
Leu Leu Glu Lys Gly Lys Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu
   1325                1330                1335

gcc cga gct gat gct gcc aag gcc ctc gct gaa gaa gct gca aag aag   4324
Ala Arg Ala Asp Ala Ala Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys
1340                1345                1350                1355

gga cgg gat acc tta caa gaa gct aat gac att ctc aac aac ctg aaa   4372
Gly Arg Asp Thr Leu Gln Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys
               1360                1365                1370

gat ttt gat agg cgc gtg aac gat aac aag acg gcc gca gag gag gca   4420
Asp Phe Asp Arg Arg Val Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala
           1375                1380                1385

cta agg aag att cct gcc atc aac cag acc atc act gaa gcc aat gaa   4468
Leu Arg Lys Ile Pro Ala Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu
       1390                1395                1400

aag acc aga gaa gcc cag cag gcc ctg ggc agt gct gcg gcg gat gcc   4516
Lys Thr Arg Glu Ala Gln Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala
   1405                1410                1415

aca gag gcc aag aac aag gcc cat gag gcg gag agg atc gca agc gct   4564
Thr Glu Ala Lys Asn Lys Ala His Glu Ala Glu Arg Ile Ala Ser Ala
1420                1425                1430                1435

gtc caa aag aat gcc acc agc acc aag gca gaa gct gaa aga act ttt   4612
Val Gln Lys Asn Ala Thr Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe
               1440                1445                1450

gca gaa gtt aca gat ctg gat aat gag gtg aac aat atg ttg aag caa   4660
Ala Glu Val Thr Asp Leu Asp Asn Glu Val Asn Asn Met Leu Lys Gln
           1455                1460                1465
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ctg cag gaa gca gaa aaa gag cta aag aga aaa caa gat gac gct gac   4708
Leu Gln Glu Ala Glu Lys Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp
       1470                1475                1480

cag gac atg atg atg gca ggg atg gct tca cag gct gct caa gaa gcc   4756
Gln Asp Met Met Met Ala Gly Met Ala Ser Gln Ala Ala Gln Glu Ala
   1485                1490                1495

gag atc aat gcc aga aaa gcc aaa aac tct gtt act agc ctc ctc agc   4804
Glu Ile Asn Ala Arg Lys Ala Lys Asn Ser Val Thr Ser Leu Leu Ser
1500                1505                1510                1515

att att aat gac ctc ttg gag cag ctg ggg cag ctg gat aca gtg gac   4852
Ile Ile Asn Asp Leu Leu Glu Gln Leu Gly Gln Leu Asp Thr Val Asp
               1520                1525                1530

ctg aat aag cta aac gag att gaa ggc acc cta aac aaa gcc aaa gat   4900
Leu Asn Lys Leu Asn Glu Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp
           1535                1540                1545

gaa atg aag gtc agc gat ctt gat agg aaa gtg tct gac ctg gag aat   4948
Glu Met Lys Val Ser Asp Leu Asp Arg Lys Val Ser Asp Leu Glu Asn
       1550                1555                1560

gaa gcc aag aag cag gag gct gcc atc atg gac tat aac cga gat atc   4996
Glu Ala Lys Lys Gln Glu Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile
   1565                1570                1575

gag gag atc atg aag gac att cgc aat ctg gag gac atc agg aag acc   5044
Glu Glu Ile Met Lys Asp Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr
1580                1585                1590                1595

tta cca tct ggc tgc ttc aac acc ccg tcc att gaa aag ccc           5086
Leu Pro Ser Gly Cys Phe Asn Thr Pro Ser Ile Glu Lys Pro
               1600                1605

tagtgtcttt agggctggaa ggcagcatcc ctctgacagg ggggcagttg tgaggccaca 5146

gagtgccttg acacaaagat tacatttttc agacccccac tcctctgctg ctgtccatca 5206

ctgtcctttt gaaccaggaa aagtcacaga gtttaaagag aagcaaatta aacatcctga 5266

atcgggaaca aagggtttta tctaataaag tgtctcttcc                       5306
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<210> 14
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<212> PRT
<213> Homo sapiens

<400> 14

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Met Arg Gly Ser His Arg Ala Ala Pro Ala Leu Arg Pro Arg Gly Arg
  1               5                  10                  15

Leu Trp Pro Val Leu Ala Val Leu Ala Ala Ala Ala Ala Ala Gly Cys
             20                  25                  30

Ala Gln Ala Ala Met Asp Glu Cys Thr Asp Glu Gly Gly Arg Pro Gln
         35                  40                  45

Arg Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val
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     50                  55                  60

Ala Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr
 65                  70                  75                  80

Gly Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln
                 85                  90                  95

Pro His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln
            100                 105                 110

Ala Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln
        115                 120                 125

Tyr Pro Ser Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp
    130                 135                 140

Ile Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe
145                 150                 155                 160

Ala Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln
                165                 170                 175

Tyr Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly
            180                 185                 190

Phe Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu
        195                 200                 205

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

Leu Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu
225                 230                 235                 240

Gln Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu
                245                 250                 255

Asn Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser
            260                 265                 270

Tyr Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys
        275                 280                 285

Asn Gly His Ala Ser Glu Cys Met Lys Asn Glu Phe Asp Lys Leu Val
    290                 295                 300

Cys Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu
305                 310                 315                 320

Pro Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala
                325                 330                 335

Ser Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr
            340                 345                 350

Phe Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr
        355                 360                 365

Asn Cys Gln Asp Asn Thr Asp Gly Ala His Cys Glu Arg Cys Arg Glu
    370                 375                 380
```

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Asn Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys Ser Ser Cys His Cys
385                 390                 395                 400

Ser Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys
                405                 410                 415

Ser Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro
            420                 425                 430

Gly Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp
        435                 440                 445

Pro Ser Gly Ser Ile Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val
    450                 455                 460

Cys Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly
465                 470                 475                 480

Phe Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly Cys Thr Pro Cys Phe
                485                 490                 495

Cys Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val
            500                 505                 510

Tyr Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Ala
        515                 520                 525

Glu Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Glu Arg
    530                 535                 540

Gln Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile
545                 550                 555                 560

Ala Pro Ala Lys Phe Leu Gly Lys Gln Val Leu Ser Tyr Gly Gln Asn
                565                 570                 575

Leu Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala
            580                 585                 590

Glu Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu
        595                 600                 605

Ile Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Val
    610                 615                 620

Phe Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Thr
625                 630                 635                 640

Pro Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile
                645                 650                 655

Arg Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr
            660                 665                 670

Leu Ala Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu
        675                 680                 685

Ser Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Met Cys
    690                 695                 700
```

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Leu Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu Gly Pro Tyr Ser Pro
705                 710                 715                 720

Cys Val Leu Cys Ala Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu
                725                 730                 735

Thr Gly Val Cys Asn Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu
            740                 745                 750

Lys Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Ala Gly Thr Ser Ser
        755                 760                 765

Asp Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Val Val
    770                 775                 780

Pro Lys Thr Lys Glu Val Val Cys Thr Asn Cys Pro Thr Gly Thr Thr
785                 790                 795                 800

Gly Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu
                805                 810                 815

Gly Arg Asn Gly Pro Val Arg Leu Cys Arg Leu Cys Gln Cys Ser Asp
            820                 825                 830

Asn Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu
        835                 840                 845

Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys
    850                 855                 860

Lys Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys
865                 870                 875                 880

Cys Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr Met Lys Gln Gln Ser
                885                 890                 895

Ser Cys Asn Pro Val Thr Gly Gln Cys Glu Cys Leu Pro His Val Thr
            900                 905                 910

Gly Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe Tyr Asn Leu Gln Ser
        915                 920                 925

Gly Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn
    930                 935                 940

Gly Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile
945                 950                 955                 960

Thr Gly Gln His Cys Glu Arg Cys Glu Val Asn His Phe Gly Phe Gly
                965                 970                 975

Pro Glu Gly Cys Lys Pro Cys Asp Cys His Pro Glu Gly Ser Leu Ser
            980                 985                 990

Leu Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val
        995                1000                1005

Gly Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser
   1010                1015                1020

Trp Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp
```

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1025                1030                1035                1040

Lys Val Ala Asp His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile
                1045                1050                1055

Ala Asn Leu Gly Thr Gly Asp Glu Met Val Thr Asp Gln Ala Phe Glu
            1060                1065                1070

Asp Arg Leu Lys Glu Ala Glu Arg Glu Val Met Asp Leu Leu Arg Glu
        1075                1080                1085

Ala Gln Asp Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln
    1090                1095                1100

Arg Val Asn Asn Thr Leu Ser Ser Gln Ile Ser Arg Leu Gln Asn Ile
1105                1110                1115                1120

Arg Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala Glu Gln Ala Arg Ala
                1125                1130                1135

His Val Glu Asn Thr Glu Arg Leu Ile Glu Ile Ala Ser Arg Glu Leu
            1140                1145                1150

Glu Lys Ala Lys Val Ala Ala Ala Asn Val Ser Val Thr Gln Pro Glu
        1155                1160                1165

Ser Thr Gly Asp Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg
    1170                1175                1180

Lys Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val
1185                1190                1195                1200

Ala Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala Tyr Asn Leu Leu Leu
                1205                1210                1215

Arg Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe Glu Ile Glu Glu Leu
            1220                1225                1230

Asn Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys
        1235                1240                1245

Gln Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala
    1250                1255                1260

Val Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser Pro Leu Asp Ser Glu
1265                1270                1275                1280

Thr Leu Glu Asn Glu Ala Asn Asn Ile Lys Met Glu Ala Glu Asn Leu
                1285                1290                1295

Glu Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu
            1300                1305                1310

Asp Met Arg Gly Lys Glu Leu Glu Val Lys Asn Leu Leu Glu Lys Gly
        1315                1320                1325

Lys Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala
    1330                1335                1340

Ala Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Asp Thr Leu
1345                1350                1355                1360
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Gln Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg
               1365                1370                1375

Val Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Lys Ile Pro
           1380                1385                1390

Ala Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu Lys Thr Arg Glu Ala
       1395                1400                1405

Gln Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn
   1410                1415                1420

Lys Ala His Glu Ala Glu Arg Ile Ala Ser Ala Val Gln Lys Asn Ala
1425                1430                1435                1440

Thr Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe Ala Glu Val Thr Asp
               1445                1450                1455

Leu Asp Asn Glu Val Asn Asn Met Leu Lys Gln Leu Gln Glu Ala Glu
           1460                1465                1470

Lys Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met
       1475                1480                1485

Ala Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Ile Asn Ala Arg
   1490                1495                1500

Lys Ala Lys Asn Ser Val Thr Ser Leu Leu Ser Ile Ile Asn Asp Leu
1505                1510                1515                1520

Leu Glu Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn
               1525                1530                1535

Glu Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp Glu Met Lys Val Ser
           1540                1545                1550

Asp Leu Asp Arg Lys Val Ser Asp Leu Glu Asn Glu Ala Lys Lys Gln
       1555                1560                1565

Glu Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Glu Glu Ile Met Lys
   1570                1575                1580

Asp Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr Leu Pro Ser Gly Cys
1585                1590                1595                1600

Phe Asn Thr Pro Ser Ile Glu Lys Pro
               1605
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tgc atg ccc gag ttc gtc aac gcc gct ttc aac gtg act gtg gtg gcc   96
Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala
             20                  25                  30

acc aac acg tgt ggg act ccg ccc gag gaa tac tgt gtg cag acc ggg   144
Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly
         35                  40                  45

gtg acc ggg gtc acc aag tcc tgt cac ctg tgc gac gcc ggg cag ccc   192
Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Pro
     50                  55                  60

cac ctg cag cac ggg gca gcc ttc ctg acc gac tac aac aac cag gcc   240
His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala
 65                  70                  75                  80

gac acc acc tgg tgg caa agc cag acc atg ctg gcc ggg gtg cag tac   288
Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr
                 85                  90                  95

ccc agc tcc atc aac ctc acg ctg cac ctg gga aaa gct ttt gac atc   336
Pro Ser Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile
            100                 105                 110

acc tat gtg cgt ctc aag ttc cac acc agc cgc ccg gag agc ttt gcc   384
Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala
        115                 120                 125

att tac aag cgc aca cgg gaa gac ggg ccc tgg att cct tac cag tac   432
Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr
    130                 135                 140

tac agt ggt tcc tgc gag aac acc tac tcc aag gca aac cgc ggc ttc   480
Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe
145                 150                 155                 160

atc agg aca gga ggg gac gag cag cag gcc ttg tgt act gat gaa ttc   528
Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe
                165                 170                 175

agt gac att tct ccc ctc act ggg ggc aac gtg gcc ttt tct acc ctg   576
Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu
            180                 185                 190

gaa gga agg ccc agc gcc tat aac ttt gac aat agc cct gtg ctg cag   624
Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln
        195                 200                 205

gaa tgg gta act gcc act gac atc aga gta act ctt aat cgc ctg aac   672
Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn
    210                 215                 220

act ttt gga gat gaa gtg ttt aac gat ccc aaa gtt ctc aag tcc tat   720
Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr
225                 230                 235                 240

tat tat gcc atc tct gat ttt gct gta ggt ggc aga tgt aaa tgt aat   768
Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn
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                245                 250                 255

gga cac gca agc gag tgt atg aag aac gaa ttt gat aag ctg gtg tgt   816
Gly His Ala Ser Glu Cys Met Lys Asn Glu Phe Asp Lys Leu Val Cys
            260                 265                 270

aat tgc aaa cat aac aca tat gga gta gac tgt gaa aag tgt ctt cct   864
Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro
        275                 280                 285

ttc ttc aat gac cgg ccg tgg agg agg gca act gcg gaa agt gcc agt   912
Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser
    290                 295                 300

gaa tgc ctg ccc tgt gat tgc aat ggt cga tcc cag gaa tgc tac ttc   960
Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe
305                 310                 315                 320

gac cct gaa ctc tat cgt tcc act ggc cat ggg ggc cac tgt acc aac  1008
Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn
                325                 330                 335

tgc cag gat aac aca gat ggc gcc cac tgt gag agg tgc cga gag aac  1056
Cys Gln Asp Asn Thr Asp Gly Ala His Cys Glu Arg Cys Arg Glu Asn
            340                 345                 350

ttc ttc cgc ctt ggc aac aat gaa gcc tgc tct tca tgc cac tgt agt  1104
Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys Ser Ser Cys His Cys Ser
        355                 360                 365

cct gtg ggc tct cta agc aca cag tgt gat agt tac ggc aga tgc agc  1152
Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser
    370                 375                 380

tgt aag cca gga gtg atg ggg gac aaa tgt gac cgt tgc cag cct gga  1200
Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly
385                 390                 395                 400

ttc cat tct ctc act gaa gca gga tgc agg cca tgc tct tgt gat ccc  1248
Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro
                405                 410                 415

tct ggc agc ata gat gaa tgt aat gtt gaa aca gga aga tgt gtt tgc  1296
Ser Gly Ser Ile Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys
            420                 425                 430

aaa gac aat gtc gaa ggc ttc aat tgt gaa aga tgc aaa cct gga ttt  1344
Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe
        435                 440                 445

ttt aat ctg gaa tca tct aat cct cgg ggt tgc aca ccc tgc ttc tgc  1392
Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly Cys Thr Pro Cys Phe Cys
    450                 455                 460

ttt ggg cat tct tct gtc tgt aca aac gct gtt ggc tac agt gtt tat  1440
Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr
465                 470                 475                 480

tct atc tcc tct acc ttt cag att gat gag gat ggg tgg cgt gcg gaa  1488
Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Ala Glu
                485                 490                 495
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cag aga gat ggc tct gaa gca tct ctc gag tgg tcc tct gag agg caa   1536
Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Glu Arg Gln
            500                 505                 510

gat atc gcc gtg atc tca gac agc tac ttt cct cgg tac ttc att gct   1584
Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala
        515                 520                 525

cct gca aag ttc ttg ggc aag cag gtg ttg agt tat ggt cag aac ctc   1632
Pro Ala Lys Phe Leu Gly Lys Gln Val Leu Ser Tyr Gly Gln Asn Leu
    530                 535                 540

tcc ttc tcc ttt cga gtg gac agg cga gat act cgc ctc tct gcc gaa   1680
Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu
545                 550                 555                 560

gac ctt gtg ctt gag gga gct ggc tta aga gta tct gta ccc ttg atc   1728
Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile
                565                 570                 575

gct cag ggc aat tcc tat cca agt gag acc act gtg aag tat gtc ttc   1776
Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Val Phe
            580                 585                 590

agg ctc cat gaa gca aca gat tac cct tgg agg cct gct ctt acc cct   1824
Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Thr Pro
        595                 600                 605

ttt gaa ttt cag aag ctc cta aac aac ttg acc tct atc aag ata cgt   1872
Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg
    610                 615                 620

ggg aca tac agt gag aga agt gct gga tat ttg gat gat gtc acc ctg   1920
Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu
625                 630                 635                 640

gca agt gct cgt cct ggg cct gga gtc cct gca act tgg gtg gag tcc   1968
Ala Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser
                645                 650                 655

tgc acc tgt cct gtg gga tat gga ggg cag ttt tgt gag atg tgc ctc   2016
Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Met Cys Leu
            660                 665                 670

tca ggt tac aga aga gaa act cct aat ctt gga cca tac agt cca tgt   2064
Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu Gly Pro Tyr Ser Pro Cys
        675                 680                 685

gtg ctt tgc gcc tgc aat gga cac agc gag acc tgt gat cct gag aca   2112
Val Leu Cys Ala Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr
    690                 695                 700

ggt gtt tgt aac tgc aga gac aat acg gct ggc ccg cac tgt gag aag   2160
Gly Val Cys Asn Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys
705                 710                 715                 720

tgc agt gat ggg tac tat gga gat tca act gca ggc acc tcc tcc gat   2208
Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Ala Gly Thr Ser Ser Asp
                725                 730                 735
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tgc caa ccc tgt ccg tgt cct gga ggt tca agt tgt gct gtt gtt ccc   2256
Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Val Val Pro
            740                 745                 750

aag aca aag gag gtg gtg tgc acc aac tgt cct act ggc acc act ggt   2304
Lys Thr Lys Glu Val Val Cys Thr Asn Cys Pro Thr Gly Thr Thr Gly
        755                 760                 765

aag aga tgt gag ctc tgt gat gat ggc tac ttt gga gac ccc ctg ggt   2352
Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly
    770                 775                 780

aga aac ggc cct gtg aga ctt tgc cgc ctg tgc cag tgc agt gac aac   2400
Arg Asn Gly Pro Val Arg Leu Cys Arg Leu Cys Gln Cys Ser Asp Asn
785                 790                 795                 800

atc gat ccc aac gca gtt gga aat tgc aat cgc ttg acg gga gaa tgc   2448
Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys
                805                 810                 815

ctg aag tgc atc tat aac act gct ggc ttc tat tgt gac cgg tgc aaa   2496
Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys
            820                 825                 830

gac gga ttt ttt gga aat ccc ctg gct ccc aat cca gca gac aaa tgc   2544
Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys
        835                 840                 845

aaa gcc tgc aat tgc aat ccg tat ggg acc atg aag cag cag agc agc   2592
Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr Met Lys Gln Gln Ser Ser
    850                 855                 860

tgt aac ccc gtg acg ggg cag tgt gaa tgt ttg cct cac gtg act ggc   2640
Cys Asn Pro Val Thr Gly Gln Cys Glu Cys Leu Pro His Val Thr Gly
865                 870                 875                 880

cag gac tgt ggt gct tgt gac cct gga ttc tac aat ctg cag agt ggg   2688
Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe Tyr Asn Leu Gln Ser Gly
                885                 890                 895

caa ggc tgt gag agg tgt gac tgc cat gcc ttg ggc tcc acc aat ggg   2736
Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly
            900                 905                 910

cag tgt gac atc cgc acc ggc cag tgt gag tgc cag ccc ggc atc act   2784
Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr
        915                 920                 925

ggt cag cac tgt gag cgc tgt gag gtc aac cac ttt ggg ttt gga cct   2832
Gly Gln His Cys Glu Arg Cys Glu Val Asn His Phe Gly Phe Gly Pro
    930                 935                 940

gaa ggc tgc aaa ccc tgt gac tgt cat cct gag gga tct ctt tca ctt   2880
Glu Gly Cys Lys Pro Cys Asp Cys His Pro Glu Gly Ser Leu Ser Leu
945                 950                 955                 960

cag tgc aaa gat gat ggt cgc tgt gaa tgc aga gaa ggc ttt gtg gga   2928
Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly
                965                 970                 975

aat cgc tgt gac cag tgt gaa gaa aac tat ttc tac aat cgg tct tgg   2976
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Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp
            980                 985                 990

cct ggc tgc cag gaa tgt cca gct tgt tac cgg ctg gta aag gat aag   3024
Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys
        995                1000                1005

gtt gct gat cat aga gtg aag ctc cag gaa tta gag agt ctc ata gca   3072
Val Ala Asp His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala
   1010                1015                1020

aac ctt gga act ggg gat gag atg gtg aca gat caa gcc ttc gag gat   3120
Asn Leu Gly Thr Gly Asp Glu Met Val Thr Asp Gln Ala Phe Glu Asp
1025                1030                1035                1040

aga cta aag gaa gca gag agg gaa gtt atg gac ctc ctt cgt gag gcc   3168
Arg Leu Lys Glu Ala Glu Arg Glu Val Met Asp Leu Leu Arg Glu Ala
               1045                1050                1055

cag gat gtc aaa gat gtt gac cag aat ttg atg gat cgc cta cag aga   3216
Gln Asp Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg
           1060                1065                1070

gtg aat aac act ctg tcc agc caa att agc cgt tta cag aat atc cgg   3264
Val Asn Asn Thr Leu Ser Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg
       1075                1080                1085

aat acc att gaa gag act gga aac ttg gct gaa caa gcg cgt gcc cat   3312
Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala Glu Gln Ala Arg Ala His
   1090                1095                1100

gta gag aac aca gag cgg ttg att gaa atc gca tcc aga gaa ctt gag   3360
Val Glu Asn Thr Glu Arg Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu
1105                1110                1115                1120

aaa gca aaa gtc gct gct gcc aat gtg tca gtc act cag cca gaa tct   3408
Lys Ala Lys Val Ala Ala Ala Asn Val Ser Val Thr Gln Pro Glu Ser
               1125                1130                1135

aca ggg gac cca aac aac atg act ctt ttg gca gaa gag gct cga aag   3456
Thr Gly Asp Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Lys
           1140                1145                1150

ctt gct gaa cgt cat aaa cag gaa gct gat gac att gtt cga gtg gca   3504
Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala
       1155                1160                1165

aag aca gcc aat gat acg tca act gag gca tac aac ctg ctt ctg agg   3552
Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala Tyr Asn Leu Leu Leu Arg
   1170                1175                1180

aca ctg gca gga gaa aat caa aca gca ttt gag att gaa gag ctt aat   3600
Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe Glu Ile Glu Glu Leu Asn
1185                1190                1195                1200

agg aag tat gaa caa gcg aag aac atc tca cag gat ctg gaa aaa caa   3648
Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln
               1205                1210                1215

gct gcc cga gta cat gag gag gcc aaa agg gcc ggt gac aaa gct gtg   3696
Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val
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          1220                1225                1230

gag atc tat gcc agc gtg gct cag ctg agc cct ttg gac tct gag aca   3744
Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser Pro Leu Asp Ser Glu Thr
       1235                1240                1245

ctg gag aat gaa gca aat aac ata aag atg gaa gct gag aat ctg gaa   3792
Leu Glu Asn Glu Ala Asn Asn Ile Lys Met Glu Ala Glu Asn Leu Glu
   1250                1255                1260

caa ctg att gac cag aaa tta aaa gat tat gag gac ctc aga gaa gat   3840
Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp
1265                1270                1275                1280

atg aga ggg aag gaa ctt gaa gtc aag aac ctt ctg gag aaa ggc aag   3888
Met Arg Gly Lys Glu Leu Glu Val Lys Asn Leu Leu Glu Lys Gly Lys
               1285                1290                1295

act gaa cag cag acc gca gac caa ctc cta gcc cga gct gat gct gcc   3936
Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala
          1300                1305                1310

aag gcc ctc gct gaa gaa gct gca aag aag gga cgg gat acc tta caa   3984
Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Asp Thr Leu Gln
       1315                1320                1325

gaa gct aat gac att ctc aac aac ctg aaa gat ttt gat agg cgc gtg   4032
Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val
   1330                1335                1340

aac gat aac aag acg gcc gca gag gag gca cta agg aag att cct gcc   4080
Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Lys Ile Pro Ala
1345                1350                1355                1360

atc aac cag acc atc act gaa gcc aat gaa aag acc aga gaa gcc cag   4128
Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln
               1365                1370                1375

cag gcc ctg ggc agt gct gcg gcg gat gcc aca gag gcc aag aac aag   4176
Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys
          1380                1385                1390

gcc cat gag gcg gag agg atc gca agc gct gtc caa aag aat gcc acc   4224
Ala His Glu Ala Glu Arg Ile Ala Ser Ala Val Gln Lys Asn Ala Thr
       1395                1400                1405

agc acc aag gca gaa gct gaa aga act ttt gca gaa gtt aca gat ctg   4272
Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe Ala Glu Val Thr Asp Leu
   1410                1415                1420

gat aat gag gtg aac aat atg ttg aag caa ctg cag gaa gca gaa aaa   4320
Asp Asn Glu Val Asn Asn Met Leu Lys Gln Leu Gln Glu Ala Glu Lys
1425                1430                1435                1440

gag cta aag aga aaa caa gat gac gct gac cag gac atg atg atg gca   4368
Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala
               1445                1450                1455

ggg atg gct tca cag gct gct caa gaa gcc gag atc aat gcc aga aaa   4416
Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Ile Asn Ala Arg Lys
          1460                1465                1470
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gcc aaa aac tct gtt act agc ctc ctc agc att att aat gac ctc ttg   4464
Ala Lys Asn Ser Val Thr Ser Leu Leu Ser Ile Ile Asn Asp Leu Leu
       1475                1480                1485

gag cag ctg ggg cag ctg gat aca gtg gac ctg aat aag cta aac gag   4512
Glu Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu
   1490                1495                1500

att gaa ggc acc cta aac aaa gcc aaa gat gaa atg aag gtc agc gat   4560
Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp Glu Met Lys Val Ser Asp
1505                1510                1515                1520

ctt gat agg aaa gtg tct gac ctg gag aat gaa gcc aag aag cag gag   4608
Leu Asp Arg Lys Val Ser Asp Leu Glu Asn Glu Ala Lys Lys Gln Glu
               1525                1530                1535

gct gcc atc atg gac tat aac cga gat atc gag gag atc atg aag gac   4656
Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Glu Glu Ile Met Lys Asp
           1540                1545                1550

att cgc aat ctg gag gac atc agg aag acc tta cca tct ggc tgc ttc   4704
Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr Leu Pro Ser Gly Cys Phe
       1555                1560                1565

aac acc ccg tcc att gaa aag ccc tagtgtcttt agggctggaa ggcagcatcc  4758
Asn Thr Pro Ser Ile Glu Lys Pro
   1570                1575

ctctgacagg ggggcagttg tgaggccaca gagtgccttg acacaaagat tacatttttc 4818

agacccccac tcctctgctg ctgtccatca ctgtcctttt gaaccaggaa aagtcacaga 4878

gtttaaagag aagcaaatta aacatcctga atcgggaaca aagggtttta tctaataaag 4938

tgtctcttcc                                                        4948
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<400> 16

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Gln Ala Ala Met Asp Glu Cys Thr Asp Glu Gly Gly Arg Pro Gln Arg
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Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala
             20                  25                  30

Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly
         35                  40                  45

Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Pro
     50                  55                  60

His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala
 65                  70                  75                  80

Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr
                 85                  90                  95
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Pro Ser Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile
            100                 105                 110

Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala
        115                 120                 125

Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr
    130                 135                 140

Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe
145                 150                 155                 160

Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe
                165                 170                 175

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

Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln
        195                 200                 205

Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn
    210                 215                 220

Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr
225                 230                 235                 240

Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn
                245                 250                 255

Gly His Ala Ser Glu Cys Met Lys Asn Glu Phe Asp Lys Leu Val Cys
            260                 265                 270

Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro
        275                 280                 285

Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser
    290                 295                 300

Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe
305                 310                 315                 320

Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn
                325                 330                 335

Cys Gln Asp Asn Thr Asp Gly Ala His Cys Glu Arg Cys Arg Glu Asn
            340                 345                 350

Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys Ser Ser Cys His Cys Ser
        355                 360                 365

Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser
    370                 375                 380

Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly
385                 390                 395                 400

Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro
                405                 410                 415
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Ser Gly Ser Ile Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys
            420                 425                 430

Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe
        435                 440                 445

Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly Cys Thr Pro Cys Phe Cys
    450                 455                 460

Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr
465                 470                 475                 480

Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Ala Glu
                485                 490                 495

Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Glu Arg Gln
            500                 505                 510

Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala
        515                 520                 525

Pro Ala Lys Phe Leu Gly Lys Gln Val Leu Ser Tyr Gly Gln Asn Leu
    530                 535                 540

Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu
545                 550                 555                 560

Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile
                565                 570                 575

Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Val Phe
            580                 585                 590

Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Thr Pro
        595                 600                 605

Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg
    610                 615                 620

Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu
625                 630                 635                 640

Ala Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser
                645                 650                 655

Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Met Cys Leu
            660                 665                 670

Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu Gly Pro Tyr Ser Pro Cys
        675                 680                 685

Val Leu Cys Ala Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr
    690                 695                 700

Gly Val Cys Asn Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys
705                 710                 715                 720

Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Ala Gly Thr Ser Ser Asp
                725                 730                 735

Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Val Val Pro
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```
            740                 745                 750

Lys Thr Lys Glu Val Val Cys Thr Asn Cys Pro Thr Gly Thr Thr Gly
        755                 760                 765

Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly
    770                 775                 780

Arg Asn Gly Pro Val Arg Leu Cys Arg Leu Cys Gln Cys Ser Asp Asn
785                 790                 795                 800

Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys
                805                 810                 815

Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys
            820                 825                 830

Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys
        835                 840                 845

Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr Met Lys Gln Gln Ser Ser
    850                 855                 860

Cys Asn Pro Val Thr Gly Gln Cys Glu Cys Leu Pro His Val Thr Gly
865                 870                 875                 880

Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe Tyr Asn Leu Gln Ser Gly
                885                 890                 895

Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly
            900                 905                 910

Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr
        915                 920                 925

Gly Gln His Cys Glu Arg Cys Glu Val Asn His Phe Gly Phe Gly Pro
    930                 935                 940

Glu Gly Cys Lys Pro Cys Asp Cys His Pro Glu Gly Ser Leu Ser Leu
945                 950                 955                 960

Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly
                965                 970                 975

Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp
            980                 985                 990

Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys
        995                1000                1005

Val Ala Asp His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala
   1010                1015                1020

Asn Leu Gly Thr Gly Asp Glu Met Val Thr Asp Gln Ala Phe Glu Asp
1025                1030                1035                1040

Arg Leu Lys Glu Ala Glu Arg Glu Val Met Asp Leu Leu Arg Glu Ala
               1045                1050                1055

Gln Asp Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg
           1060                1065                1070
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Val Asn Asn Thr Leu Ser Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg
      1075                1080                1085

Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala Glu Gln Ala Arg Ala His
   1090                1095                1100

Val Glu Asn Thr Glu Arg Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu
1105                1110                1115                1120

Lys Ala Lys Val Ala Ala Ala Asn Val Ser Val Thr Gln Pro Glu Ser
               1125                1130                1135

Thr Gly Asp Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Lys
           1140                1145                1150

Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala
      1155                1160                1165

Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala Tyr Asn Leu Leu Leu Arg
   1170                1175                1180

Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe Glu Ile Glu Glu Leu Asn
1185                1190                1195                1200

Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln
               1205                1210                1215

Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val
           1220                1225                1230

Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser Pro Leu Asp Ser Glu Thr
      1235                1240                1245

Leu Glu Asn Glu Ala Asn Asn Ile Lys Met Glu Ala Glu Asn Leu Glu
   1250                1255                1260

Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp
1265                1270                1275                1280

Met Arg Gly Lys Glu Leu Glu Val Lys Asn Leu Leu Glu Lys Gly Lys
               1285                1290                1295

Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala
           1300                1305                1310

Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Asp Thr Leu Gln
      1315                1320                1325

Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val
   1330                1335                1340

Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Lys Ile Pro Ala
1345                1350                1355                1360

Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln
               1365                1370                1375

Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys
           1380                1385                1390
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Ala His Glu Ala Glu Arg Ile Ala Ser Ala Val Gln Lys Asn Ala Thr
       1395                1400                1405

Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe Ala Glu Val Thr Asp Leu
   1410                1415                1420

Asp Asn Glu Val Asn Asn Met Leu Lys Gln Leu Gln Glu Ala Glu Lys
1425                1430                1435                1440

Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala
               1445                1450                1455

Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Ile Asn Ala Arg Lys
           1460                1465                1470

Ala Lys Asn Ser Val Thr Ser Leu Leu Ser Ile Ile Asn Asp Leu Leu
       1475                1480                1485

Glu Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu
   1490                1495                1500

Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp Glu Met Lys Val Ser Asp
1505                1510                1515                1520

Leu Asp Arg Lys Val Ser Asp Leu Glu Asn Glu Ala Lys Lys Gln Glu
               1525                1530                1535

Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Glu Glu Ile Met Lys Asp
           1540                1545                1550

Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr Leu Pro Ser Gly Cys Phe
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Asn Thr Pro Ser Ile Glu Lys Pro
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ggcctcggga tacgccgcta ggcgagtgca gcgcggcacc ccagcctttg ccgaggggcc 180

cgccgcagcg gg atg acg ggc ggc ggg cgg gcc gcg ctg gcc ctg cag ccc 231
Met Thr Gly Gly Gly Arg Ala Ala Leu Ala Leu Gln Pro
1 5 10

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cgg ggg cgg ctg tgg ccg ctg ttg gct gtg ctg gcg gct gtg gcg ggc   279
Arg Gly Arg Leu Trp Pro Leu Leu Ala Val Leu Ala Ala Val Ala Gly
     15                  20                  25

tgt gtc cgg gcg gcc atg gac gag tgc gcg gat gag ggc ggg cgg ccg   327
Cys Val Arg Ala Ala Met Asp Glu Cys Ala Asp Glu Gly Gly Arg Pro
 30                  35                  40                  45

cag cgc tgc atg ccg gag ttt gtt aat gcc gcc ttc aat gtg acc gtg   375
Gln Arg Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val
                 50                  55                  60

gtg gct acc aac acg tgt ggg act ccg ccc gag gag tac tgc gtg cag   423
Val Ala Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln
             65                  70                  75

act ggg gtg acc gga gtc act aag tcc tgt cac ctg tgc gac gcc ggc   471
Thr Gly Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly
         80                  85                  90

cag cag cac ctg caa cac ggg gca gcc ttc ctg acc gac tac aac aac   519
Gln Gln His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn
     95                  100                 105

cag gcc gac acc acc tgg tgg caa agc cag act atg ctg gcc ggg gtg   567
Gln Ala Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val
110                 115                 120                 125

cag tac ccc aac tcc atc aac ctc acg ctg cac ctg gga aag gct ttt   615
Gln Tyr Pro Asn Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe
                130                 135                 140

gac atc act tac gtg cgc ctc aag ttc cac acc agc cgt cca gag agc   663
Asp Ile Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser
            145                 150                 155

ttc gcc atc tat aag cgc act cgg gaa gac ggg ccc tgg att cct tat   711
Phe Ala Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr
        160                 165                 170

cag tac tac agt ggg tcc tgt gag aac acg tac tca aag gct aac cgt   759
Gln Tyr Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg
    175                 180                 185

ggc ttc atc agg acc gga ggg gac gag cag cag gcc ttg tgt act gat   807
Gly Phe Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp
190                 195                 200                 205

gaa ttc agt gac att tcc ccc ctc acc ggt ggc aac gtg gcc ttt tca   855
Glu Phe Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser
                210                 215                 220

acc ctg gaa gga cgg ccg agt gcc tac aac ttt gac aac agc cct gtg   903
Thr Leu Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val
            225                 230                 235

ctc cag gaa tgg gta act gcc act gac atc aga gtg acg ctc aat cgc   951
Leu Gln Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg
        240                 245                 250

ctg aac acc ttt gga gat gaa gtg ttt aac gac ccc aaa gtt ctc aag   999
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Leu Asn Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys
    255                 260                 265

tct tac tat tac gca atc tca gac ttt gct gtg ggc ggc agg tgt aaa  1047
Ser Tyr Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys
270                 275                 280                 285

tgt aac gga cat gcc agc gag tgt gta aag aac gag ttt gac aaa ctc  1095
Cys Asn Gly His Ala Ser Glu Cys Val Lys Asn Glu Phe Asp Lys Leu
                290                 295                 300

atg tgc aac tgc aaa cat aac aca tac gga gtt gac tgt gaa aag tgc  1143
Met Cys Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys
            305                 310                 315

ctg cct ttc ttc aat gac cgg ccg tgg agg agg gcg act gct gag agc  1191
Leu Pro Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser
        320                 325                 330

gcc agc gag tgc ctt cct tgt gac tgc aat ggc cga tcc caa gag tgc  1239
Ala Ser Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys
    335                 340                 345

tac ttt gat cct gaa cta tac cgt tcc act gga cat ggt ggc cac tgt  1287
Tyr Phe Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys
350                 355                 360                 365

acc aac tgc cgg gat aac aca gat ggt gcc aag tgc gag agg tgc cgg  1335
Thr Asn Cys Arg Asp Asn Thr Asp Gly Ala Lys Cys Glu Arg Cys Arg
                370                 375                 380

gag aat ttc ttc cgc ctg ggg aac act gaa gcc tgc tct ccg tgc cac  1383
Glu Asn Phe Phe Arg Leu Gly Asn Thr Glu Ala Cys Ser Pro Cys His
            385                 390                 395

tgc agc cct gtt ggt tct ctc agc aca cag tgt gac agt tac ggc aga  1431
Cys Ser Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg
        400                 405                 410

tgc agc tgt aag cca gga gtg atg ggt gac aag tgt gac cgt tgt cag  1479
Cys Ser Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln
    415                 420                 425

cct ggg ttc cat tcc ctc act gag gca gga tgc agg cca tgc tcc tgc  1527
Pro Gly Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys
430                 435                 440                 445

gat cct tcg ggc agc aca gac gag tgt aat gtt gaa aca gga aga tgc  1575
Asp Pro Ser Gly Ser Thr Asp Glu Cys Asn Val Glu Thr Gly Arg Cys
                450                 455                 460

gtt tgc aaa gac aat gtt gaa ggc ttc aac tgt gag aga tgc aaa cct  1623
Val Cys Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro
            465                 470                 475

gga ttt ttt aat ctg gag tca tct aat cct aag ggc tgc aca ccc tgc  1671
Gly Phe Phe Asn Leu Glu Ser Ser Asn Pro Lys Gly Cys Thr Pro Cys
        480                 485                 490

ttc tgc ttt ggc cat tct tct gtg tgc aca aat gct gtt ggc tac agt  1719
Phe Cys Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser
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    495                 500                 505

gtt tat gac atc tcc tcc acc ttt cag att gat gag gat ggg tgg cgc   1767
Val Tyr Asp Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg
510                 515                 520                 525

gtg gag cag aga gat ggc tcg gag gcg tct ctg gag tgg tcc tca gac   1815
Val Glu Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Asp
                530                 535                 540

agg caa tat att gcc gta atc tca gac agt tac ttt cct aga tac ttc   1863
Arg Gln Tyr Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe
            545                 550                 555

atc gcc cct gtg aag ttc ctg ggc aac cag gtc ctg agt tat ggg cag   1911
Ile Ala Pro Val Lys Phe Leu Gly Asn Gln Val Leu Ser Tyr Gly Gln
        560                 565                 570

aat ctt tcc ttc tcc ttc cga gtg gac aga cga gac act cgc ctc tcc   1959
Asn Leu Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser
    575                 580                 585

gca gag gac ctt gtg ctc gaa gga gct ggc ttg aga gta tcc gtg ccc   2007
Ala Glu Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro
590                 595                 600                 605

ttg atc gct cag ggc aac tcc tac ccc agc gag acc act gtg aag tac   2055
Leu Ile Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr
                610                 615                 620

atc ttc agg ctc cat gaa gca acg gat tac cct tgg agg ccc gct ctc   2103
Ile Phe Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu
            625                 630                 635

tcc ccg ttt gaa ttt cag aag ctc ctg aac aac ttg acc tct atc aag   2151
Ser Pro Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys
        640                 645                 650

atc cgt ggt aca tac agc gag agg agc gct ggg tac ttg gat gat gtc   2199
Ile Arg Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val
    655                 660                 665

acc ttg caa agt gct cgc cct ggg ccc gga gtc cct gca acg tgg gtg   2247
Thr Leu Gln Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val
670                 675                 680                 685

gag tcc tgc acc tgt cca gtg gga tac ggg gga cag ttc tgt gag acg   2295
Glu Ser Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Thr
                690                 695                 700

tgc ctc cca ggg tac aga aga gaa act cca agc ctt gga cct tat agc   2343
Cys Leu Pro Gly Tyr Arg Arg Glu Thr Pro Ser Leu Gly Pro Tyr Ser
            705                 710                 715

ccg tgt gtg ctc tgt acc tgt aat ggg cac agt gag acc tgt gac ccg   2391
Pro Cys Val Leu Cys Thr Cys Asn Gly His Ser Glu Thr Cys Asp Pro
        720                 725                 730

gag aca ggt gtc tgt gac tgc aga gac aat aca gcc ggc ccc cac tgt   2439
Glu Thr Gly Val Cys Asp Cys Arg Asp Asn Thr Ala Gly Pro His Cys
    735                 740                 745
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gag aaa tgt agc gat ggg tac tat ggg gac tca acc ctg ggc acc tcc   2487
Glu Lys Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Leu Gly Thr Ser
750                 755                 760                 765

tct gac tgc cag cct tgt ccc tgc ccc ggt ggc tca agt tgt gcc att   2535
Ser Asp Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Ile
                770                 775                 780

gtc cca aag aca aag gaa gtg gtg tgc acg cac tgt ccg act ggc act   2583
Val Pro Lys Thr Lys Glu Val Val Cys Thr His Cys Pro Thr Gly Thr
            785                 790                 795

gcc ggc aag aga tgt gaa ctc tgt gat gac ggc tac ttt gga gac cct   2631
Ala Gly Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro
        800                 805                 810

ctg ggc agc aat ggg ccc gtg aga ctg tgc cgc ccg tgc cag tgt aac   2679
Leu Gly Ser Asn Gly Pro Val Arg Leu Cys Arg Pro Cys Gln Cys Asn
    815                 820                 825

gac aac ata gac ccc aac gcg gtt ggc aac tgc aac cgc ctg acg ggc   2727
Asp Asn Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly
830                 835                 840                 845

gag tgc ctg aag tgc atc tat aac acg gct ggt ttc tac tgc gac cgg   2775
Glu Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg
                850                 855                 860

tgc aag gaa ggg ttt ttc gga aat ccc ctg gct ccc aat cca gcc gac   2823
Cys Lys Glu Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp
            865                 870                 875

aaa tgc aaa gcc tgc gcc tgc aac tac ggg aca gtg cag caa cag agc   2871
Lys Cys Lys Ala Cys Ala Cys Asn Tyr Gly Thr Val Gln Gln Gln Ser
        880                 885                 890

agc tgt aac ccg gtg acc gga caa tgc cag tgt ctg cct cat gtg tct   2919
Ser Cys Asn Pro Val Thr Gly Gln Cys Gln Cys Leu Pro His Val Ser
    895                 900                 905

ggc cgc gac tgc ggt act tgt gac cct ggc tac tac aac ctg cag agc   2967
Gly Arg Asp Cys Gly Thr Cys Asp Pro Gly Tyr Tyr Asn Leu Gln Ser
910                 915                 920                 925

ggg caa ggc tgc gag agg tgt gac tgc cat gct ttg ggt tcc acc aat   3015
Gly Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn
                930                 935                 940

ggg cag tgt gac atc cgc acc ggg cag tgt gag tgc cag cct ggc atc   3063
Gly Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile
            945                 950                 955

acc ggt cag cac tgt gag cgc tgt gag acc aac cac ttt ggg ttt gga   3111
Thr Gly Gln His Cys Glu Arg Cys Glu Thr Asn His Phe Gly Phe Gly
        960                 965                 970

cct gaa ggc tgc aaa cct tgt gac tgt cac cat gaa gga tcc ctt tcg   3159
Pro Glu Gly Cys Lys Pro Cys Asp Cys His His Glu Gly Ser Leu Ser
    975                 980                 985
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ctc cag tgt aaa gac gac ggc cgt tgt gaa tgc agg gaa ggc ttt gtg   3207
Leu Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val
990                 995                1000                1005

ggc aat cgc tgt gac cag tgt gaa gag aac tat ttc tac aat cgg tcc   3255
Gly Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser
               1010                1015                1020

tgg cct ggc tgc cag gag tgt ccg gct tgt tac cga ctt gtg aag gat   3303
Trp Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp
          1025                1030                1035

aag gct gct gag cat cga gtg aaa ctc cag gag tta gag agc ctc atc   3351
Lys Ala Ala Glu His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile
       1040                1045                1050

gcc aac ctt ggc act ggg gat gac atg gtg aca gat caa gcc ttt gag   3399
Ala Asn Leu Gly Thr Gly Asp Asp Met Val Thr Asp Gln Ala Phe Glu
   1055                1060                1065

gac aga ctt aag gaa gca gaa agg gag gtg aca gac ctt ctc cgt gag   3447
Asp Arg Leu Lys Glu Ala Glu Arg Glu Val Thr Asp Leu Leu Arg Glu
1070                1075                1080                1085

gct cag gaa gtc aaa gat gta gat caa aat ctg atg gat cgc ctt cag   3495
Ala Gln Glu Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln
               1090                1095                1100

aga gta aat agc agc ctg cat agc caa att agc cga ctg cag aat atc   3543
Arg Val Asn Ser Ser Leu His Ser Gln Ile Ser Arg Leu Gln Asn Ile
          1105                1110                1115

cgg aat act atc gaa gag acc ggg atc ttg gct gag cga gca cgg tcc   3591
Arg Asn Thr Ile Glu Glu Thr Gly Ile Leu Ala Glu Arg Ala Arg Ser
       1120                1125                1130

cga gtg gag agt aca gag cag ctg att gag atc gcc tcc agg gag ctc   3639
Arg Val Glu Ser Thr Glu Gln Leu Ile Glu Ile Ala Ser Arg Glu Leu
   1135                1140                1145

gag aaa gca aaa atg gcc gcc aat gtg tca atc act cag cca gag tct   3687
Glu Lys Ala Lys Met Ala Ala Asn Val Ser Ile Thr Gln Pro Glu Ser
1150                1155                1160                1165

aca ggg gag cca aac aac atg acc ctc ttg gca gaa gaa gcc cga agg   3735
Thr Gly Glu Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Arg
               1170                1175                1180

ctt gca gag cgt cat aaa cag gaa gcc gat gac att gta cga gtg gca   3783
Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala
          1185                1190                1195

aag aca gcc aac gag act tca gct gag gca tat aat ctg ctt ttg agg   3831
Lys Thr Ala Asn Glu Thr Ser Ala Glu Ala Tyr Asn Leu Leu Leu Arg
       1200                1205                1210

acc ctg gca gga gaa aat caa act gcg ctg gag att gaa gaa ctt aac   3879
Thr Leu Ala Gly Glu Asn Gln Thr Ala Leu Glu Ile Glu Glu Leu Asn
   1215                1220                1225

cgg aag tac gaa caa gca aag aac atc tct cag gac ctg gag aag cag   3927
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Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln
1230                1235                1240                1245

gct gcc cga gtc cat gag gaa gcc aag cgt gca ggt gac aaa gcc gta   3975
Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val
                1250                1255                1260

gag atc tat gcc agt gtg gcc cag ctg acc cct gtg gac tct gag gcc   4023
Glu Ile Tyr Ala Ser Val Ala Gln Leu Thr Pro Val Asp Ser Glu Ala
            1265                1270                1275

ctg gag aat gaa gca aat aaa atc aag aaa gaa gct gca gac ctg gac   4071
Leu Glu Asn Glu Ala Asn Lys Ile Lys Lys Glu Ala Ala Asp Leu Asp
        1280                1285                1290

cgt ctg att gac cag aag cta aag gat tac gag gac ctc agg gaa gac   4119
Arg Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp
    1295                1300                1305

atg aga gga aag gaa cat gaa gtg aag aac ctt cta gag aag ggg aaa   4167
Met Arg Gly Lys Glu His Glu Val Lys Asn Leu Leu Glu Lys Gly Lys
1310                1315                1320                1325

gct gaa cag cag acc gcc gac caa ctc cta gct cga gcc gat gct gcc   4215
Ala Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala
                1330                1335                1340

aag gcc ctt gct gaa gaa gct gct aag aag gga cgc agt acc tta caa   4263
Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Ser Thr Leu Gln
            1345                1350                1355

gaa gcc aat gac att ctc aac aac ctg aaa gat ttt gat aga cgt gtg   4311
Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val
        1360                1365                1370

aac gat aac aag aca gcc gcg gaa gaa gct cta agg aga att ccc gcc   4359
Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Arg Ile Pro Ala
    1375                1380                1385

atc aac cgg acc ata gct gaa gcc aat gag aag aca agg gag gcc cag   4407
Ile Asn Arg Thr Ile Ala Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln
1390                1395                1400                1405

cta gcg ctg ggc aat gct gcc gct gac gcc acg gag gcc aag aac aag   4455
Leu Ala Leu Gly Asn Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys
                1410                1415                1420

gcc cat gag gca gag agg atc gcc agc gcc gcg cag aag aat gcc acc   4503
Ala His Glu Ala Glu Arg Ile Ala Ser Ala Ala Gln Lys Asn Ala Thr
            1425                1430                1435

agt acc aag gcg gac gca gaa aga acc ttc ggg gaa gtt aca gat ctg   4551
Ser Thr Lys Ala Asp Ala Glu Arg Thr Phe Gly Glu Val Thr Asp Leu
        1440                1445                1450

gat aat gag gtg aac ggt atg ctg agg cag cta gag gag gca gag aat   4599
Asp Asn Glu Val Asn Gly Met Leu Arg Gln Leu Glu Glu Ala Glu Asn
    1455                1460                1465

gag ctg aag agg aag caa gat gac gcc gac cag gac atg atg atg gcg   4647
Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala
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ggg atg gct tcg caa gcc gct cag gag gct gag ctc aat gcc aga aag   4695
Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Leu Asn Ala Arg Lys
                1490                1495                1500

gcc aaa aac tct gtc agc agc ctc ctc agc cag ctg aac aac ctc ttg   4743
Ala Lys Asn Ser Val Ser Ser Leu Leu Ser Gln Leu Asn Asn Leu Leu
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gat cag cta gga cag ctg gac aca gtg gac ctg aac aag ctc aat gag   4791
Asp Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu
        1520                1525                1530

atc gaa ggc tcc ctg aac aaa gcc aaa gac gaa atg aag gcc agc gac   4839
Ile Glu Gly Ser Leu Asn Lys Ala Lys Asp Glu Met Lys Ala Ser Asp
    1535                1540                1545

ctg gac agg aag gtg tct gac ctg gag agc gag gct cgg aag cag gaa   4887
Leu Asp Arg Lys Val Ser Asp Leu Glu Ser Glu Ala Arg Lys Gln Glu
1550                1555                1560                1565

gca gcc atc atg gac tat aac cgg gac ata gca gag atc att aag gat   4935
Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Ala Glu Ile Ile Lys Asp
                1570                1575                1580

att cac aac ctg gag gac atc aag aag acc cta cca acc ggc tgc ttc   4983
Ile His Asn Leu Glu Asp Ile Lys Lys Thr Leu Pro Thr Gly Cys Phe
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aac acc ccg tct atc gag aag ccc tagtggcgag agggctgtaa ggcagtgtcc  5037
Asn Thr Pro Ser Ile Glu Lys Pro
        1600                1605

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Ala Ala Met Asp Glu Cys Ala Asp Glu Gly Gly Arg Pro Gln Arg Cys
         35                  40                  45

Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala Thr
     50                  55                  60

Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly Val
 65                  70                  75                  80

Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Gln His
                 85                  90                  95

Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala Asp
            100                 105                 110

Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr Pro
        115                 120                 125

Asn Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile Thr
    130                 135                 140

Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala Ile
145                 150                 155                 160

Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr Tyr
                165                 170                 175

Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe Ile
            180                 185                 190

Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe Ser
        195                 200                 205

Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu Glu
    210                 215                 220

Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln Glu
225                 230                 235                 240

Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn Thr
                245                 250                 255

Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr Tyr
            260                 265                 270

Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn Gly
        275                 280                 285

His Ala Ser Glu Cys Val Lys Asn Glu Phe Asp Lys Leu Met Cys Asn
    290                 295                 300

Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro Phe
```

305 310 315 320

Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser Glu
325 330 335

Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe Asp
340 345 350

Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn Cys
355 360 365

Arg Asp Asn Thr Asp Gly Ala Lys Cys Glu Arg Cys Arg Glu Asn Phe
370 375 380

Phe Arg Leu Gly Asn Thr Glu Ala Cys Ser Pro Cys His Cys Ser Pro
385 390 395 400

Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser Cys
405 410 415

Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly Phe
420 425 430

His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro Ser
435 440 445

Gly Ser Thr Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys Lys
450 455 460

Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe Phe
465 470 475 480

Asn Leu Glu Ser Ser Asn Pro Lys Gly Cys Thr Pro Cys Phe Cys Phe
485 490 495

Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr Asp
500 505 510

Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Val Glu Gln
515 520 525

Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Asp Arg Gln Tyr
530 535 540

Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala Pro
545 550 555 560

Val Lys Phe Leu Gly Asn Gln Val Leu Ser Tyr Gly Gln Asn Leu Ser
565 570 575

Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu Asp
580 585 590

Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile Ala
595 600 605

Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Ile Phe Arg
610 615 620

Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Ser Pro Phe
625 630 635 640

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Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg Gly
                645                 650                 655

Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu Gln
            660                 665                 670

Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser Cys
        675                 680                 685

Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Thr Cys Leu Pro
    690                 695                 700

Gly Tyr Arg Arg Glu Thr Pro Ser Leu Gly Pro Tyr Ser Pro Cys Val
705                 710                 715                 720

Leu Cys Thr Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr Gly
                725                 730                 735

Val Cys Asp Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys Cys
            740                 745                 750

Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Leu Gly Thr Ser Ser Asp Cys
        755                 760                 765

Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Ile Val Pro Lys
    770                 775                 780

Thr Lys Glu Val Val Cys Thr His Cys Pro Thr Gly Thr Ala Gly Lys
785                 790                 795                 800

Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly Ser
                805                 810                 815

Asn Gly Pro Val Arg Leu Cys Arg Pro Cys Gln Cys Asn Asp Asn Ile
            820                 825                 830

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

Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys Glu
    850                 855                 860

Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Lys
865                 870                 875                 880

Ala Cys Ala Cys Asn Tyr Gly Thr Val Gln Gln Gln Ser Ser Cys Asn
                885                 890                 895

Pro Val Thr Gly Gln Cys Gln Cys Leu Pro His Val Ser Gly Arg Asp
            900                 905                 910

Cys Gly Thr Cys Asp Pro Gly Tyr Tyr Asn Leu Gln Ser Gly Gln Gly
        915                 920                 925

Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly Gln Cys
    930                 935                 940

Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr Gly Gln
945                 950                 955                 960
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His Cys Glu Arg Cys Glu Thr Asn His Phe Gly Phe Gly Pro Glu Gly
                965                 970                 975

Cys Lys Pro Cys Asp Cys His His Glu Gly Ser Leu Ser Leu Gln Cys
            980                 985                 990

Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly Asn Arg
        995                1000                1005

Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp Pro Gly
   1010                1015                1020

Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys Ala Ala
1025                1030                1035                1040

Glu His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala Asn Leu
                1045                1050                1055

Gly Thr Gly Asp Asp Met Val Thr Asp Gln Ala Phe Glu Asp Arg Leu
            1060                1065                1070

Lys Glu Ala Glu Arg Glu Val Thr Asp Leu Leu Arg Glu Ala Gln Glu
        1075                1080                1085

Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg Val Asn
   1090                1095                1100

Ser Ser Leu His Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg Asn Thr
1105                1110                1115                1120

Ile Glu Glu Thr Gly Ile Leu Ala Glu Arg Ala Arg Ser Arg Val Glu
                1125                1130                1135

Ser Thr Glu Gln Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu Lys Ala
            1140                1145                1150

Lys Met Ala Ala Asn Val Ser Ile Thr Gln Pro Glu Ser Thr Gly Glu
        1155                1160                1165

Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Arg Leu Ala Glu
   1170                1175                1180

Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala Lys Thr Ala
1185                1190                1195                1200

Asn Glu Thr Ser Ala Glu Ala Tyr Asn Leu Leu Leu Arg Thr Leu Ala
                1205                1210                1215

Gly Glu Asn Gln Thr Ala Leu Glu Ile Glu Glu Leu Asn Arg Lys Tyr
            1220                1225                1230

Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln Ala Ala Arg
        1235                1240                1245

Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val Glu Ile Tyr
   1250                1255                1260

Ala Ser Val Ala Gln Leu Thr Pro Val Asp Ser Glu Ala Leu Glu Asn
1265                1270                1275                1280

Glu Ala Asn Lys Ile Lys Lys Glu Ala Ala Asp Leu Asp Arg Leu Ile
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                1285                1290                1295

Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp Met Arg Gly
            1300                1305                1310

Lys Glu His Glu Val Lys Asn Leu Leu Glu Lys Gly Lys Ala Glu Gln
        1315                1320                1325

Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala Lys Ala Leu
    1330                1335                1340

Ala Glu Glu Ala Ala Lys Lys Gly Arg Ser Thr Leu Gln Glu Ala Asn
1345                1350                1355                1360

Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val Asn Asp Asn
                1365                1370                1375

Lys Thr Ala Ala Glu Glu Ala Leu Arg Arg Ile Pro Ala Ile Asn Arg
            1380                1385                1390

Thr Ile Ala Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln Leu Ala Leu
        1395                1400                1405

Gly Asn Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys Ala His Glu
    1410                1415                1420

Ala Glu Arg Ile Ala Ser Ala Ala Gln Lys Asn Ala Thr Ser Thr Lys
1425                1430                1435                1440

Ala Asp Ala Glu Arg Thr Phe Gly Glu Val Thr Asp Leu Asp Asn Glu
                1445                1450                1455

Val Asn Gly Met Leu Arg Gln Leu Glu Glu Ala Glu Asn Glu Leu Lys
            1460                1465                1470

Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala Gly Met Ala
        1475                1480                1485

Ser Gln Ala Ala Gln Glu Ala Glu Leu Asn Ala Arg Lys Ala Lys Asn
    1490                1495                1500

Ser Val Ser Ser Leu Leu Ser Gln Leu Asn Asn Leu Leu Asp Gln Leu
1505                1510                1515                1520

Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu Ile Glu Gly
                1525                1530                1535

Ser Leu Asn Lys Ala Lys Asp Glu Met Lys Ala Ser Asp Leu Asp Arg
            1540                1545                1550

Lys Val Ser Asp Leu Glu Ser Glu Ala Arg Lys Gln Glu Ala Ala Ile
        1555                1560                1565

Met Asp Tyr Asn Arg Asp Ile Ala Glu Ile Ile Lys Asp Ile His Asn
    1570                1575                1580

Leu Glu Asp Ile Lys Lys Thr Leu Pro Thr Gly Cys Phe Asn Thr Pro
1585                1590                1595                1600

Ser Ile Glu Lys Pro
                1605
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Ala Met Asp Glu Cys Ala Asp Glu Gly Gly Arg Pro Gln Arg Cys Met
  1               5                  10                  15

ccg gag ttt gtt aat gcc gcc ttc aat gtg acc gtg gtg gct acc aac   96
Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala Thr Asn
             20                  25                  30

acg tgt ggg act ccg ccc gag gag tac tgc gtg cag act ggg gtg acc   144
Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly Val Thr
         35                  40                  45

gga gtc act aag tcc tgt cac ctg tgc gac gcc ggc cag cag cac ctg   192
Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Gln His Leu
     50                  55                  60

caa cac ggg gca gcc ttc ctg acc gac tac aac aac cag gcc gac acc   240
Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala Asp Thr
 65                  70                  75                  80

acc tgg tgg caa agc cag act atg ctg gcc ggg gtg cag tac ccc aac   288
Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr Pro Asn
                 85                  90                  95

tcc atc aac ctc acg ctg cac ctg gga aag gct ttt gac atc act tac   336
Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile Thr Tyr
            100                 105                 110

gtg cgc ctc aag ttc cac acc agc cgt cca gag agc ttc gcc atc tat   384
Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala Ile Tyr
        115                 120                 125

aag cgc act cgg gaa gac ggg ccc tgg att cct tat cag tac tac agt   432
Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr Tyr Ser
    130                 135                 140

ggg tcc tgt gag aac acg tac tca aag gct aac cgt ggc ttc atc agg   480
Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe Ile Arg
145                 150                 155                 160

acc gga ggg gac gag cag cag gcc ttg tgt act gat gaa ttc agt gac   528
Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe Ser Asp
                165                 170                 175

att tcc ccc ctc acc ggt ggc aac gtg gcc ttt tca acc ctg gaa gga   576
Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu Glu Gly
            180                 185                 190

cgg ccg agt gcc tac aac ttt gac aac agc cct gtg ctc cag gaa tgg   624
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Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln Glu Trp
        195                 200                 205

gta act gcc act gac atc aga gtg acg ctc aat cgc ctg aac acc ttt   672
Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn Thr Phe
    210                 215                 220

gga gat gaa gtg ttt aac gac ccc aaa gtt ctc aag tct tac tat tac   720
Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr Tyr Tyr
225                 230                 235                 240

gca atc tca gac ttt gct gtg ggc ggc agg tgt aaa tgt aac gga cat   768
Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn Gly His
                245                 250                 255

gcc agc gag tgt gta aag aac gag ttt gac aaa ctc atg tgc aac tgc   816
Ala Ser Glu Cys Val Lys Asn Glu Phe Asp Lys Leu Met Cys Asn Cys
            260                 265                 270

aaa cat aac aca tac gga gtt gac tgt gaa aag tgc ctg cct ttc ttc   864
Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro Phe Phe
        275                 280                 285

aat gac cgg ccg tgg agg agg gcg act gct gag agc gcc agc gag tgc   912
Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser Glu Cys
    290                 295                 300

ctt cct tgt gac tgc aat ggc cga tcc caa gag tgc tac ttt gat cct   960
Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe Asp Pro
305                 310                 315                 320

gaa cta tac cgt tcc act gga cat ggt ggc cac tgt acc aac tgc cgg  1008
Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn Cys Arg
                325                 330                 335

gat aac aca gat ggt gcc aag tgc gag agg tgc cgg gag aat ttc ttc  1056
Asp Asn Thr Asp Gly Ala Lys Cys Glu Arg Cys Arg Glu Asn Phe Phe
            340                 345                 350

cgc ctg ggg aac act gaa gcc tgc tct ccg tgc cac tgc agc cct gtt  1104
Arg Leu Gly Asn Thr Glu Ala Cys Ser Pro Cys His Cys Ser Pro Val
        355                 360                 365

ggt tct ctc agc aca cag tgt gac agt tac ggc aga tgc agc tgt aag  1152
Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser Cys Lys
    370                 375                 380

cca gga gtg atg ggt gac aag tgt gac cgt tgt cag cct ggg ttc cat  1200
Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly Phe His
385                 390                 395                 400

tcc ctc act gag gca gga tgc agg cca tgc tcc tgc gat cct tcg ggc  1248
Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro Ser Gly
                405                 410                 415

agc aca gac gag tgt aat gtt gaa aca gga aga tgc gtt tgc aaa gac  1296
Ser Thr Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys Lys Asp
            420                 425                 430

aat gtt gaa ggc ttc aac tgt gag aga tgc aaa cct gga ttt ttt aat  1344
Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe Phe Asn
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        435                 440                 445

ctg gag tca tct aat cct aag ggc tgc aca ccc tgc ttc tgc ttt ggc   1392
Leu Glu Ser Ser Asn Pro Lys Gly Cys Thr Pro Cys Phe Cys Phe Gly
    450                 455                 460

cat tct tct gtg tgc aca aat gct gtt ggc tac agt gtt tat gac atc   1440
His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr Asp Ile
465                 470                 475                 480

tcc tcc acc ttt cag att gat gag gat ggg tgg cgc gtg gag cag aga   1488
Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Val Glu Gln Arg
                485                 490                 495

gat ggc tcg gag gcg tct ctg gag tgg tcc tca gac agg caa tat att   1536
Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Asp Arg Gln Tyr Ile
            500                 505                 510

gcc gta atc tca gac agt tac ttt cct aga tac ttc atc gcc cct gtg   1584
Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala Pro Val
        515                 520                 525

aag ttc ctg ggc aac cag gtc ctg agt tat ggg cag aat ctt tcc ttc   1632
Lys Phe Leu Gly Asn Gln Val Leu Ser Tyr Gly Gln Asn Leu Ser Phe
    530                 535                 540

tcc ttc cga gtg gac aga cga gac act cgc ctc tcc gca gag gac ctt   1680
Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu Asp Leu
545                 550                 555                 560

gtg ctc gaa gga gct ggc ttg aga gta tcc gtg ccc ttg atc gct cag   1728
Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile Ala Gln
                565                 570                 575

ggc aac tcc tac ccc agc gag acc act gtg aag tac atc ttc agg ctc   1776
Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Ile Phe Arg Leu
            580                 585                 590

cat gaa gca acg gat tac cct tgg agg ccc gct ctc tcc ccg ttt gaa   1824
His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Ser Pro Phe Glu
        595                 600                 605

ttt cag aag ctc ctg aac aac ttg acc tct atc aag atc cgt ggt aca   1872
Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg Gly Thr
    610                 615                 620

tac agc gag agg agc gct ggg tac ttg gat gat gtc acc ttg caa agt   1920
Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu Gln Ser
625                 630                 635                 640

gct cgc cct ggg ccc gga gtc cct gca acg tgg gtg gag tcc tgc acc   1968
Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser Cys Thr
                645                 650                 655

tgt cca gtg gga tac ggg gga cag ttc tgt gag acg tgc ctc cca ggg   2016
Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Thr Cys Leu Pro Gly
            660                 665                 670

tac aga aga gaa act cca agc ctt gga cct tat agc ccg tgt gtg ctc   2064
Tyr Arg Arg Glu Thr Pro Ser Leu Gly Pro Tyr Ser Pro Cys Val Leu
        675                 680                 685
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tgt acc tgt aat ggg cac agt gag acc tgt gac ccg gag aca ggt gtc   2112
Cys Thr Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr Gly Val
    690                 695                 700

tgt gac tgc aga gac aat aca gcc ggc ccc cac tgt gag aaa tgt agc   2160
Cys Asp Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys Cys Ser
705                 710                 715                 720

gat ggg tac tat ggg gac tca acc ctg ggc acc tcc tct gac tgc cag   2208
Asp Gly Tyr Tyr Gly Asp Ser Thr Leu Gly Thr Ser Ser Asp Cys Gln
                725                 730                 735

cct tgt ccc tgc ccc ggt ggc tca agt tgt gcc att gtc cca aag aca   2256
Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Ile Val Pro Lys Thr
            740                 745                 750

aag gaa gtg gtg tgc acg cac tgt ccg act ggc act gcc ggc aag aga   2304
Lys Glu Val Val Cys Thr His Cys Pro Thr Gly Thr Ala Gly Lys Arg
        755                 760                 765

tgt gaa ctc tgt gat gac ggc tac ttt gga gac cct ctg ggc agc aat   2352
Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly Ser Asn
    770                 775                 780

ggg ccc gtg aga ctg tgc cgc ccg tgc cag tgt aac gac aac ata gac   2400
Gly Pro Val Arg Leu Cys Arg Pro Cys Gln Cys Asn Asp Asn Ile Asp
785                 790                 795                 800

ccc aac gcg gtt ggc aac tgc aac cgc ctg acg ggc gag tgc ctg aag   2448
Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys Leu Lys
                805                 810                 815

tgc atc tat aac acg gct ggt ttc tac tgc gac cgg tgc aag gaa ggg   2496
Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys Glu Gly
            820                 825                 830

ttt ttc gga aat ccc ctg gct ccc aat cca gcc gac aaa tgc aaa gcc   2544
Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Lys Ala
        835                 840                 845

tgc gcc tgc aac tac ggg aca gtg cag caa cag agc agc tgt aac ccg   2592
Cys Ala Cys Asn Tyr Gly Thr Val Gln Gln Gln Ser Ser Cys Asn Pro
    850                 855                 860

gtg acc gga caa tgc cag tgt ctg cct cat gtg tct ggc cgc gac tgc   2640
Val Thr Gly Gln Cys Gln Cys Leu Pro His Val Ser Gly Arg Asp Cys
865                 870                 875                 880

ggt act tgt gac cct ggc tac tac aac ctg cag agc ggg caa ggc tgc   2688
Gly Thr Cys Asp Pro Gly Tyr Tyr Asn Leu Gln Ser Gly Gln Gly Cys
                885                 890                 895

gag agg tgt gac tgc cat gct ttg ggt tcc acc aat ggg cag tgt gac   2736
Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly Gln Cys Asp
            900                 905                 910

atc cgc acc ggg cag tgt gag tgc cag cct ggc atc acc ggt cag cac   2784
Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr Gly Gln His
        915                 920                 925
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tgt gag cgc tgt gag acc aac cac ttt ggg ttt gga cct gaa ggc tgc   2832
Cys Glu Arg Cys Glu Thr Asn His Phe Gly Phe Gly Pro Glu Gly Cys
    930                 935                 940

aaa cct tgt gac tgt cac cat gaa gga tcc ctt tcg ctc cag tgt aaa   2880
Lys Pro Cys Asp Cys His His Glu Gly Ser Leu Ser Leu Gln Cys Lys
945                 950                 955                 960

gac gac ggc cgt tgt gaa tgc agg gaa ggc ttt gtg ggc aat cgc tgt   2928
Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly Asn Arg Cys
                965                 970                 975

gac cag tgt gaa gag aac tat ttc tac aat cgg tcc tgg cct ggc tgc   2976
Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp Pro Gly Cys
            980                 985                 990

cag gag tgt ccg gct tgt tac cga ctt gtg aag gat aag gct gct gag   3024
Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys Ala Ala Glu
        995                1000                1005

cat cga gtg aaa ctc cag gag tta gag agc ctc atc gcc aac ctt ggc   3072
His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala Asn Leu Gly
   1010                1015                1020

act ggg gat gac atg gtg aca gat caa gcc ttt gag gac aga ctt aag   3120
Thr Gly Asp Asp Met Val Thr Asp Gln Ala Phe Glu Asp Arg Leu Lys
1025                1030                1035                1040

gaa gca gaa agg gag gtg aca gac ctt ctc cgt gag gct cag gaa gtc   3168
Glu Ala Glu Arg Glu Val Thr Asp Leu Leu Arg Glu Ala Gln Glu Val
               1045                1050                1055

aaa gat gta gat caa aat ctg atg gat cgc ctt cag aga gta aat agc   3216
Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg Val Asn Ser
           1060                1065                1070

agc ctg cat agc caa att agc cga ctg cag aat atc cgg aat act atc   3264
Ser Leu His Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg Asn Thr Ile
       1075                1080                1085

gaa gag acc ggg atc ttg gct gag cga gca cgg tcc cga gtg gag agt   3312
Glu Glu Thr Gly Ile Leu Ala Glu Arg Ala Arg Ser Arg Val Glu Ser
   1090                1095                1100

aca gag cag ctg att gag atc gcc tcc agg gag ctc gag aaa gca aaa   3360
Thr Glu Gln Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu Lys Ala Lys
1105                1110                1115                1120

atg gcc gcc aat gtg tca atc act cag cca gag tct aca ggg gag cca   3408
Met Ala Ala Asn Val Ser Ile Thr Gln Pro Glu Ser Thr Gly Glu Pro
               1125                1130                1135

aac aac atg acc ctc ttg gca gaa gaa gcc cga agg ctt gca gag cgt   3456
Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Arg Leu Ala Glu Arg
           1140                1145                1150

cat aaa cag gaa gcc gat gac att gta cga gtg gca aag aca gcc aac   3504
His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala Lys Thr Ala Asn
       1155                1160                1165

gag act tca gct gag gca tat aat ctg ctt ttg agg acc ctg gca gga   3552
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Glu Thr Ser Ala Glu Ala Tyr Asn Leu Leu Leu Arg Thr Leu Ala Gly
   1170                1175                1180

gaa aat caa act gcg ctg gag att gaa gaa ctt aac cgg aag tac gaa   3600
Glu Asn Gln Thr Ala Leu Glu Ile Glu Glu Leu Asn Arg Lys Tyr Glu
1185                1190                1195                1200

caa gca aag aac atc tct cag gac ctg gag aag cag gct gcc cga gtc   3648
Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln Ala Ala Arg Val
               1205                1210                1215

cat gag gaa gcc aag cgt gca ggt gac aaa gcc gta gag atc tat gcc   3696
His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val Glu Ile Tyr Ala
           1220                1225                1230

agt gtg gcc cag ctg acc cct gtg gac tct gag gcc ctg gag aat gaa   3744
Ser Val Ala Gln Leu Thr Pro Val Asp Ser Glu Ala Leu Glu Asn Glu
       1235                1240                1245

gca aat aaa atc aag aaa gaa gct gca gac ctg gac cgt ctg att gac   3792
Ala Asn Lys Ile Lys Lys Glu Ala Ala Asp Leu Asp Arg Leu Ile Asp
   1250                1255                1260

cag aag cta aag gat tac gag gac ctc agg gaa gac atg aga gga aag   3840
Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp Met Arg Gly Lys
1265                1270                1275                1280

gaa cat gaa gtg aag aac ctt cta gag aag ggg aaa gct gaa cag cag   3888
Glu His Glu Val Lys Asn Leu Leu Glu Lys Gly Lys Ala Glu Gln Gln
               1285                1290                1295

acc gcc gac caa ctc cta gct cga gcc gat gct gcc aag gcc ctt gct   3936
Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala Lys Ala Leu Ala
           1300                1305                1310

gaa gaa gct gct aag aag gga cgc agt acc tta caa gaa gcc aat gac   3984
Glu Glu Ala Ala Lys Lys Gly Arg Ser Thr Leu Gln Glu Ala Asn Asp
       1315                1320                1325

att ctc aac aac ctg aaa gat ttt gat aga cgt gtg aac gat aac aag   4032
Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val Asn Asp Asn Lys
   1330                1335                1340

aca gcc gcg gaa gaa gct cta agg aga att ccc gcc atc aac cgg acc   4080
Thr Ala Ala Glu Glu Ala Leu Arg Arg Ile Pro Ala Ile Asn Arg Thr
1345                1350                1355                1360

ata gct gaa gcc aat gag aag aca agg gag gcc cag cta gcg ctg ggc   4128
Ile Ala Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln Leu Ala Leu Gly
               1365                1370                1375

aat gct gcc gct gac gcc acg gag gcc aag aac aag gcc cat gag gca   4176
Asn Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys Ala His Glu Ala
           1380                1385                1390

gag agg atc gcc agc gcc gcg cag aag aat gcc acc agt acc aag gcg   4224
Glu Arg Ile Ala Ser Ala Ala Gln Lys Asn Ala Thr Ser Thr Lys Ala
       1395                1400                1405

gac gca gaa aga acc ttc ggg gaa gtt aca gat ctg gat aat gag gtg   4272
Asp Ala Glu Arg Thr Phe Gly Glu Val Thr Asp Leu Asp Asn Glu Val
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   1410                1415                1420

aac ggt atg ctg agg cag cta gag gag gca gag aat gag ctg aag agg   4320
Asn Gly Met Leu Arg Gln Leu Glu Glu Ala Glu Asn Glu Leu Lys Arg
1425                1430                1435                1440

aag caa gat gac gcc gac cag gac atg atg atg gcg ggg atg gct tcg   4368
Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala Gly Met Ala Ser
                1445                1450                1455

caa gcc gct cag gag gct gag ctc aat gcc aga aag gcc aaa aac tct   4416
Gln Ala Ala Gln Glu Ala Glu Leu Asn Ala Arg Lys Ala Lys Asn Ser
            1460                1465                1470

gtc agc agc ctc ctc agc cag ctg aac aac ctc ttg gat cag cta gga   4464
Val Ser Ser Leu Leu Ser Gln Leu Asn Asn Leu Leu Asp Gln Leu Gly
        1475                1480                1485

cag ctg gac aca gtg gac ctg aac aag ctc aat gag atc gaa ggc tcc   4512
Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu Ile Glu Gly Ser
    1490                1495                1500

ctg aac aaa gcc aaa gac gaa atg aag gcc agc gac ctg gac agg aag   4560
Leu Asn Lys Ala Lys Asp Glu Met Lys Ala Ser Asp Leu Asp Arg Lys
1505                1510                1515                1520

gtg tct gac ctg gag agc gag gct cgg aag cag gaa gca gcc atc atg   4608
Val Ser Asp Leu Glu Ser Glu Ala Arg Lys Gln Glu Ala Ala Ile Met
                1525                1530                1535

gac tat aac cgg gac ata gca gag atc att aag gat att cac aac ctg   4656
Asp Tyr Asn Arg Asp Ile Ala Glu Ile Ile Lys Asp Ile His Asn Leu
            1540                1545                1550

gag gac atc aag aag acc cta cca acc ggc tgc ttc aac acc ccg tct   4704
Glu Asp Ile Lys Lys Thr Leu Pro Thr Gly Cys Phe Asn Thr Pro Ser
        1555                1560                1565

atc gag aag ccc tagtggcgag agggctgtaa ggcagtgtcc ctgacagggg       4756
Ile Glu Lys Pro
   1570

accctgtgag gcctcggtgc cttgacacaa agattacact tttcagaccc ccacttctct 4816

gctgctctcc atcactgtcc ttttgaccca agaaaagtca gagtttaaag agaagcaagt 4876

taaacatctt taaccaggaa caaagggttt tgcctaataa agtctctcct ccacttctgt 4936

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ccaggagaac atggctcaaa gatgcttagg gttcctcctg ttttcattga ctaggaagat 5356
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gaatgtttcc caaatcctca ggcagctgat aaaaagtctg gatgggcagc tcgcacgcac 5416

cactacgtga ggtagctttt gatattttta taagcaggac ttaatgcaga agaaacagat 5476

gtgataacca ctcaagtttt tttccccaag tagtactaat tcttaaagct ttgttagtgt 5536

tagtcttgga actgttggta agatagctgt caaaacagtt gtcctctaag gtcatgacca 5596

atgaaagaag agcaaatctc cttttcccca tattttctgg gaagtggctg taatcgggat 5656

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aggctgccaa ccccatctag ttcctgcact ttgtcggtcc gcccactcca agcctttcct 5896

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aagaaggcgt ggcctcacca agttcagtgc tgattggcta gttcctctat tccgagctca 6736

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gttttctcca gcttttgtgg tatattttta aacagaattt tatttttaa aatgaaagtt 6916

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ccaataatct gtattttatg taatgaaatg gacagaatgg ctgctgtaga atgcggggtg 7036

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cttccccccct cagggagggc aataaagcgc aacacttggc attttttttat gtttaaaaag 7216

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<400> 20

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Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala Thr Asn
            20                  25                  30

Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly Val Thr
        35                  40                  45

Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Gln His Leu
    50                  55                  60

Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala Asp Thr
65                  70                  75                  80

Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr Pro Asn
                85                  90                  95

Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile Thr Tyr
            100                 105                 110

Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala Ile Tyr
        115                 120                 125

Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr Tyr Ser
    130                 135                 140

Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe Ile Arg
145                 150                 155                 160

Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe Ser Asp
                165                 170                 175

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

Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln Glu Trp
        195                 200                 205

Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn Thr Phe
    210                 215                 220

Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr Tyr Tyr
225                 230                 235                 240

Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn Gly His
                245                 250                 255

Ala Ser Glu Cys Val Lys Asn Glu Phe Asp Lys Leu Met Cys Asn Cys
            260                 265                 270
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Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro Phe Phe
        275                 280                 285

Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser Glu Cys
    290                 295                 300

Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe Asp Pro
305                 310                 315                 320

Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn Cys Arg
                325                 330                 335

Asp Asn Thr Asp Gly Ala Lys Cys Glu Arg Cys Arg Glu Asn Phe Phe
            340                 345                 350

Arg Leu Gly Asn Thr Glu Ala Cys Ser Pro Cys His Cys Ser Pro Val
        355                 360                 365

Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser Cys Lys
    370                 375                 380

Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly Phe His
385                 390                 395                 400

Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro Ser Gly
                405                 410                 415

Ser Thr Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys Lys Asp
            420                 425                 430

Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe Phe Asn
        435                 440                 445

Leu Glu Ser Ser Asn Pro Lys Gly Cys Thr Pro Cys Phe Cys Phe Gly
    450                 455                 460

His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr Asp Ile
465                 470                 475                 480

Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Val Glu Gln Arg
                485                 490                 495

Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Asp Arg Gln Tyr Ile
            500                 505                 510

Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala Pro Val
        515                 520                 525

Lys Phe Leu Gly Asn Gln Val Leu Ser Tyr Gly Gln Asn Leu Ser Phe
    530                 535                 540

Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu Asp Leu
545                 550                 555                 560

Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile Ala Gln
                565                 570                 575

Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Ile Phe Arg Leu
            580                 585                 590
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His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Ser Pro Phe Glu
        595                 600                 605

Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg Gly Thr
    610                 615                 620

Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu Gln Ser
625                 630                 635                 640

Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser Cys Thr
                645                 650                 655

Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Thr Cys Leu Pro Gly
            660                 665                 670

Tyr Arg Arg Glu Thr Pro Ser Leu Gly Pro Tyr Ser Pro Cys Val Leu
        675                 680                 685

Cys Thr Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr Gly Val
    690                 695                 700

Cys Asp Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys Cys Ser
705                 710                 715                 720

Asp Gly Tyr Tyr Gly Asp Ser Thr Leu Gly Thr Ser Ser Asp Cys Gln
                725                 730                 735

Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Ile Val Pro Lys Thr
            740                 745                 750

Lys Glu Val Val Cys Thr His Cys Pro Thr Gly Thr Ala Gly Lys Arg
        755                 760                 765

Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly Ser Asn
    770                 775                 780

Gly Pro Val Arg Leu Cys Arg Pro Cys Gln Cys Asn Asp Asn Ile Asp
785                 790                 795                 800

Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys Leu Lys
                805                 810                 815

Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys Glu Gly
            820                 825                 830

Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Lys Ala
        835                 840                 845

Cys Ala Cys Asn Tyr Gly Thr Val Gln Gln Gln Ser Ser Cys Asn Pro
    850                 855                 860

Val Thr Gly Gln Cys Gln Cys Leu Pro His Val Ser Gly Arg Asp Cys
865                 870                 875                 880

Gly Thr Cys Asp Pro Gly Tyr Tyr Asn Leu Gln Ser Gly Gln Gly Cys
                885                 890                 895

Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly Gln Cys Asp
            900                 905                 910

Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr Gly Gln His
```

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        915                 920                 925

Cys Glu Arg Cys Glu Thr Asn His Phe Gly Phe Gly Pro Glu Gly Cys
    930                 935                 940

Lys Pro Cys Asp Cys His His Glu Gly Ser Leu Ser Leu Gln Cys Lys
945                 950                 955                 960

Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly Asn Arg Cys
                965                 970                 975

Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp Pro Gly Cys
            980                 985                 990

Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys Ala Ala Glu
        995                1000                1005

His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala Asn Leu Gly
   1010                1015                1020

Thr Gly Asp Asp Met Val Thr Asp Gln Ala Phe Glu Asp Arg Leu Lys
1025                1030                1035                1040

Glu Ala Glu Arg Glu Val Thr Asp Leu Leu Arg Glu Ala Gln Glu Val
                1045                1050                1055

Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg Val Asn Ser
            1060                1065                1070

Ser Leu His Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg Asn Thr Ile
        1075                1080                1085

Glu Glu Thr Gly Ile Leu Ala Glu Arg Ala Arg Ser Arg Val Glu Ser
   1090                1095                1100

Thr Glu Gln Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu Lys Ala Lys
1105                1110                1115                1120

Met Ala Ala Asn Val Ser Ile Thr Gln Pro Glu Ser Thr Gly Glu Pro
                1125                1130                1135

Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Arg Leu Ala Glu Arg
            1140                1145                1150

His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala Lys Thr Ala Asn
        1155                1160                1165

Glu Thr Ser Ala Glu Ala Tyr Asn Leu Leu Leu Arg Thr Leu Ala Gly
   1170                1175                1180

Glu Asn Gln Thr Ala Leu Glu Ile Glu Glu Leu Asn Arg Lys Tyr Glu
1185                1190                1195                1200

Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln Ala Ala Arg Val
                1205                1210                1215

His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val Glu Ile Tyr Ala
            1220                1225                1230

Ser Val Ala Gln Leu Thr Pro Val Asp Ser Glu Ala Leu Glu Asn Glu
        1235                1240                1245
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Ala Asn Lys Ile Lys Lys Glu Ala Ala Asp Leu Asp Arg Leu Ile Asp
   1250                1255                1260

Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp Met Arg Gly Lys
1265                1270                1275                1280

Glu His Glu Val Lys Asn Leu Leu Glu Lys Gly Lys Ala Glu Gln Gln
               1285                1290                1295

Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala Lys Ala Leu Ala
           1300                1305                1310

Glu Glu Ala Ala Lys Lys Gly Arg Ser Thr Leu Gln Glu Ala Asn Asp
       1315                1320                1325

Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val Asn Asp Asn Lys
   1330                1335                1340

Thr Ala Ala Glu Glu Ala Leu Arg Arg Ile Pro Ala Ile Asn Arg Thr
1345                1350                1355                1360

Ile Ala Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln Leu Ala Leu Gly
               1365                1370                1375

Asn Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys Ala His Glu Ala
           1380                1385                1390

Glu Arg Ile Ala Ser Ala Ala Gln Lys Asn Ala Thr Ser Thr Lys Ala
       1395                1400                1405

Asp Ala Glu Arg Thr Phe Gly Glu Val Thr Asp Leu Asp Asn Glu Val
   1410                1415                1420

Asn Gly Met Leu Arg Gln Leu Glu Glu Ala Glu Asn Glu Leu Lys Arg
1425                1430                1435                1440

Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala Gly Met Ala Ser
               1445                1450                1455

Gln Ala Ala Gln Glu Ala Glu Leu Asn Ala Arg Lys Ala Lys Asn Ser
           1460                1465                1470

Val Ser Ser Leu Leu Ser Gln Leu Asn Asn Leu Leu Asp Gln Leu Gly
       1475                1480                1485

Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu Ile Glu Gly Ser
   1490                1495                1500

Leu Asn Lys Ala Lys Asp Glu Met Lys Ala Ser Asp Leu Asp Arg Lys
1505                1510                1515                1520

Val Ser Asp Leu Glu Ser Glu Ala Arg Lys Gln Glu Ala Ala Ile Met
               1525                1530                1535

Asp Tyr Asn Arg Asp Ile Ala Glu Ile Ile Lys Asp Ile His Asn Leu
           1540                1545                1550

Glu Asp Ile Lys Lys Thr Leu Pro Thr Gly Cys Phe Asn Thr Pro Ser
       1555                1560                1565
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Ile Glu Lys Pro
1570

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<210> 22
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<210> 23
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<220>
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<212> DNA
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<220>
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<210> 25
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<210> 26
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<220>
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<210> 32
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<400> 32
ggaggtggtc agcctctaca 20

<210> 33
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<210> 34
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<400> 34
aatggtgcca gactcagg 18

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<400> 35

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       Met Ala Lys Arg Leu Cys Ala Gly Ser Ala Leu Cys Val Arg
         1               5                  10

ggc ccc cgg ggc ccc gcg ccg ctg ctg ctg gtc ggg ctg gcg ctg ctg   157
Gly Pro Arg Gly Pro Ala Pro Leu Leu Leu Val Gly Leu Ala Leu Leu
 15                  20                  25                  30

ggc gcg gcg cgg gcg cgg gag gag gcg ggc ggc ggc ttc agc ctg cac   205
Gly Ala Ala Arg Ala Arg Glu Glu Ala Gly Gly Gly Phe Ser Leu His
                 35                  40                  45

ccg ccc tac ttc aac ctg gcc gag ggc gcc cgc atc gcc gcc tcc gcg   253
Pro Pro Tyr Phe Asn Leu Ala Glu Gly Ala Arg Ile Ala Ala Ser Ala
             50                  55                  60

acc tgc gga gag gag gcc ccg gcg cgc ggc tcc ccg cgc ccc acc gag   301
Thr Cys Gly Glu Glu Ala Pro Ala Arg Gly Ser Pro Arg Pro Thr Glu
         65                  70                  75

gac ctt tac tgc aag ctg gta ggg ggc ccc gtg gcc ggc ggc gac ccc   349
Asp Leu Tyr Cys Lys Leu Val Gly Gly Pro Val Ala Gly Gly Asp Pro
     80                  85                  90

aac cag acc atc cgg ggc cag tac tgc gac atc tgc acg gct gcc aac   397
Asn Gln Thr Ile Arg Gly Gln Tyr Cys Asp Ile Cys Thr Ala Ala Asn
 95                  100                 105                 110

agc aac aag gca cac ccc gcg agc aat gcc atc gat ggc acg gag cgc   445
Ser Asn Lys Ala His Pro Ala Ser Asn Ala Ile Asp Gly Thr Glu Arg
                115                 120                 125

tgg tgg cag agt cca ccg ctg tcc cgc ggc ctg gag tac aac gag gtc   493
Trp Trp Gln Ser Pro Pro Leu Ser Arg Gly Leu Glu Tyr Asn Glu Val
            130                 135                 140

aac gtc acc ctg gac ctg ggc cag gtc ttc cac gtg gcc tac gtc ctc   541
Asn Val Thr Leu Asp Leu Gly Gln Val Phe His Val Ala Tyr Val Leu
        145                 150                 155

atc aag ttt gcc aac tca ccc cgg ccg gac ctc tgg gtg ctg gag cgg   589
Ile Lys Phe Ala Asn Ser Pro Arg Pro Asp Leu Trp Val Leu Glu Arg
    160                 165                 170

tcc atg gac ttc ggc cgc acc tac cag ccc tgg cag ttc ttt gcc tcc   637
Ser Met Asp Phe Gly Arg Thr Tyr Gln Pro Trp Gln Phe Phe Ala Ser
175                 180                 185                 190

tct aag agg gac tgt ctg gag cgg ttc ggg cca cag acg ctg gag cgc   685
Ser Lys Arg Asp Cys Leu Glu Arg Phe Gly Pro Gln Thr Leu Glu Arg
                195                 200                 205

atc aca cgg gac gac gca gcc atc tgc acc acc gag tac tca cgc atc   733
Ile Thr Arg Asp Asp Ala Ala Ile Cys Thr Thr Glu Tyr Ser Arg Ile
            210                 215                 220
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gtg ccc ctg gag aac gga gag atc gtg gtg tcc ctg gtg aac gga cgt   781
Val Pro Leu Glu Asn Gly Glu Ile Val Val Ser Leu Val Asn Gly Arg
        225                 230                 235

ccg ggc gcc atg aat ttc tcc tac tcg ccg ctg cta cgt gag ttc acc   829
Pro Gly Ala Met Asn Phe Ser Tyr Ser Pro Leu Leu Arg Glu Phe Thr
    240                 245                 250

aag gcc acc aac gtc cgc ctg cgc ttc ctg cgt acc aac acg ctg ctg   877
Lys Ala Thr Asn Val Arg Leu Arg Phe Leu Arg Thr Asn Thr Leu Leu
255                 260                 265                 270

ggc cat ctc atg ggg aag gcg ctg cgg gac ccc acg gtc acc cgc cgg   925
Gly His Leu Met Gly Lys Ala Leu Arg Asp Pro Thr Val Thr Arg Arg
                275                 280                 285

tat tat tac agc atc aag gat atc agc atc gga ggc cgc tgt gtc tgc   973
Tyr Tyr Tyr Ser Ile Lys Asp Ile Ser Ile Gly Gly Arg Cys Val Cys
            290                 295                 300

cac ggc cac gcg gat gcc tgc gat gcc aaa gac ccc acg gac ccg ttc   1021
His Gly His Ala Asp Ala Cys Asp Ala Lys Asp Pro Thr Asp Pro Phe
        305                 310                 315

agg ctg cag tgc acc tgc cag cac aac acc tgc ggg ggc acc tgc gac   1069
Arg Leu Gln Cys Thr Cys Gln His Asn Thr Cys Gly Gly Thr Cys Asp
    320                 325                 330

cgc tgc tgc ccc ggc ttc aat cag cag ccg tgg aag cct gcg act gcc   1117
Arg Cys Cys Pro Gly Phe Asn Gln Gln Pro Trp Lys Pro Ala Thr Ala
335                 340                 345                 350

aac agt gcc aac gag tgc cag tcc tgt aac tgc tac ggc cat gcc acc   1165
Asn Ser Ala Asn Glu Cys Gln Ser Cys Asn Cys Tyr Gly His Ala Thr
                355                 360                 365

gac tgt tac tac gac cct gag gtg gac cgg cgc cgc gcc agc cag agc   1213
Asp Cys Tyr Tyr Asp Pro Glu Val Asp Arg Arg Arg Ala Ser Gln Ser
            370                 375                 380

ctg gat ggc acc tat cag ggt ggg ggt gtc tgt atc gac tgc cag cac   1261
Leu Asp Gly Thr Tyr Gln Gly Gly Gly Val Cys Ile Asp Cys Gln His
        385                 390                 395

cac acc gcc ggc gtc aac tgt gag cgc tgc ctg ccc ggc ttc tac cgc   1309
His Thr Ala Gly Val Asn Cys Glu Arg Cys Leu Pro Gly Phe Tyr Arg
    400                 405                 410

tct ccc aac cac cct ctc gac tcg ccc cac gtc tgc cgc cgc tgc aac   1357
Ser Pro Asn His Pro Leu Asp Ser Pro His Val Cys Arg Arg Cys Asn
415                 420                 425                 430

tgc gag tcc gac ttc acg gat ggc acc tgc gag gac ctg acg ggt cga   1405
Cys Glu Ser Asp Phe Thr Asp Gly Thr Cys Glu Asp Leu Thr Gly Arg
                435                 440                 445

tgc tac tgc cgg ccc aac ttc tct ggg gag cgg tgt gac gtg tgt gcc   1453
Cys Tyr Cys Arg Pro Asn Phe Ser Gly Glu Arg Cys Asp Val Cys Ala
            450                 455                 460

gag ggc ttc acg ggc ttc cca agc tgc tac ccg acg ccc tcg tcc tcc   1501
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Glu Gly Phe Thr Gly Phe Pro Ser Cys Tyr Pro Thr Pro Ser Ser Ser
        465                 470                 475

aat gac acc agg gag cag gtg ctg cca gct ggc cag att gtg aat tgt   1549
Asn Asp Thr Arg Glu Gln Val Leu Pro Ala Gly Gln Ile Val Asn Cys
    480                 485                 490

gac tgc agc gcg gca ggg acc cag ggc aac gcc tgc cgg aag gac cca   1597
Asp Cys Ser Ala Ala Gly Thr Gln Gly Asn Ala Cys Arg Lys Asp Pro
495                 500                 505                 510

agg gtg gga cgc tgt ctg tgc aaa ccc aac ttc caa ggc acc cat tgt   1645
Arg Val Gly Arg Cys Leu Cys Lys Pro Asn Phe Gln Gly Thr His Cys
                515                 520                 525

gag ctc tgc gcg cca ggg ttc tac ggc ccc ggc tgc cag ccc tgc cag   1693
Glu Leu Cys Ala Pro Gly Phe Tyr Gly Pro Gly Cys Gln Pro Cys Gln
            530                 535                 540

tgt tcc agc cct gga gtg gcc gat gac cgc tgt gac cct gac aca ggc   1741
Cys Ser Ser Pro Gly Val Ala Asp Asp Arg Cys Asp Pro Asp Thr Gly
        545                 550                 555

cag tgc agg tgc cga gtg ggc ttc gag ggg gcc aca tgt gat cgc tgt   1789
Gln Cys Arg Cys Arg Val Gly Phe Glu Gly Ala Thr Cys Asp Arg Cys
    560                 565                 570

gcc ccc ggc tac ttt cac ttc cct ctc tgc cag ttg tgt ggc tgc agc   1837
Ala Pro Gly Tyr Phe His Phe Pro Leu Cys Gln Leu Cys Gly Cys Ser
575                 580                 585                 590

cct gca gga acc ttg ccc gag ggc tgc gat gag gcc ggc cgc tgc cta   1885
Pro Ala Gly Thr Leu Pro Glu Gly Cys Asp Glu Ala Gly Arg Cys Leu
                595                 600                 605

tgc cag cct gag ttt gct gga cct cat tgt gac cgg tgc cgc cct ggc   1933
Cys Gln Pro Glu Phe Ala Gly Pro His Cys Asp Arg Cys Arg Pro Gly
            610                 615                 620

tac cat ggt ttc ccc aac tgc caa gca tgc acc tgc gac cct cgg gga   1981
Tyr His Gly Phe Pro Asn Cys Gln Ala Cys Thr Cys Asp Pro Arg Gly
        625                 630                 635

gcc ctg gac cag ctc tgt ggg gcg gga ggt ttg tgc cgc tgc cgc ccc   2029
Ala Leu Asp Gln Leu Cys Gly Ala Gly Gly Leu Cys Arg Cys Arg Pro
    640                 645                 650

ggc tac aca ggc act gcc tgc cag gaa tgc agc ccc ggc ttt cac ggc   2077
Gly Tyr Thr Gly Thr Ala Cys Gln Glu Cys Ser Pro Gly Phe His Gly
655                 660                 665                 670

ttc ccc agc tgt gtc ccc tgc cac tgc tct gct gaa ggc tcc ctg cac   2125
Phe Pro Ser Cys Val Pro Cys His Cys Ser Ala Glu Gly Ser Leu His
                675                 680                 685

gca gcc tgt gac ccc cgg agt ggg cag tgc agc tgc cgg ccc cgt gtg   2173
Ala Ala Cys Asp Pro Arg Ser Gly Gln Cys Ser Cys Arg Pro Arg Val
            690                 695                 700

acg ggg ctg cgg tgt gac acg tgt gtg ccc ggt gcc tac aac ttc ccc   2221
Thr Gly Leu Arg Cys Asp Thr Cys Val Pro Gly Ala Tyr Asn Phe Pro
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        705                 710                 715

tac tgc gaa gct ggc tct tgc cac cct gcc ggt ctg gcc cca gtg gat   2269
Tyr Cys Glu Ala Gly Ser Cys His Pro Ala Gly Leu Ala Pro Val Asp
    720                 725                 730

cct gcc ctt cct gag gca cag gtt ccc tgt atg tgc cgg gct cac gtg   2317
Pro Ala Leu Pro Glu Ala Gln Val Pro Cys Met Cys Arg Ala His Val
735                 740                 745                 750

gag ggg ccg agc tgt gac cgc tgc aaa cct ggg ttc tgg gga ctg agc   2365
Glu Gly Pro Ser Cys Asp Arg Cys Lys Pro Gly Phe Trp Gly Leu Ser
                755                 760                 765

ccc agc aac ccc gag ggc tgt acc cgc tgc agc tgc gac ctc agg ggc   2413
Pro Ser Asn Pro Glu Gly Cys Thr Arg Cys Ser Cys Asp Leu Arg Gly
            770                 775                 780

aca ctg ggt gga gtt gct gag tgc cag ccg ggc acc ggc cag tgc ttc   2461
Thr Leu Gly Gly Val Ala Glu Cys Gln Pro Gly Thr Gly Gln Cys Phe
        785                 790                 795

tgc aag ccc cac gtg tgc ggc cag gcc tgc gcg tcc tgc aag gat ggc   2509
Cys Lys Pro His Val Cys Gly Gln Ala Cys Ala Ser Cys Lys Asp Gly
    800                 805                 810

ttc ttt gga ctg gat cag gct gac tat ttt ggc tgc cgc agc tgc cgg   2557
Phe Phe Gly Leu Asp Gln Ala Asp Tyr Phe Gly Cys Arg Ser Cys Arg
815                 820                 825                 830

tgt gac att ggc ggt gca ctg ggc cag agc tgt gaa ccg agg acg ggc   2605
Cys Asp Ile Gly Gly Ala Leu Gly Gln Ser Cys Glu Pro Arg Thr Gly
                835                 840                 845

gtc tgc cgg tgc cgc ccc aac acc cag ggc ccc acc tgc agc gag cct   2653
Val Cys Arg Cys Arg Pro Asn Thr Gln Gly Pro Thr Cys Ser Glu Pro
            850                 855                 860

gcg agg gac cac tac ctc ccg gac ctg cac cac ctg cgc ctg gag ctg   2701
Ala Arg Asp His Tyr Leu Pro Asp Leu His His Leu Arg Leu Glu Leu
        865                 870                 875

gag gag gct gcc aca cct gag ggt cac gcc gtg cgc ttt ggc ttc aac   2749
Glu Glu Ala Ala Thr Pro Glu Gly His Ala Val Arg Phe Gly Phe Asn
    880                 885                 890

ccc ctc gag ttc gag aac ttc agc tgg agg ggc tac gcg cag atg gca   2797
Pro Leu Glu Phe Glu Asn Phe Ser Trp Arg Gly Tyr Ala Gln Met Ala
895                 900                 905                 910

cct gtc cag ccc agg atc gtg gcc agg ctg aac ctg acc tcc ccc gac   2845
Pro Val Gln Pro Arg Ile Val Ala Arg Leu Asn Leu Thr Ser Pro Asp
                915                 920                 925

ctt ttc tgg ctc gtc ttc cga tac gtc aac cgg ggg gcc atg agt gtg   2893
Leu Phe Trp Leu Val Phe Arg Tyr Val Asn Arg Gly Ala Met Ser Val
            930                 935                 940

agc ggg cgg gtc tct gtg cga gag gag ggc agg tcg gcc gcc tgt gcc   2941
Ser Gly Arg Val Ser Val Arg Glu Glu Gly Arg Ser Ala Ala Cys Ala
        945                 950                 955
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aac tgc aca gca cag agt cag ccc gtg gcc ttc cca ccc agc acg gag   2989
Asn Cys Thr Ala Gln Ser Gln Pro Val Ala Phe Pro Pro Ser Thr Glu
    960                 965                 970

cct gcc ttc atc acc gtg ccc cag agg ggc ttc gga gag ccc ttt gtg   3037
Pro Ala Phe Ile Thr Val Pro Gln Arg Gly Phe Gly Glu Pro Phe Val
975                 980                 985                 990

ctg aac cct ggc acc tgg gcc ctg cgt gtg gag gcc gaa ggg gtg ctc   3085
Leu Asn Pro Gly Thr Trp Ala Leu Arg Val Glu Ala Glu Gly Val Leu
                995                1000                1005

ctg gac tac gtg gtt ctg ctg cct agc gca tac tac gag gcg gcg ctc   3133
Leu Asp Tyr Val Val Leu Leu Pro Ser Ala Tyr Tyr Glu Ala Ala Leu
           1010                1015                1020

ctg cag ctg cgg gtg act gag gcc tgc aca tac cgt ccc tct gcc cag   3181
Leu Gln Leu Arg Val Thr Glu Ala Cys Thr Tyr Arg Pro Ser Ala Gln
       1025                1030                1035

cag tct ggc gac aac tgc ctc ctc tac aca cac ctc ccc ctg gat ggc   3229
Gln Ser Gly Asp Asn Cys Leu Leu Tyr Thr His Leu Pro Leu Asp Gly
   1040                1045                1050

ttc ccc tcg gcc gcc ggg ctg gag gcc ctg tgt cgc cag gac aac agc   3277
Phe Pro Ser Ala Ala Gly Leu Glu Ala Leu Cys Arg Gln Asp Asn Ser
1055                1060                1065                1070

ctg ccc cgg ccc tgc ccc acg gag cag ctc agc ccg tcg cac ccg cca   3325
Leu Pro Arg Pro Cys Pro Thr Glu Gln Leu Ser Pro Ser His Pro Pro
               1075                1080                1085

ctg atc acc tgc acg ggc agt gat gtg gac gtc cag ctt caa gtg gca   3373
Leu Ile Thr Cys Thr Gly Ser Asp Val Asp Val Gln Leu Gln Val Ala
           1090                1095                1100

gtg cca cag cca ggc cgc tat gcc cta gtg gtg gag tac gcc aat gag   3421
Val Pro Gln Pro Gly Arg Tyr Ala Leu Val Val Glu Tyr Ala Asn Glu
       1105                1110                1115

gat gcc cgc cag gag gtg ggc gtg gct gtg cac acc cca cag cgg gcc   3469
Asp Ala Arg Gln Glu Val Gly Val Ala Val His Thr Pro Gln Arg Ala
   1120                1125                1130

ccc cag cag ggg ctg ctc tcc ctg cac ccc tgc ctg tac agc acc ctg   3517
Pro Gln Gln Gly Leu Leu Ser Leu His Pro Cys Leu Tyr Ser Thr Leu
1135                1140                1145                1150

tgc cgg ggc act gcc cgg gat acc cag gac cac ctg gct gtc ttc cac   3565
Cys Arg Gly Thr Ala Arg Asp Thr Gln Asp His Leu Ala Val Phe His
               1155                1160                1165

ctg gac tcg gag gcc agc gtg agg ctc aca gcc gag cag gca cgc ttc   3613
Leu Asp Ser Glu Ala Ser Val Arg Leu Thr Ala Glu Gln Ala Arg Phe
           1170                1175                1180

ttc ctg cac ggg gtc act ctg gtg ccc att gag gag ttc agc ccg gag   3661
Phe Leu His Gly Val Thr Leu Val Pro Ile Glu Glu Phe Ser Pro Glu
       1185                1190                1195
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ttc gtg gag ccc cgg gtc agc tgc atc agc agc cac ggc gcc ttt ggc   3709
Phe Val Glu Pro Arg Val Ser Cys Ile Ser Ser His Gly Ala Phe Gly
   1200                1205                1210

ccc aac agt gcc gcc tgt ctg ccc tcg cgc ttc cca aag ccg ccc cag   3757
Pro Asn Ser Ala Ala Cys Leu Pro Ser Arg Phe Pro Lys Pro Pro Gln
1215                1220                1225                1230

ccc atc atc ctc agg gac tgc cag gtg atc ccg ctg ccg ccc ggc ctc   3805
Pro Ile Ile Leu Arg Asp Cys Gln Val Ile Pro Leu Pro Pro Gly Leu
               1235                1240                1245

ccg ctg acc cac gcg cag gat ctc act cca gcc acg tcc cca gct gga   3853
Pro Leu Thr His Ala Gln Asp Leu Thr Pro Ala Thr Ser Pro Ala Gly
           1250                1255                1260

ccc cga cct cgg ccc ccc acc gct gtg gac cct gat gca gag ccc acc   3901
Pro Arg Pro Arg Pro Pro Thr Ala Val Asp Pro Asp Ala Glu Pro Thr
       1265                1270                1275

ctg ctg cgt gag ccc cag gcc acc gtg gtc ttc acc acc cat gtg ccc   3949
Leu Leu Arg Glu Pro Gln Ala Thr Val Val Phe Thr Thr His Val Pro
   1280                1285                1290

acg ctg ggc cgc tat gcc ttc ctg ctg cac ggc tac cag cca gcc cac   3997
Thr Leu Gly Arg Tyr Ala Phe Leu Leu His Gly Tyr Gln Pro Ala His
1295                1300                1305                1310

ccc acc ttc ccc gtg gaa gtc ctc atc aac gcc ggc cgc gtg tgg cag   4045
Pro Thr Phe Pro Val Glu Val Leu Ile Asn Ala Gly Arg Val Trp Gln
               1315                1320                1325

ggc cac gcc aac gcc agc ttc tgt cca cat ggc tac ggc tgc cgc acc   4093
Gly His Ala Asn Ala Ser Phe Cys Pro His Gly Tyr Gly Cys Arg Thr
           1330                1335                1340

ctg gtg gtg tgt gag ggc cag gcc ctg ctg gac gtg acc cac agc gag   4141
Leu Val Val Cys Glu Gly Gln Ala Leu Leu Asp Val Thr His Ser Glu
       1345                1350                1355

ctc act gtg acc gtg cgt gtg ccc gag ggc cgg tgg ctc tgg ctg gat   4189
Leu Thr Val Thr Val Arg Val Pro Glu Gly Arg Trp Leu Trp Leu Asp
   1360                1365                1370

tat gta ctc gtg gtc cct gag aac gtc tac agc ttt ggc tac ctc cgg   4237
Tyr Val Leu Val Val Pro Glu Asn Val Tyr Ser Phe Gly Tyr Leu Arg
1375                1380                1385                1390

gag gag ccc ctg gat aaa tcc tat gac ttc atc agc cac tgc gca gcc   4285
Glu Glu Pro Leu Asp Lys Ser Tyr Asp Phe Ile Ser His Cys Ala Ala
               1395                1400                1405

cag ggc tac cac atc agc ccc agc agc tca tcc ctg ttc tgc cga aac   4333
Gln Gly Tyr His Ile Ser Pro Ser Ser Ser Ser Leu Phe Cys Arg Asn
           1410                1415                1420

gct gct gct tcc ctc tcc ctc ttc tat aac aac gga gcc cgt cca tgt   4381
Ala Ala Ala Ser Leu Ser Leu Phe Tyr Asn Asn Gly Ala Arg Pro Cys
       1425                1430                1435

ggc tgc cac gaa gta ggt gct aca ggc ccc acg tgt gag ccc ttc ggg   4429
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Gly Cys His Glu Val Gly Ala Thr Gly Pro Thr Cys Glu Pro Phe Gly
   1440                1445                1450

ggc cag tgt ccc tgc cat gcc cat gtc att ggc cgt gac tgc tcc cgc   4477
Gly Gln Cys Pro Cys His Ala His Val Ile Gly Arg Asp Cys Ser Arg
1455                1460                1465                1470

tgt gcc acc gga tac tgg ggc ttc ccc aac tgc agg ccc tgt gac tgc   4525
Cys Ala Thr Gly Tyr Trp Gly Phe Pro Asn Cys Arg Pro Cys Asp Cys
               1475                1480                1485

ggt gcc cgc ctc tgt gac gag ctc acg ggc cag tgc atc tgc ccg cca   4573
Gly Ala Arg Leu Cys Asp Glu Leu Thr Gly Gln Cys Ile Cys Pro Pro
           1490                1495                1500

cgc acc atc ccg ccc gac tgc ctg ctg tgc cag ccc cag acc ttt ggc   4621
Arg Thr Ile Pro Pro Asp Cys Leu Leu Cys Gln Pro Gln Thr Phe Gly
       1505                1510                1515

tgc cac ccc ctg gtc ggc tgt gag gag tgt aac tgc tca ggg ccc ggc   4669
Cys His Pro Leu Val Gly Cys Glu Glu Cys Asn Cys Ser Gly Pro Gly
   1520                1525                1530

atc cag gag ctc aca gac cct acc tgt gac aca gac agc ggc cag tgc   4717
Ile Gln Glu Leu Thr Asp Pro Thr Cys Asp Thr Asp Ser Gly Gln Cys
1535                1540                1545                1550

aag tgc aga ccc aac gtg act ggg cgc cgc tgt gat acc tgc tct ccg   4765
Lys Cys Arg Pro Asn Val Thr Gly Arg Arg Cys Asp Thr Cys Ser Pro
               1555                1560                1565

ggc ttc cat ggc tac ccc cgc tgc cgc ccc tgt gac tgt cac gag gcg   4813
Gly Phe His Gly Tyr Pro Arg Cys Arg Pro Cys Asp Cys His Glu Ala
           1570                1575                1580

ggc act gcg cct ggc gtg tgt gac ccc ctc aca ggg cag tgc tac tgt   4861
Gly Thr Ala Pro Gly Val Cys Asp Pro Leu Thr Gly Gln Cys Tyr Cys
       1585                1590                1595

aag gag aac gtg cag ggc ccc aaa tgt gac cag tgc agc ctt ggg acc   4909
Lys Glu Asn Val Gln Gly Pro Lys Cys Asp Gln Cys Ser Leu Gly Thr
   1600                1605                1610

ttc tca ctg gat gct gcc aac ccc aaa ggt tgc acc cgc tgc ttc tgc   4957
Phe Ser Leu Asp Ala Ala Asn Pro Lys Gly Cys Thr Arg Cys Phe Cys
1615                1620                1625                1630

ttt ggg gcc acg gag cgc tgc cgg agc tcg tcc tac acc cgc cag gag   5005
Phe Gly Ala Thr Glu Arg Cys Arg Ser Ser Ser Tyr Thr Arg Gln Glu
               1635                1640                1645

ttc gtg gat atg gag gga tgg gtg ctg ctg agc act gac cgg cag gtg   5053
Phe Val Asp Met Glu Gly Trp Val Leu Leu Ser Thr Asp Arg Gln Val
           1650                1655                1660

gtg ccc cac gag cgg cag cca ggg acg gag atg ctc cgt gca gac ctg   5101
Val Pro His Glu Arg Gln Pro Gly Thr Glu Met Leu Arg Ala Asp Leu
       1665                1670                1675

cgg cac gtg cct gag gct gtg ccc gag gct ttc ccc gag ctg tac tgg   5149
Arg His Val Pro Glu Ala Val Pro Glu Ala Phe Pro Glu Leu Tyr Trp
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   1680                1685                1690

cag gcc cca ccc tcc tac ctg ggg gac cgg gtg tca tcc tac ggt ggg   5197
Gln Ala Pro Pro Ser Tyr Leu Gly Asp Arg Val Ser Ser Tyr Gly Gly
1695               1700                1705                1710

acc ctc cgt tat gaa ctg cac tca gag acc cag cgg gga gat gtc ttt   5245
Thr Leu Arg Tyr Glu Leu His Ser Glu Thr Gln Arg Gly Asp Val Phe
                1715                1720                1725

gtc ccc atg gag agc agg ccg gat gtg gtg ctg cag ggc aac cag atg   5293
Val Pro Met Glu Ser Arg Pro Asp Val Val Leu Gln Gly Asn Gln Met
            1730                1735                1740

agc atc aca ttc ctg gag ccg gca tac ccc acg cct ggc cac gtt cac   5341
Ser Ile Thr Phe Leu Glu Pro Ala Tyr Pro Thr Pro Gly His Val His
        1745                1750                1755

cgt ggg cag ctg cag ctg gtg gag ggg aac ttc cgg cat acg gag act   5389
Arg Gly Gln Leu Gln Leu Val Glu Gly Asn Phe Arg His Thr Glu Thr
    1760                1765                1770

cgc aac act gtg tcc cgc gag gag ctc atg atg gtg ctg gcc agc ctg   5437
Arg Asn Thr Val Ser Arg Glu Glu Leu Met Met Val Leu Ala Ser Leu
1775                1780                1785                1790

gag cag ctg cag atc cgt gcc ctc ttc tca cag atc tcc tcg gct gtc   5485
Glu Gln Leu Gln Ile Arg Ala Leu Phe Ser Gln Ile Ser Ser Ala Val
                1795                1800                1805

tcc ctg cgc agg gtg gca ctg gag gtg gcc agc cca gca ggc cag ggg   5533
Ser Leu Arg Arg Val Ala Leu Glu Val Ala Ser Pro Ala Gly Gln Gly
            1810                1815                1820

gcc ctg gcc agc aat gtg gag ctg tgc ctg tgc ccc gcc agc tac cgg   5581
Ala Leu Ala Ser Asn Val Glu Leu Cys Leu Cys Pro Ala Ser Tyr Arg
        1825                1830                1835

ggg gac tca tgc cag gaa tgt gcc ccc ggc ttc tat cgg gac gtc aaa   5629
Gly Asp Ser Cys Gln Glu Cys Ala Pro Gly Phe Tyr Arg Asp Val Lys
    1840                1845                1850

ggt ctc ttc ctg ggc cga tgt gtc cct tgt cag tgc cat gga cac tca   5677
Gly Leu Phe Leu Gly Arg Cys Val Pro Cys Gln Cys His Gly His Ser
1855                1860                1865                1870

gac cgc tgc ctc cct ggc tct ggc gtc tgt gtg gac tgc cag cac aac   5725
Asp Arg Cys Leu Pro Gly Ser Gly Val Cys Val Asp Cys Gln His Asn
                1875                1880                1885

acc gaa ggg gcc cac tgt gag cgc tgc cag gct ggc ttc atg agc agc   5773
Thr Glu Gly Ala His Cys Glu Arg Cys Gln Ala Gly Phe Met Ser Ser
            1890                1895                1900

agg gac gac ccc agc gcc ccc tgt gtc agc tgc ccc tgc ccc ctc tca   5821
Arg Asp Asp Pro Ser Ala Pro Cys Val Ser Cys Pro Cys Pro Leu Ser
        1905                1910                1915

gtg cct tcc aac aac ttc gcc gag ggc tgt gtc ctg cga ggc ggc cgc   5869
Val Pro Ser Asn Asn Phe Ala Glu Gly Cys Val Leu Arg Gly Gly Arg
    1920                1925                1930
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acc cag tgc ctc tgc aaa cct ggt tat gca ggt gcc tcc tgc gag cgg   5917
Thr Gln Cys Leu Cys Lys Pro Gly Tyr Ala Gly Ala Ser Cys Glu Arg
1935              1940                1945                1950

tgt gcg ccc gga ttc ttt ggg aac cca ctg gtg ctg ggc agc tcc tgc   5965
Cys Ala Pro Gly Phe Phe Gly Asn Pro Leu Val Leu Gly Ser Ser Cys
               1955                1960                1965

cag cca tgc gac tgc agc ggc aac ggt gac ccc aac ttg ctc ttc agc   6013
Gln Pro Cys Asp Cys Ser Gly Asn Gly Asp Pro Asn Leu Leu Phe Ser
          1970                1975                1980

gac tgc gac ccc ctg acg ggc gcc tgc cgt ggc tgc ctg cgc cac acc   6061
Asp Cys Asp Pro Leu Thr Gly Ala Cys Arg Gly Cys Leu Arg His Thr
       1985                1990                1995

act ggg ccc cgc tgc gag atc tgt gcc ccc ggc ttc tac ggc aac gcc   6109
Thr Gly Pro Arg Cys Glu Ile Cys Ala Pro Gly Phe Tyr Gly Asn Ala
   2000                2005                2010

ctg ctg ccc ggc aac tgc acc cgg tgc gac tgt acc cca tgt ggg aca   6157
Leu Leu Pro Gly Asn Cys Thr Arg Cys Asp Cys Thr Pro Cys Gly Thr
2015                2020                2025                2030

gag gcc tgc gac ccc cac agc ggg cac tgc ctg tgc aag gcg ggc gtg   6205
Glu Ala Cys Asp Pro His Ser Gly His Cys Leu Cys Lys Ala Gly Val
               2035                2040                2045

act ggg cgg cgc tgt gac cgc tgc cag gag gga cat ttt ggt ttc aat   6253
Thr Gly Arg Arg Cys Asp Arg Cys Gln Glu Gly His Phe Gly Phe Asn
          2050                2055                2060

ggc tgc ggg ggc tgc cgc ccg tgt gct tgt gga ccg gcc gcc gag ggc   6301
Gly Cys Gly Gly Cys Arg Pro Cys Ala Cys Gly Pro Ala Ala Glu Gly
       2065                2070                2075

tcc gag tgc cac ccc cag agc gga cag tgc cac tgc cga cca ggg acc   6349
Ser Glu Cys His Pro Gln Ser Gly Gln Cys His Cys Arg Pro Gly Thr
   2080                2085                2090

atg gga ccc cag tgc cgc gag tgt gcc cct ggc tac tgg ggg ctc cct   6397
Met Gly Pro Gln Cys Arg Glu Cys Ala Pro Gly Tyr Trp Gly Leu Pro
2095                2100                2105                2110

gag cag ggc tgc agg cgc tgc cag tgc cct ggg ggc cgc tgt gac cct   6445
Glu Gln Gly Cys Arg Arg Cys Gln Cys Pro Gly Gly Arg Cys Asp Pro
               2115                2120                2125

cac acg ggc cgc tgc aac tgc ccc ccg ggg ctc agc ggg gag cgc tgc   6493
His Thr Gly Arg Cys Asn Cys Pro Pro Gly Leu Ser Gly Glu Arg Cys
          2130                2135                2140

gac acc tgc agc cag cag cat cag gtg cct gtt cca ggc ggg cct gtg   6541
Asp Thr Cys Ser Gln Gln His Gln Val Pro Val Pro Gly Gly Pro Val
       2145                2150                2155

ggc cac agc atc cac tgt gaa gtg tgt gac cac tgt gtg gtc ctg ctc   6589
Gly His Ser Ile His Cys Glu Val Cys Asp His Cys Val Val Leu Leu
   2160                2165                2170
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ctg gat gac ctg gaa cgg gcc ggc gcc ctc ctc ccc gcc att cac gag   6637
Leu Asp Asp Leu Glu Arg Ala Gly Ala Leu Leu Pro Ala Ile His Glu
2175                2180                2185                2190

caa ctg cgt ggc atc aat gcc agc tcc atg gcc tgg gcc cgt ctg cac   6685
Gln Leu Arg Gly Ile Asn Ala Ser Ser Met Ala Trp Ala Arg Leu His
                2195                2200                2205

agg ctg aac gcc tcc atc gct gac ctg cag agc cag ctc cgg agc ccc   6733
Arg Leu Asn Ala Ser Ile Ala Asp Leu Gln Ser Gln Leu Arg Ser Pro
            2210                2215                2220

ctg ggc ccc cgc cat gag acg gca cag cag ctg gag gtg ctg gag cag   6781
Leu Gly Pro Arg His Glu Thr Ala Gln Gln Leu Glu Val Leu Glu Gln
        2225                2230                2235

cag agc aca agc ctc ggg cag gac gca cgg cgg cta ggc ggc cag gcc   6829
Gln Ser Thr Ser Leu Gly Gln Asp Ala Arg Arg Leu Gly Gly Gln Ala
    2240                2245                2250

gtg ggg acc cga gac cag gcg agc caa ttg ctg gcc ggc acc gag gcc   6877
Val Gly Thr Arg Asp Gln Ala Ser Gln Leu Leu Ala Gly Thr Glu Ala
2255                2260                2265                2270

aca ctg ggc cat gcg aag acg ctg ttg gcg gcc atc cgg gct gtg gac   6925
Thr Leu Gly His Ala Lys Thr Leu Leu Ala Ala Ile Arg Ala Val Asp
                2275                2280                2285

cgc acc ctg agc gag ctc atg tcc cag acg ggc cac ctg ggg ctg gcc   6973
Arg Thr Leu Ser Glu Leu Met Ser Gln Thr Gly His Leu Gly Leu Ala
            2290                2295                2300

aat gcc tcg gct cca tca ggt gag cag ctg ctc cgg aca ctg gcc gag   7021
Asn Ala Ser Ala Pro Ser Gly Glu Gln Leu Leu Arg Thr Leu Ala Glu
        2305                2310                2315

gtg gag cgg ctg ctc tgg gag atg cgg gcc cgg gac ctg ggg gcc ccg   7069
Val Glu Arg Leu Leu Trp Glu Met Arg Ala Arg Asp Leu Gly Ala Pro
    2320                2325                2330

cag gca gca gct gag gct gag ttg gct gca gca cag aga ttg ctg gcc   7117
Gln Ala Ala Ala Glu Ala Glu Leu Ala Ala Ala Gln Arg Leu Leu Ala
2335                2340                2345                2350

cgg gtg cag gag cag ctg agc agc ctc tgg gag gag aac cag gca ctg   7165
Arg Val Gln Glu Gln Leu Ser Ser Leu Trp Glu Glu Asn Gln Ala Leu
                2355                2360                2365

gcc aca caa acc cgc gac cgg ctg gcc cag cac gag gcc ggc ctc atg   7213
Ala Thr Gln Thr Arg Asp Arg Leu Ala Gln His Glu Ala Gly Leu Met
            2370                2375                2380

gac ctg cga gag gct ttg aac cgg gca gtg gac gcc aca cgg gag gcc   7261
Asp Leu Arg Glu Ala Leu Asn Arg Ala Val Asp Ala Thr Arg Glu Ala
        2385                2390                2395

cag gag ctc aac agc cgc aac cag gag cgc ctg gag gaa gcc ctg caa   7309
Gln Glu Leu Asn Ser Arg Asn Gln Glu Arg Leu Glu Glu Ala Leu Gln
    2400                2405                2410

agg aag cag gag ctg tcc cgg gac aat gcc acc ctg cag gcc act ctg   7357
```

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Arg Lys Gln Glu Leu Ser Arg Asp Asn Ala Thr Leu Gln Ala Thr Leu
2415                2420                2425                2430

cat gcg gct agg gac acc ctg gcc agc gtc ttc aga ttg ctg cac agc   7405
His Ala Ala Arg Asp Thr Leu Ala Ser Val Phe Arg Leu Leu His Ser
                2435                2440                2445

ctg gac cag gct aag gag gag ctg gag cgc ctc gcc gcc agc ctg gac   7453
Leu Asp Gln Ala Lys Glu Glu Leu Glu Arg Leu Ala Ala Ser Leu Asp
            2450                2455                2460

ggg gct cgg acc cca ctg ctg cag agg atg cag acc ttc tcc ccg gcg   7501
Gly Ala Arg Thr Pro Leu Leu Gln Arg Met Gln Thr Phe Ser Pro Ala
        2465                2470                2475

ggc agc aag ctg cgt cta gtg gag gcc gcc gag gcc cac gca cag cag   7549
Gly Ser Lys Leu Arg Leu Val Glu Ala Ala Glu Ala His Ala Gln Gln
    2480                2485                2490

ctg ggc cag ctg gca ctc aat ctg tcc agc atc atc ctg gac gtc aac   7597
Leu Gly Gln Leu Ala Leu Asn Leu Ser Ser Ile Ile Leu Asp Val Asn
2495                2500                2505                2510

cag gac cgc ctc acc cag agg gcc atc gag gcc tcc aac gcc tac agc   7645
Gln Asp Arg Leu Thr Gln Arg Ala Ile Glu Ala Ser Asn Ala Tyr Ser
                2515                2520                2525

cgc atc ctg cag gcc gtg cag gct gcc gag gat gct gct ggc cag gcc   7693
Arg Ile Leu Gln Ala Val Gln Ala Ala Glu Asp Ala Ala Gly Gln Ala
            2530                2535                2540

ctg cag cag gcg gac cac acg tgg gcg acg gtg gtg cgg cag ggc ctg   7741
Leu Gln Gln Ala Asp His Thr Trp Ala Thr Val Val Arg Gln Gly Leu
        2545                2550                2555

gtg gac cga gcc cag cag ctc ctg gcc aac agc act gca cta gaa gag   7789
Val Asp Arg Ala Gln Gln Leu Leu Ala Asn Ser Thr Ala Leu Glu Glu
    2560                2565                2570

gcc atg ctc cag gaa cag cag agg ctg ggc ctt gtg tgg gct gcc ctc   7837
Ala Met Leu Gln Glu Gln Gln Arg Leu Gly Leu Val Trp Ala Ala Leu
2575                2580                2585                2590

cag ggt gcc agg acc cag ctc cga gat gtc cgg gcc aag aag gac cag   7885
Gln Gly Ala Arg Thr Gln Leu Arg Asp Val Arg Ala Lys Lys Asp Gln
                2595                2600                2605

ctg gag gcg cac atc cag gcg gcg cag gcc atg ctt gcc atg gac aca   7933
Leu Glu Ala His Ile Gln Ala Ala Gln Ala Met Leu Ala Met Asp Thr
            2610                2615                2620

gac gag aca agc aag aag atc gca cat gcc aag gct gtg gct gct gaa   7981
Asp Glu Thr Ser Lys Lys Ile Ala His Ala Lys Ala Val Ala Ala Glu
        2625                2630                2635

gcc cag gac acc gcc acc cgt gtg cag tcc cag ctg cag gcc atg cag   8029
Ala Gln Asp Thr Ala Thr Arg Val Gln Ser Gln Leu Gln Ala Met Gln
    2640                2645                2650

gag aat gtg gag cgg tgg cag ggc cag tac gag ggc ctg cgg ggc cag   8077
Glu Asn Val Glu Arg Trp Gln Gly Gln Tyr Glu Gly Leu Arg Gly Gln
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2655                2660                2665                2670

gac ctg ggc cag gca gtg ctt gac gca ggc cac tca gtg tcc acc ctg   8125
Asp Leu Gly Gln Ala Val Leu Asp Ala Gly His Ser Val Ser Thr Leu
                2675                2680                2685

gag aag acg ctg ccc cag ctg ctg gcc aag ctg agc atc ctg gag aac   8173
Glu Lys Thr Leu Pro Gln Leu Leu Ala Lys Leu Ser Ile Leu Glu Asn
            2690                2695                2700

cgt ggg gtg cac aac gcc agc ctg gcc ctg tcc gcc agc att ggc cgc   8221
Arg Gly Val His Asn Ala Ser Leu Ala Leu Ser Ala Ser Ile Gly Arg
        2705                2710                2715

gtg cga gag ctc att gcc cag gcc cgg ggg gct gcc agt aag gtc aag   8269
Val Arg Glu Leu Ile Ala Gln Ala Arg Gly Ala Ala Ser Lys Val Lys
    2720                2725                2730

gtg ccc atg aag ttc aac ggg cgc tca                               8296
Val Pro Met Lys Phe Asn Gly Arg Ser
2735                2740
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<210> 36
<211> 2743
<212> PRT
<213> Homo sapiens

<400> 36

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

Arg Gly Pro Ala Pro Leu Leu Leu Val Gly Leu Ala Leu Leu Gly Ala
             20                  25                  30

Ala Arg Ala Arg Glu Glu Ala Gly Gly Gly Phe Ser Leu His Pro Pro
         35                  40                  45

Tyr Phe Asn Leu Ala Glu Gly Ala Arg Ile Ala Ala Ser Ala Thr Cys
     50                  55                  60

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

Tyr Cys Lys Leu Val Gly Gly Pro Val Ala Gly Gly Asp Pro Asn Gln
                 85                  90                  95

Thr Ile Arg Gly Gln Tyr Cys Asp Ile Cys Thr Ala Ala Asn Ser Asn
            100                 105                 110

Lys Ala His Pro Ala Ser Asn Ala Ile Asp Gly Thr Glu Arg Trp Trp
        115                 120                 125

Gln Ser Pro Pro Leu Ser Arg Gly Leu Glu Tyr Asn Glu Val Asn Val
    130                 135                 140

Thr Leu Asp Leu Gly Gln Val Phe His Val Ala Tyr Val Leu Ile Lys
145                 150                 155                 160

Phe Ala Asn Ser Pro Arg Pro Asp Leu Trp Val Leu Glu Arg Ser Met
                165                 170                 175
```

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Asp Phe Gly Arg Thr Tyr Gln Pro Trp Gln Phe Phe Ala Ser Ser Lys
            180                 185                 190

Arg Asp Cys Leu Glu Arg Phe Gly Pro Gln Thr Leu Glu Arg Ile Thr
        195                 200                 205

Arg Asp Asp Ala Ala Ile Cys Thr Thr Glu Tyr Ser Arg Ile Val Pro
    210                 215                 220

Leu Glu Asn Gly Glu Ile Val Val Ser Leu Val Asn Gly Arg Pro Gly
225                 230                 235                 240

Ala Met Asn Phe Ser Tyr Ser Pro Leu Leu Arg Glu Phe Thr Lys Ala
                245                 250                 255

Thr Asn Val Arg Leu Arg Phe Leu Arg Thr Asn Thr Leu Leu Gly His
            260                 265                 270

Leu Met Gly Lys Ala Leu Arg Asp Pro Thr Val Thr Arg Arg Tyr Tyr
        275                 280                 285

Tyr Ser Ile Lys Asp Ile Ser Ile Gly Gly Arg Cys Val Cys His Gly
    290                 295                 300

His Ala Asp Ala Cys Asp Ala Lys Asp Pro Thr Asp Pro Phe Arg Leu
305                 310                 315                 320

Gln Cys Thr Cys Gln His Asn Thr Cys Gly Gly Thr Cys Asp Arg Cys
                325                 330                 335

Cys Pro Gly Phe Asn Gln Gln Pro Trp Lys Pro Ala Thr Ala Asn Ser
            340                 345                 350

Ala Asn Glu Cys Gln Ser Cys Asn Cys Tyr Gly His Ala Thr Asp Cys
        355                 360                 365

Tyr Tyr Asp Pro Glu Val Asp Arg Arg Arg Ala Ser Gln Ser Leu Asp
    370                 375                 380

Gly Thr Tyr Gln Gly Gly Gly Val Cys Ile Asp Cys Gln His His Thr
385                 390                 395                 400

Ala Gly Val Asn Cys Glu Arg Cys Leu Pro Gly Phe Tyr Arg Ser Pro
                405                 410                 415

Asn His Pro Leu Asp Ser Pro His Val Cys Arg Arg Cys Asn Cys Glu
            420                 425                 430

Ser Asp Phe Thr Asp Gly Thr Cys Glu Asp Leu Thr Gly Arg Cys Tyr
        435                 440                 445

Cys Arg Pro Asn Phe Ser Gly Glu Arg Cys Asp Val Cys Ala Glu Gly
    450                 455                 460

Phe Thr Gly Phe Pro Ser Cys Tyr Pro Thr Pro Ser Ser Ser Asn Asp
465                 470                 475                 480

Thr Arg Glu Gln Val Leu Pro Ala Gly Gln Ile Val Asn Cys Asp Cys
                485                 490                 495
```

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Ser Ala Ala Gly Thr Gln Gly Asn Ala Cys Arg Lys Asp Pro Arg Val
            500                 505                 510

Gly Arg Cys Leu Cys Lys Pro Asn Phe Gln Gly Thr His Cys Glu Leu
        515                 520                 525

Cys Ala Pro Gly Phe Tyr Gly Pro Gly Cys Gln Pro Cys Gln Cys Ser
    530                 535                 540

Ser Pro Gly Val Ala Asp Asp Arg Cys Asp Pro Asp Thr Gly Gln Cys
545                 550                 555                 560

Arg Cys Arg Val Gly Phe Glu Gly Ala Thr Cys Asp Arg Cys Ala Pro
                565                 570                 575

Gly Tyr Phe His Phe Pro Leu Cys Gln Leu Cys Gly Cys Ser Pro Ala
            580                 585                 590

Gly Thr Leu Pro Glu Gly Cys Asp Glu Ala Gly Arg Cys Leu Cys Gln
        595                 600                 605

Pro Glu Phe Ala Gly Pro His Cys Asp Arg Cys Arg Pro Gly Tyr His
    610                 615                 620

Gly Phe Pro Asn Cys Gln Ala Cys Thr Cys Asp Pro Arg Gly Ala Leu
625                 630                 635                 640

Asp Gln Leu Cys Gly Ala Gly Gly Leu Cys Arg Cys Arg Pro Gly Tyr
                645                 650                 655

Thr Gly Thr Ala Cys Gln Glu Cys Ser Pro Gly Phe His Gly Phe Pro
            660                 665                 670

Ser Cys Val Pro Cys His Cys Ser Ala Glu Gly Ser Leu His Ala Ala
        675                 680                 685

Cys Asp Pro Arg Ser Gly Gln Cys Ser Cys Arg Pro Arg Val Thr Gly
    690                 695                 700

Leu Arg Cys Asp Thr Cys Val Pro Gly Ala Tyr Asn Phe Pro Tyr Cys
705                 710                 715                 720

Glu Ala Gly Ser Cys His Pro Ala Gly Leu Ala Pro Val Asp Pro Ala
                725                 730                 735

Leu Pro Glu Ala Gln Val Pro Cys Met Cys Arg Ala His Val Glu Gly
            740                 745                 750

Pro Ser Cys Asp Arg Cys Lys Pro Gly Phe Trp Gly Leu Ser Pro Ser
        755                 760                 765

Asn Pro Glu Gly Cys Thr Arg Cys Ser Cys Asp Leu Arg Gly Thr Leu
    770                 775                 780

Gly Gly Val Ala Glu Cys Gln Pro Gly Thr Gly Gln Cys Phe Cys Lys
785                 790                 795                 800

Pro His Val Cys Gly Gln Ala Cys Ala Ser Cys Lys Asp Gly Phe Phe
                805                 810                 815

Gly Leu Asp Gln Ala Asp Tyr Phe Gly Cys Arg Ser Cys Arg Cys Asp
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            820                 825                 830

Ile Gly Gly Ala Leu Gly Gln Ser Cys Glu Pro Arg Thr Gly Val Cys
        835                 840                 845

Arg Cys Arg Pro Asn Thr Gln Gly Pro Thr Cys Ser Glu Pro Ala Arg
    850                 855                 860

Asp His Tyr Leu Pro Asp Leu His His Leu Arg Leu Glu Leu Glu Glu
865                 870                 875                 880

Ala Ala Thr Pro Glu Gly His Ala Val Arg Phe Gly Phe Asn Pro Leu
                885                 890                 895

Glu Phe Glu Asn Phe Ser Trp Arg Gly Tyr Ala Gln Met Ala Pro Val
            900                 905                 910

Gln Pro Arg Ile Val Ala Arg Leu Asn Leu Thr Ser Pro Asp Leu Phe
        915                 920                 925

Trp Leu Val Phe Arg Tyr Val Asn Arg Gly Ala Met Ser Val Ser Gly
    930                 935                 940

Arg Val Ser Val Arg Glu Glu Gly Arg Ser Ala Ala Cys Ala Asn Cys
945                 950                 955                 960

Thr Ala Gln Ser Gln Pro Val Ala Phe Pro Pro Ser Thr Glu Pro Ala
                965                 970                 975

Phe Ile Thr Val Pro Gln Arg Gly Phe Gly Glu Pro Phe Val Leu Asn
            980                 985                 990

Pro Gly Thr Trp Ala Leu Arg Val Glu Ala Glu Gly Val Leu Leu Asp
        995                1000                1005

Tyr Val Val Leu Leu Pro Ser Ala Tyr Tyr Glu Ala Ala Leu Leu Gln
   1010                1015                1020

Leu Arg Val Thr Glu Ala Cys Thr Tyr Arg Pro Ser Ala Gln Gln Ser
1025                1030                1035                1040

Gly Asp Asn Cys Leu Leu Tyr Thr His Leu Pro Leu Asp Gly Phe Pro
                1045                1050                1055

Ser Ala Ala Gly Leu Glu Ala Leu Cys Arg Gln Asp Asn Ser Leu Pro
            1060                1065                1070

Arg Pro Cys Pro Thr Glu Gln Leu Ser Pro Ser His Pro Pro Leu Ile
        1075                1080                1085

Thr Cys Thr Gly Ser Asp Val Asp Val Gln Leu Gln Val Ala Val Pro
   1090                1095                1100

Gln Pro Gly Arg Tyr Ala Leu Val Val Glu Tyr Ala Asn Glu Asp Ala
1105                1110                1115                1120

Arg Gln Glu Val Gly Val Ala Val His Thr Pro Gln Arg Ala Pro Gln
                1125                1130                1135

Gln Gly Leu Leu Ser Leu His Pro Cys Leu Tyr Ser Thr Leu Cys Arg
            1140                1145                1150
```

```
Gly Thr Ala Arg Asp Thr Gln Asp His Leu Ala Val Phe His Leu Asp
       1155                1160                1165

Ser Glu Ala Ser Val Arg Leu Thr Ala Glu Gln Ala Arg Phe Phe Leu
   1170                1175                1180

His Gly Val Thr Leu Val Pro Ile Glu Glu Phe Ser Pro Glu Phe Val
1185                1190                1195                1200

Glu Pro Arg Val Ser Cys Ile Ser Ser His Gly Ala Phe Gly Pro Asn
               1205                1210                1215

Ser Ala Ala Cys Leu Pro Ser Arg Phe Pro Lys Pro Pro Gln Pro Ile
           1220                1225                1230

Ile Leu Arg Asp Cys Gln Val Ile Pro Leu Pro Pro Gly Leu Pro Leu
       1235                1240                1245

Thr His Ala Gln Asp Leu Thr Pro Ala Thr Ser Pro Ala Gly Pro Arg
   1250                1255                1260

Pro Arg Pro Pro Thr Ala Val Asp Pro Asp Ala Glu Pro Thr Leu Leu
1265                1270                1275                1280

Arg Glu Pro Gln Ala Thr Val Val Phe Thr Thr His Val Pro Thr Leu
               1285                1290                1295

Gly Arg Tyr Ala Phe Leu Leu His Gly Tyr Gln Pro Ala His Pro Thr
           1300                1305                1310

Phe Pro Val Glu Val Leu Ile Asn Ala Gly Arg Val Trp Gln Gly His
       1315                1320                1325

Ala Asn Ala Ser Phe Cys Pro His Gly Tyr Gly Cys Arg Thr Leu Val
   1330                1335                1340

Val Cys Glu Gly Gln Ala Leu Leu Asp Val Thr His Ser Glu Leu Thr
1345                1350                1355                1360

Val Thr Val Arg Val Pro Glu Gly Arg Trp Leu Trp Leu Asp Tyr Val
               1365                1370                1375

Leu Val Val Pro Glu Asn Val Tyr Ser Phe Gly Tyr Leu Arg Glu Glu
           1380                1385                1390

Pro Leu Asp Lys Ser Tyr Asp Phe Ile Ser His Cys Ala Ala Gln Gly
       1395                1400                1405

Tyr His Ile Ser Pro Ser Ser Ser Ser Leu Phe Cys Arg Asn Ala Ala
   1410                1415                1420

Ala Ser Leu Ser Leu Phe Tyr Asn Asn Gly Ala Arg Pro Cys Gly Cys
1425                1430                1435                1440

His Glu Val Gly Ala Thr Gly Pro Thr Cys Glu Pro Phe Gly Gly Gln
               1445                1450                1455

Cys Pro Cys His Ala His Val Ile Gly Arg Asp Cys Ser Arg Cys Ala
           1460                1465                1470
```

```
Thr Gly Tyr Trp Gly Phe Pro Asn Cys Arg Pro Cys Asp Cys Gly Ala
       1475                1480                1485

Arg Leu Cys Asp Glu Leu Thr Gly Gln Cys Ile Cys Pro Pro Arg Thr
   1490                1495                1500

Ile Pro Pro Asp Cys Leu Leu Cys Gln Pro Gln Thr Phe Gly Cys His
1505                1510                1515                1520

Pro Leu Val Gly Cys Glu Glu Cys Asn Cys Ser Gly Pro Gly Ile Gln
               1525                1530                1535

Glu Leu Thr Asp Pro Thr Cys Asp Thr Asp Ser Gly Gln Cys Lys Cys
           1540                1545                1550

Arg Pro Asn Val Thr Gly Arg Arg Cys Asp Thr Cys Ser Pro Gly Phe
       1555                1560                1565

His Gly Tyr Pro Arg Cys Arg Pro Cys Asp Cys His Glu Ala Gly Thr
   1570                1575                1580

Ala Pro Gly Val Cys Asp Pro Leu Thr Gly Gln Cys Tyr Cys Lys Glu
1585                1590                1595                1600

Asn Val Gln Gly Pro Lys Cys Asp Gln Cys Ser Leu Gly Thr Phe Ser
               1605                1610                1615

Leu Asp Ala Ala Asn Pro Lys Gly Cys Thr Arg Cys Phe Cys Phe Gly
           1620                1625                1630

Ala Thr Glu Arg Cys Arg Ser Ser Ser Tyr Thr Arg Gln Glu Phe Val
       1635                1640                1645

Asp Met Glu Gly Trp Val Leu Leu Ser Thr Asp Arg Gln Val Val Pro
   1650                1655                1660

His Glu Arg Gln Pro Gly Thr Glu Met Leu Arg Ala Asp Leu Arg His
1665                1670                1675                1680

Val Pro Glu Ala Val Pro Glu Ala Phe Pro Glu Leu Tyr Trp Gln Ala
               1685                1690                1695

Pro Pro Ser Tyr Leu Gly Asp Arg Val Ser Ser Tyr Gly Gly Thr Leu
           1700                1705                1710

Arg Tyr Glu Leu His Ser Glu Thr Gln Arg Gly Asp Val Phe Val Pro
       1715                1720                1725

Met Glu Ser Arg Pro Asp Val Val Leu Gln Gly Asn Gln Met Ser Ile
   1730                1735                1740

Thr Phe Leu Glu Pro Ala Tyr Pro Thr Pro Gly His Val His Arg Gly
1745                1750                1755                1760

Gln Leu Gln Leu Val Glu Gly Asn Phe Arg His Thr Glu Thr Arg Asn
               1765                1770                1775

Thr Val Ser Arg Glu Glu Leu Met Met Val Leu Ala Ser Leu Glu Gln
           1780                1785                1790

Leu Gln Ile Arg Ala Leu Phe Ser Gln Ile Ser Ser Ala Val Ser Leu
```

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      1795                1800                1805

Arg Arg Val Ala Leu Glu Val Ala Ser Pro Ala Gly Gln Gly Ala Leu
   1810                1815                1820

Ala Ser Asn Val Glu Leu Cys Leu Cys Pro Ala Ser Tyr Arg Gly Asp
1825                1830                1835                1840

Ser Cys Gln Glu Cys Ala Pro Gly Phe Tyr Arg Asp Val Lys Gly Leu
               1845                1850                1855

Phe Leu Gly Arg Cys Val Pro Cys Gln Cys His Gly His Ser Asp Arg
           1860                1865                1870

Cys Leu Pro Gly Ser Gly Val Cys Val Asp Cys Gln His Asn Thr Glu
       1875                1880                1885

Gly Ala His Cys Glu Arg Cys Gln Ala Gly Phe Met Ser Ser Arg Asp
   1890                1895                1900

Asp Pro Ser Ala Pro Cys Val Ser Cys Pro Cys Pro Leu Ser Val Pro
1905                1910                1915                1920

Ser Asn Asn Phe Ala Glu Gly Cys Val Leu Arg Gly Gly Arg Thr Gln
               1925                1930                1935

Cys Leu Cys Lys Pro Gly Tyr Ala Gly Ala Ser Cys Glu Arg Cys Ala
           1940                1945                1950

Pro Gly Phe Phe Gly Asn Pro Leu Val Leu Gly Ser Ser Cys Gln Pro
       1955                1960                1965

Cys Asp Cys Ser Gly Asn Gly Asp Pro Asn Leu Leu Phe Ser Asp Cys
   1970                1975                1980

Asp Pro Leu Thr Gly Ala Cys Arg Gly Cys Leu Arg His Thr Thr Gly
1985                1990                1995                2000

Pro Arg Cys Glu Ile Cys Ala Pro Gly Phe Tyr Gly Asn Ala Leu Leu
               2005                2010                2015

Pro Gly Asn Cys Thr Arg Cys Asp Cys Thr Pro Cys Gly Thr Glu Ala
           2020                2025                2030

Cys Asp Pro His Ser Gly His Cys Leu Cys Lys Ala Gly Val Thr Gly
       2035                2040                2045

Arg Arg Cys Asp Arg Cys Gln Glu Gly His Phe Gly Phe Asn Gly Cys
   2050                2055                2060

Gly Gly Cys Arg Pro Cys Ala Cys Gly Pro Ala Ala Glu Gly Ser Glu
2065                2070                2075                2080

Cys His Pro Gln Ser Gly Gln Cys His Cys Arg Pro Gly Thr Met Gly
               2085                2090                2095

Pro Gln Cys Arg Glu Cys Ala Pro Gly Tyr Trp Gly Leu Pro Glu Gln
           2100                2105                2110

Gly Cys Arg Arg Cys Gln Cys Pro Gly Gly Arg Cys Asp Pro His Thr
       2115                2120                2125
```

```
Gly Arg Cys Asn Cys Pro Pro Gly Leu Ser Gly Glu Arg Cys Asp Thr
   2130                2135                2140

Cys Ser Gln Gln His Gln Val Pro Val Pro Gly Gly Pro Val Gly His
2145                2150                2155                2160

Ser Ile His Cys Glu Val Cys Asp His Cys Val Val Leu Leu Leu Asp
                2165                2170                2175

Asp Leu Glu Arg Ala Gly Ala Leu Leu Pro Ala Ile His Glu Gln Leu
            2180                2185                2190

Arg Gly Ile Asn Ala Ser Ser Met Ala Trp Ala Arg Leu His Arg Leu
        2195                2200                2205

Asn Ala Ser Ile Ala Asp Leu Gln Ser Gln Leu Arg Ser Pro Leu Gly
   2210                2215                2220

Pro Arg His Glu Thr Ala Gln Gln Leu Glu Val Leu Glu Gln Gln Ser
2225                2230                2235                2240

Thr Ser Leu Gly Gln Asp Ala Arg Arg Leu Gly Gly Gln Ala Val Gly
                2245                2250                2255

Thr Arg Asp Gln Ala Ser Gln Leu Leu Ala Gly Thr Glu Ala Thr Leu
            2260                2265                2270

Gly His Ala Lys Thr Leu Leu Ala Ala Ile Arg Ala Val Asp Arg Thr
        2275                2280                2285

Leu Ser Glu Leu Met Ser Gln Thr Gly His Leu Gly Leu Ala Asn Ala
   2290                2295                2300

Ser Ala Pro Ser Gly Glu Gln Leu Leu Arg Thr Leu Ala Glu Val Glu
2305                2310                2315                2320

Arg Leu Leu Trp Glu Met Arg Ala Arg Asp Leu Gly Ala Pro Gln Ala
                2325                2330                2335

Ala Ala Glu Ala Glu Leu Ala Ala Ala Gln Arg Leu Leu Ala Arg Val
            2340                2345                2350

Gln Glu Gln Leu Ser Ser Leu Trp Glu Glu Asn Gln Ala Leu Ala Thr
        2355                2360                2365

Gln Thr Arg Asp Arg Leu Ala Gln His Glu Ala Gly Leu Met Asp Leu
   2370                2375                2380

Arg Glu Ala Leu Asn Arg Ala Val Asp Ala Thr Arg Glu Ala Gln Glu
2385                2390                2395                2400

Leu Asn Ser Arg Asn Gln Glu Arg Leu Glu Glu Ala Leu Gln Arg Lys
                2405                2410                2415

Gln Glu Leu Ser Arg Asp Asn Ala Thr Leu Gln Ala Thr Leu His Ala
            2420                2425                2430

Ala Arg Asp Thr Leu Ala Ser Val Phe Arg Leu Leu His Ser Leu Asp
        2435                2440                2445
```

```
Gln Ala Lys Glu Glu Leu Glu Arg Leu Ala Ala Ser Leu Asp Gly Ala
   2450                2455                2460

Arg Thr Pro Leu Leu Gln Arg Met Gln Thr Phe Ser Pro Ala Gly Ser
2465                2470                2475                2480

Lys Leu Arg Leu Val Glu Ala Ala Glu Ala His Ala Gln Gln Leu Gly
                2485                2490                2495

Gln Leu Ala Leu Asn Leu Ser Ser Ile Ile Leu Asp Val Asn Gln Asp
           2500                2505                2510

Arg Leu Thr Gln Arg Ala Ile Glu Ala Ser Asn Ala Tyr Ser Arg Ile
       2515                2520                2525

Leu Gln Ala Val Gln Ala Ala Glu Asp Ala Ala Gly Gln Ala Leu Gln
   2530                2535                2540

Gln Ala Asp His Thr Trp Ala Thr Val Val Arg Gln Gly Leu Val Asp
2545                2550                2555                2560

Arg Ala Gln Gln Leu Leu Ala Asn Ser Thr Ala Leu Glu Glu Ala Met
                2565                2570                2575

Leu Gln Glu Gln Gln Arg Leu Gly Leu Val Trp Ala Ala Leu Gln Gly
           2580                2585                2590

Ala Arg Thr Gln Leu Arg Asp Val Arg Ala Lys Lys Asp Gln Leu Glu
       2595                2600                2605

Ala His Ile Gln Ala Ala Gln Ala Met Leu Ala Met Asp Thr Asp Glu
   2610                2615                2620

Thr Ser Lys Lys Ile Ala His Ala Lys Ala Val Ala Ala Glu Ala Gln
2625                2630                2635                2640

Asp Thr Ala Thr Arg Val Gln Ser Gln Leu Gln Ala Met Gln Glu Asn
                2645                2650                2655

Val Glu Arg Trp Gln Gly Gln Tyr Glu Gly Leu Arg Gly Gln Asp Leu
           2660                2665                2670

Gly Gln Ala Val Leu Asp Ala Gly His Ser Val Ser Thr Leu Glu Lys
       2675                2680                2685

Thr Leu Pro Gln Leu Leu Ala Lys Leu Ser Ile Leu Glu Asn Arg Gly
   2690                2695                2700

Val His Asn Ala Ser Leu Ala Leu Ser Ala Ser Ile Gly Arg Val Arg
2705                2710                2715                2720

Glu Leu Ile Ala Gln Ala Arg Gly Ala Ala Ser Lys Val Lys Val Pro
                2725                2730                2735

Met Lys Phe Asn Gly Arg Ser
           2740
```