
Antibody constructs for CD70 and CD3

The present invention relates to a bispecific antibody construct comprising a first binding domain which binds to human CD70 on the surface of a target cell and a second binding domain which binds to human CD3 on the surface of a T cell. Moreover, the invention provides a polynucleotide encoding the antibody construct, a vector comprising said polynucleotide and a host cell transformed or transfected with said polynucleotide or vector. Furthermore, the invention provides a process for the production of the antibody construct of the invention, a medical use of said antibody construct and a kit comprising said antibody construct.

CD70 (CD27L, TNFSF7) is a type II integral membrane protein whose normal expression is restricted to a subset of activated T and B cells, mature dendritic cells and thymic medullar epithelial cells. The biological functions of CD70 are mediated via binding to the CD27 receptor, which is expressed on lymphocytes and NK cells. CD70 interactions regulate B-cell maturation, T-cell co-stimulation and memory T cell function. Genetic ablation of CD27 in mice, which abrogates CD70 signaling, does not impact the development of B and T cells, but interferes with memory responses to viral re-challenge.

In addition to its highly restricted normal expression, aberrant CD70 expression has been documented in 60% of Non-Hodgkin Lymphoma (NHL), 70% of clear cell renal cell carcinoma (ccRCC), 40% of papillary RCC, as well as 25% of pancreatic adenocarcinoma, 22% of laryngeal / pharyngeal carcinoma, 15% of ovarian carcinoma, and 10% of lung adenocarcinoma and glioblastoma.

Each year, 14,080 people die of metastatic RCC in the U.S. (American Cancer Society: Cancer Facts and Figures. 2015). While all patients are treated with angiogenesis inhibitors (Bevacizumab, Sunitinib, Sorafenib, Axitinib) or mTOR inhibitors (Temozolomide, Everolimus), the 5-year survival rate for patients with metastatic RCC remains dismally low at 20% (American Cancer Society: Cancer Facts and Figures 2015). A significant unmet medical need remains for this disease, and up to 10,000 patients a year presenting with CD70-expressing metastatic ccRCC could benefit from a CD70-targeted therapy in the U.S.

Diffuse large cell B cell lymphoma (DLBCL) is the largest NHL sub-type with 28,740 new cases per year in the U.S. (American Cancer Society: Cancer Facts and Figures, 2015). 71% of DLBCL tumors express CD70, and while most patients initially respond to standard of care therapy (Rituxan plus cyclophosphamide, adriamycin, vincristine, prednisone), many relapse or are refractory, and 19,790 patients die of this disease every year (American Cancer Society: Cancer Facts and Figures 2015). Therefore a clear unmet medical need remains for DLBCL, and up to 14,000 patients a year presenting with CD70-expressing DLBCL could benefit from a CD70-targeted therapy in the U.S.

Based on the number of patients dying each year in the U.S. of pancreatic (40,560), laryngeal and pharyngeal (6,300), ovarian (14,180), and lung (158,000) carcinoma (American Cancer Society: Cancer Facts and Figures, 2015), and taking into account the CD70 expression prevalence in these cancer types, up to 30,000 additional patients a year with unmet medical needs presenting with CD70-expressing solid tumors could benefit from a CD70-targeted therapy in the U.S.

As there is still a need for having available further options for the treatment cancer diseases related to the overexpression of CD70, such as the ones discussed herein above, there are provided herewith means and methods for the solution of this problem in the form of a bispecific CD70xCD3 antibody construct.

Thus, in a first aspect, the present invention provides a bispecific antibody construct comprising a first binding domain which binds to human CD70 on the surface of a target cell and a second binding domain which binds to human CD3 on the surface of a T cell.

It must be noted that as used herein, the singular forms “a”, “an”, and “the” include plural references unless the context clearly indicates otherwise. Thus, for example, reference to “a reagent” includes one or more of such different reagents and reference to “the method” includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

Unless otherwise indicated, the term “at least” preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific

embodiments of the invention described herein. Such equivalents are intended to be encompassed by the present invention.

The term “and/or” wherever used herein includes the meaning of “and”, “or” and “all or any other combination of the elements connected by said term”.

The term “about” or “approximately” as used herein means within $\pm 20\%$, preferably within $\pm 15\%$, more preferably within $\pm 10\%$, and most preferably within $\pm 5\%$ of a given value or range.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word “comprise”, and variations such as “comprises” and “comprising”, will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term “comprising” can be substituted with the term “containing” or “including” or sometimes when used herein with the term “having”.

When used herein “consisting of” excludes any element, step, or ingredient not specified in the claim element. When used herein, “consisting essentially of” does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

In each instance herein any of the terms “comprising”, “consisting essentially of” and “consisting of” may be replaced with either of the other two terms.

The term “antibody construct” refers to a molecule in which the structure and/or function is/are based on the structure and/or function of an antibody, *e.g.*, of a full-length or whole immunoglobulin molecule. An antibody construct is hence capable of binding to its specific target or antigen. Furthermore, an antibody construct according to the invention comprises the minimum structural requirements of an antibody which allow for the target binding. This minimum requirement may *e.g.* be defined by the presence of at least the three light chain CDRs (*i.e.* CDR1, CDR2 and CDR3 of the VL region) and/or the three heavy chain CDRs (*i.e.* CDR1, CDR2 and CDR3 of the VH region), preferably of all six CDRs. The antibodies on which the constructs according to the invention are based include for example monoclonal, recombinant, chimeric, deimmunized, humanized and human antibodies.

Within the definition of “antibody constructs” according to the invention are full-length or whole antibodies also including camelid antibodies and other immunoglobulin antibodies generated by biotechnological or protein engineering methods or processes. These full-length antibodies may be for example monoclonal, recombinant, chimeric, deimmunized, humanized and human antibodies. Also within the definition of “antibody constructs” are fragments of full-length antibodies, such as VH, VHH, VL, (s)dAb, Fv, Fd, Fab, Fab', F(ab')₂ or “r IgG” (“half antibody”). Antibody constructs according to the invention may also be modified fragments of antibodies, also called antibody variants, such as scFv, di-scFv or bi(s)-scFv, scFv-Fc, scFv-zipper, scFab, Fab2, Fab3, diabodies, single chain diabodies, tandem diabodies (Tandab's), tandem di-scFv, tandem tri-scFv, „minibodies“ exemplified by a structure which is as follows: (VH-VL-CH3)₂, (scFv-CH3)₂, ((scFv)₂-CH3 + CH3), ((scFv)₂-CH3) or (scFv-CH3-scFv)₂, multibodies such as triabodies or tetrabodies, and single domain antibodies such as nanobodies or single variable domain antibodies comprising merely one variable domain, which might be VHH, VH or VL, that specifically bind an antigen or epitope independently of other V regions or domains. Further preferred formats of the antibody constructs according to the invention are cross bodies, maxi bodies, hetero Fc constructs and mono Fc constructs. Examples for those formats will be described herein below.

A binding domain may typically comprise an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH); however, it does not have to comprise both. Fd fragments, for example, have two VH regions and often retain some antigen-binding function of the intact antigen-binding domain. Additional examples for the format of antibody fragments, antibody variants or binding domains include (1) a Fab fragment, a monovalent fragment having the VL, VH, CL and CH1 domains; (2) a F(ab')₂ fragment, a bivalent fragment having two Fab fragments linked by a disulfide bridge at the hinge region; (3) an Fd fragment having the two VH and CH1 domains; (4) an Fv fragment having the VL and VH domains of a single arm of an antibody, (5) a dAb fragment (Ward et al., (1989) Nature 341 :544-546), which has a VH domain; (6) an isolated complementarity determining region (CDR), and (7) a single chain Fv (scFv), the latter being preferred (for example, derived from an scFv-library). Examples for embodiments of antibody constructs according to the invention are e.g. described in WO 00/006605, WO 2005/040220, WO 2008/119567, WO 2010/037838, WO 2013/026837, WO 2013/026833, US 2014/0308285, US 2014/0302037, WO 2014/144722, WO 2014/151910, and WO 2015/048272.

Furthermore, the definition of the term “antibody construct” includes monovalent, bivalent and polyvalent / multivalent constructs and, thus, monospecific constructs, specifically binding to only one antigenic structure, as well as bispecific and polyspecific / multispecific constructs, which specifically bind more than one antigenic structure, e.g. two, three or more, through distinct binding domains. Moreover, the definition of the term “antibody construct” includes molecules consisting of only one polypeptide chain as well as molecules consisting of more than one polypeptide chain, which chains can be either identical (homodimers, homotrimers or homo oligomers) or different (heterodimer, heterotrimer or heterooligomer). Examples for the above identified antibodies and variants or derivatives thereof are described *inter alia* in Harlow and Lane, Antibodies a laboratory manual, CSHL Press (1988) and Using Antibodies: a laboratory manual, CSHL Press (1999), Kontermann and Dübel, Antibody Engineering, Springer, 2nd ed. 2010 and Little, Recombinant Antibodies for Immunotherapy, Cambridge University Press 2009.

The antibody constructs of the present invention are preferably “*in vitro* generated antibody constructs”. This term refers to an antibody construct according to the above definition where all or part of the variable region (e.g., at least one CDR) is generated in a non-immune cell selection, e.g., an *in vitro* phage display, protein chip or any other method in which candidate sequences can be tested for their ability to bind to an antigen. This term thus preferably excludes sequences generated solely by genomic rearrangement in an immune cell in an animal. A “recombinant antibody” is an antibody made through the use of recombinant DNA technology or genetic engineering.

The term “monoclonal antibody” (mAb) or monoclonal antibody construct as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations and/or post-translation modifications (e.g., isomerizations, amidations) that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site or determinant on the antigen, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (or epitopes). In addition to their specificity, the monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, hence uncontaminated by other immunoglobulins. The modifier “monoclonal” indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method.

For the preparation of monoclonal antibodies, any technique providing antibodies produced by continuous cell line cultures can be used. For example, monoclonal antibodies to be used may be made by the hybridoma method first described by Koehler *et al.*, Nature, 256: 495 (1975), or may be made by recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567). Examples for further techniques to produce human monoclonal antibodies include the trioma technique, the human B-cell hybridoma technique (Kozbor, Immunology Today 4 (1983), 72) and the EBV-hybridoma technique (Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), 77-96).

Hybridomas can then be screened using standard methods, such as enzyme-linked immunosorbent assay (ELISA) and surface plasmon resonance (BIAcore™) analysis, to identify one or more hybridomas that produce an antibody that specifically binds with a specified antigen. Any form of the relevant antigen may be used as the immunogen, e.g., recombinant antigen, naturally occurring forms, any variants or fragments thereof, as well as an antigenic peptide thereof. Surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies which bind to an epitope of a target antigen, such as CD70 or CD3 epsilon (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmberg, J. Immunol. Methods 183 (1995), 7-13).

Another exemplary method of making monoclonal antibodies includes screening protein expression libraries, e.g., phage display or ribosome display libraries. Phage display is described, for example, in Ladner *et al.*, U.S. Patent No. 5,223,409; Smith (1985) Science 228:1315-1317, Clackson *et al.*, Nature, 352: 624-628 (1991) and Marks *et al.*, J. Mol. Biol., 222: 581-597 (1991).

In addition to the use of display libraries, the relevant antigen can be used to immunize a non-human animal, e.g., a rodent (such as a mouse, hamster, rabbit or rat). In one embodiment, the non-human animal includes at least a part of a human immunoglobulin gene. For example, it is possible to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig (immunoglobulin) loci. Using the hybridoma technology, antigen-specific monoclonal antibodies derived from the genes with the desired specificity may be produced and selected. See, e.g., XENOMOUSE™, Green *et al.* (1994) Nature Genetics 7:13-21, US 2003-0070185, WO 96/34096, and WO 96/33735.

A monoclonal antibody can also be obtained from a non-human animal, and then modified, *e.g.*, humanized, deimmunized, rendered chimeric etc., using recombinant DNA techniques known in the art. Examples of modified antibody constructs include humanized variants of non-human antibodies, "affinity matured" antibodies (see, *e.g.* Hawkins *et al.* J. Mol. Biol. 254, 889-896 (1992) and Lowman *et al.*, Biochemistry 30, 10832- 10837 (1991)) and antibody mutants with altered effector function(s) (see, *e.g.*, US Patent 5,648,260, Kontermann and Dübel (2010), *loc. cit.* and Little (2009), *loc. cit.*).

In immunology, affinity maturation is the process by which B cells produce antibodies with increased affinity for antigen during the course of an immune response. With repeated exposures to the same antigen, a host will produce antibodies of successively greater affinities. Like the natural prototype, the *in vitro* affinity maturation is based on the principles of mutation and selection. The *in vitro* affinity maturation has successfully been used to optimize antibodies, antibody constructs, and antibody fragments. Random mutations inside the CDRs are introduced using radiation, chemical mutagens or error-prone PCR. In addition, the genetical diversity can be increased by chain shuffling. Two or three rounds of mutation and selection using display methods like phage display usually results in antibody fragments with affinities in the low nanomolar range.

A preferred type of an amino acid substitutional variation of the antibody constructs involves substituting one or more hypervariable region residues of a parent antibody (*e. g.* a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (*e. g.* 6-7 sites) are mutated to generate all possible amino acid substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (*e. g.* binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the binding domain and, *e.g.*, human CD70. Such contact residues and neighbouring residues are candidates for substitution according to the techniques elaborated herein. Once such variants

are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

The monoclonal antibodies and antibody constructs of the present invention specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Patent No. 4,816,567; Morrison *et al.*, Proc. Natl. Acad. Sci. USA, 81: 6851-6855 (1984)). Chimeric antibodies of interest herein include "primitized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (e.g., Old World Monkey, Ape etc.) and human constant region sequences. A variety of approaches for making chimeric antibodies have been described. See *e.g.*, Morrison *et al.*, Proc. Natl. Acad. Sci. U.S.A. 81:6851, 1985; Takeda *et al.*, Nature 314:452, 1985, Cabilly *et al.*, U.S. Patent No. 4,816,567; Boss *et al.*, U.S. Patent No. 4,816,397; Tanaguchi *et al.*, EP 0171496; EP 0173494; and GB 2177096.

An antibody, antibody construct, antibody fragment or antibody variant may also be modified by specific deletion of human T cell epitopes (a method called "deimmunization") by the methods disclosed for example in WO 98/52976 or WO 00/34317. Briefly, the heavy and light chain variable domains of an antibody can be analyzed for peptides that bind to MHC class II; these peptides represent potential T cell epitopes (as defined in WO 98/52976 and WO 00/34317). For detection of potential T cell epitopes, a computer modeling approach termed "peptide threading" can be applied, and in addition a database of human MHC class II binding peptides can be searched for motifs present in the VH and VL sequences, as described in WO 98/52976 and WO 00/34317. These motifs bind to any of the 18 major MHC class II DR allotypes, and thus constitute potential T cell epitopes. Potential T cell epitopes detected can be eliminated by substituting small numbers of amino acid residues in the variable domains, or preferably, by single amino acid substitutions. Typically, conservative substitutions are made. Often, but not exclusively, an amino acid common to a position in human germline antibody sequences may be used. Human germline sequences are disclosed *e.g.* in Tomlinson, *et al.* (1992) J. Mol. Biol. 227:776-798; Cook, G.P. *et al.* (1995) Immunol. Today Vol. 16 (5): 237-242; and Tomlinson *et al.* (1995) EMBO J. 14: 14:4628-4638. The V BASE directory provides a comprehensive

directory of human immunoglobulin variable region sequences (compiled by Tomlinson, LA. *et al.* MRC Centre for Protein Engineering, Cambridge, UK). These sequences can be used as a source of human sequence, *e.g.*, for framework regions and CDRs. Consensus human framework regions can also be used, for example as described in US Patent No. 6,300,064.

“Humanized” antibodies, antibody constructs, variants or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) are antibodies or immunoglobulins of mostly human sequences, which contain (a) minimal sequence(s) derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region (also CDR) of the recipient are replaced by residues from a hypervariable region of a non-human (*e.g.*, rodent) species (donor antibody) such as mouse, rat, hamster or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, “humanized antibodies” as used herein may also comprise residues which are found neither in the recipient antibody nor the donor antibody. These modifications are made to further refine and optimize antibody performance. The humanized antibody may also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones *et al.*, *Nature*, 321: 522-525 (1986); Reichmann *et al.*, *Nature*, 332: 323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2: 593-596 (1992).

Humanized antibodies or fragments thereof can be generated by replacing sequences of the Fv variable domain that are not directly involved in antigen binding with equivalent sequences from human Fv variable domains. Exemplary methods for generating humanized antibodies or fragments thereof are provided by Morrison (1985) *Science* 229:1202-1207; by Oi *et al.* (1986) *BioTechniques* 4:214; and by US 5,585,089; US 5,693,761; US 5,693,762; US 5,859,205; and US 6,407,213. Those methods include isolating, manipulating, and expressing the nucleic acid sequences that encode all or part of immunoglobulin Fv variable domains from at least one of a heavy or light chain. Such nucleic acids may be obtained from a hybridoma producing an antibody against a predetermined target, as described above, as well as from other sources. The recombinant DNA encoding the humanized antibody molecule can then be cloned into an appropriate expression vector.

Humanized antibodies may also be produced using transgenic animals such as mice that express human heavy and light chain genes, but are incapable of expressing the endogenous

mouse immunoglobulin heavy and light chain genes. Winter describes an exemplary CDR grafting method that may be used to prepare the humanized antibodies described herein (U.S. Patent No. 5,225,539). All of the CDRs of a particular human antibody may be replaced with at least a portion of a non-human CDR, or only some of the CDRs may be replaced with non-human CDRs. It is only necessary to replace the number of CDRs required for binding of the humanized antibody to a predetermined antigen.

A humanized antibody can be optimized by the introduction of conservative substitutions, consensus sequence substitutions, germline substitutions and/or back mutations. Such altered immunoglobulin molecules can be made by any of several techniques known in the art, (e.g., Teng *et al.*, Proc. Natl. Acad. Sci. U.S.A., 80: 7308-7312, 1983; Kozbor *et al.*, Immunology Today, 4: 7279, 1983; Olsson *et al.*, Meth. Enzymol., 92: 3-16, 1982, and EP 239 400).

The term "human antibody", "human antibody construct" and "human binding domain" includes antibodies, antibody constructs and binding domains having antibody regions such as variable and constant regions or domains which correspond substantially to human germline immunoglobulin sequences known in the art, including, for example, those described by Kabat *et al.* (1991) (*loc. cit.*). The human antibodies, antibody constructs or binding domains of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*), for example in the CDRs, and in particular, in CDR3. The human antibodies, antibody constructs or binding domains can have at least one, two, three, four, five, or more positions replaced with an amino acid residue that is not encoded by the human germline immunoglobulin sequence. The definition of human antibodies, antibody constructs and binding domains as used herein also contemplates fully human antibodies, which include only non-artificially and/or genetically altered human sequences of antibodies as those can be derived by using technologies or systems such as the Xenomouse.

In some embodiments, the antibody constructs of the invention are "isolated" or "substantially pure" antibody constructs. "Isolated" or "substantially pure", when used to describe the antibody constructs disclosed herein, means an antibody construct that has been identified, separated and/or recovered from a component of its production environment. Preferably, the antibody construct is free or substantially free of association with all other components from its production environment. Contaminant components of its production environment, such as that resulting from recombinant transfected cells, are materials that would typically interfere with

diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. The antibody constructs may e.g. constitute at least about 5%, or at least about 50% by weight of the total protein in a given sample. It is understood that the isolated protein may constitute from 5% to 99.9% by weight of the total protein content, depending on the circumstances. The polypeptide may be made at a significantly higher concentration through the use of an inducible promoter or high expression promoter, such that it is made at increased concentration levels. The definition includes the production of an antibody construct in a wide variety of organisms and/or host cells that are known in the art. In preferred embodiments, the antibody construct will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Ordinarily, however, an isolated antibody construct will be prepared by at least one purification step.

The term "binding domain" characterizes in connection with the present invention a domain which (specifically) binds to / interacts with / recognizes a given target epitope or a given target site on the target molecules (antigens), here: CD70 and CD3, respectively. The structure and function of the first binding domain (recognizing CD70), and preferably also the structure and/or function of the second binding domain (recognizing CD3), is/are based on the structure and/or function of an antibody, e.g. of a full-length or whole immunoglobulin molecule. According to the invention, the first binding domain is characterized by the presence of three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and/or three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region). The second binding domain preferably also comprises the minimum structural requirements of an antibody which allow for the target binding. More preferably, the second binding domain comprises at least three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and/or three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region). It is envisaged that the first and/or second binding domain is produced by or obtainable by phage-display or library screening methods rather than by grafting CDR sequences from a pre-existing (monoclonal) antibody into a scaffold.

According to the present invention, binding domains are in the form of one or more polypeptides. Such polypeptides may include proteinaceous parts and non-proteinaceous parts (e.g. chemical linkers or chemical cross-linking agents such as glutaraldehyde). Proteins (including fragments thereof, preferably biologically active fragments, and peptides, usually having less than 30 amino acids) comprise two or more amino acids coupled to each other via a

covalent peptide bond (resulting in a chain of amino acids). The term "polypeptide" as used herein describes a group of molecules, which usually consist of more than 30 amino acids. Polypeptides may further form multimers such as dimers, trimers and higher oligomers, *i.e.*, consisting of more than one polypeptide molecule. Polypeptide molecules forming such dimers, trimers etc. may be identical or non-identical. The corresponding higher order structures of such multimers are, consequently, termed homo- or heterodimers, homo- or heterotrimers etc. An example for a heteromultimer is an antibody molecule, which, in its naturally occurring form, consists of two identical light polypeptide chains and two identical heavy polypeptide chains. The terms "peptide", "polypeptide" and "protein" also refer to naturally modified peptides / polypeptides / proteins wherein the modification is effected *e.g.* by post-translational modifications like glycosylation, acetylation, phosphorylation and the like. A "peptide", "polypeptide" or "protein" when referred to herein may also be chemically modified such as pegylated. Such modifications are well known in the art and described herein below.

Preferably the binding domain which binds to CD70 and/or the binding domain which binds to CD3 is/are human binding domains. Antibodies and antibody constructs comprising at least one human binding domain avoid some of the problems associated with antibodies or antibody constructs that possess non-human such as rodent (*e.g.* murine, rat, hamster or rabbit) variable and/or constant regions. The presence of such rodent derived proteins can lead to the rapid clearance of the antibodies or antibody constructs or can lead to the generation of an immune response against the antibody or antibody construct by a patient. In order to avoid the use of rodent derived antibodies or antibody constructs, human or fully human antibodies / antibody constructs can be generated through the introduction of human antibody function into a rodent so that the rodent produces fully human antibodies.

The ability to clone and reconstruct megabase-sized human loci in YACs and to introduce them into the mouse germline provides a powerful approach to elucidating the functional components of very large or crudely mapped loci as well as generating useful models of human disease. Furthermore, the use of such technology for substitution of mouse loci with their human equivalents could provide unique insights into the expression and regulation of human gene products during development, their communication with other systems, and their involvement in disease induction and progression.

An important practical application of such a strategy is the "humanization" of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the

endogenous Ig genes have been inactivated offers the opportunity to study the mechanisms underlying programmed expression and assembly of antibodies as well as their role in B-cell development. Furthermore, such a strategy could provide an ideal source for production of fully human monoclonal antibodies (mAbs) – an important milestone towards fulfilling the promise of antibody therapy in human disease. Fully human antibodies or antibody constructs are expected to minimize the immunogenic and allergic responses intrinsic to mouse or mouse-derivatized mAbs and thus to increase the efficacy and safety of the administered antibodies / antibody constructs. The use of fully human antibodies or antibody constructs can be expected to provide a substantial advantage in the treatment of chronic and recurring human diseases, such as inflammation, autoimmunity, and cancer, which require repeated compound administrations.

One approach towards this goal was to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci in anticipation that such mice would produce a large repertoire of human antibodies in the absence of mouse antibodies. Large human Ig fragments would preserve the large variable gene diversity as well as the proper regulation of antibody production and expression. By exploiting the mouse machinery for antibody diversification and selection and the lack of immunological tolerance to human proteins, the reproduced human antibody repertoire in these mouse strains should yield high affinity antibodies against any antigen of interest, including human antigens. Using the hybridoma technology, antigen-specific human mAbs with the desired specificity could be readily produced and selected. This general strategy was demonstrated in connection with the generation of the first XenoMouse mouse strains (see Green et al. *Nature Genetics* 7:13-21 (1994)). The XenoMouse strains were engineered with yeast artificial chromosomes (YACs) containing 245 kb and 190 kb-sized germline configuration fragments of the human heavy chain locus and kappa light chain locus, respectively, which contained core variable and constant region sequences. The human Ig containing YACs proved to be compatible with the mouse system for both rearrangement and expression of antibodies and were capable of substituting for the inactivated mouse Ig genes. This was demonstrated by their ability to induce B cell development, to produce an adult-like human repertoire of fully human antibodies, and to generate antigen-specific human mAbs. These results also suggested that introduction of larger portions of the human Ig loci containing greater numbers of V genes, additional regulatory elements, and human Ig constant regions might recapitulate substantially the full repertoire that is characteristic of the human humoral response to infection and immunization. The work of Green et al. was recently extended to the introduction of greater than approximately 80% of the human antibody repertoire through introduction of megabase sized, germline configuration YAC

fragments of the human heavy chain loci and kappa light chain loci, respectively. See Mendez *et al.* Nature Genetics 15:146-156 (1997) and U.S. patent application Ser. No. 08/759,620.

The production of the XenoMouse mice is further discussed and delineated in U.S. patent applications Ser. No. 07/466,008, Ser. No. 07/610,515, Ser. No. 07/919,297, Ser. No. 07/922,649, Ser. No. 08/031,801, Ser. No. 08/112,848, Ser. No. 08/234,145, Ser. No. 08/376,279, Ser. No. 08/430,938, Ser. No. 08/464,584, Ser. No. 08/464,582, Ser. No. 08/463,191, Ser. No. 08/462,837, Ser. No. 08/486,853, Ser. No. 08/486,857, Ser. No. 08/486,859, Ser. No. 08/462,513, Ser. No. 08/724,752, and Ser. No. 08/759,620; and U.S. Pat. Nos. 6,162,963; 6,150,584; 6,114,598; 6,075,181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. See also Mendez *et al.* Nature Genetics 15:146-156 (1997) and Green and Jakobovits J. Exp. Med. 188:483-495 (1998), EP 0 463 151 B1, WO 94/02602, WO 96/34096, WO 98/24893, WO 00/76310, and WO 03/47336.

In an alternative approach, others, including GenPharm International, Inc., have utilized a "minilocus" approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more VH genes, one or more DH genes, one or more JH genes, a mu constant region, and a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Pat. No. 5,545,807 to Surani *et al.* and U.S. Pat. Nos. 5,545,806; 5,625,825; 5,625,126; 5,633,425; 5,661,016; 5,770,429; 5,789,650; 5,814,318; 5,877,397; 5,874,299; and 6,255,458 each to Lonberg and Kay, U.S. Pat. Nos. 5,591,669 and 6,023,010 to Krimpenfort and Berns, U.S. Pat. Nos. 5,612,205; 5,721,367; and 5,789,215 to Berns *et al.*, and U.S. Pat. No. 5,643,763 to Choi and Dunn, and GenPharm International U.S. patent application Ser. No. 07/574,748, Ser. No. 07/575,962, Ser. No. 07/810,279, Ser. No. 07/853,408, Ser. No. 07/904,068, Ser. No. 07/990,860, Ser. No. 08/053,131, Ser. No. 08/096,762, Ser. No. 08/155,301, Ser. No. 08/161,739, Ser. No. 08/165,699, Ser. No. 08/209,741. See also EP 0 546 073 B1, WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Pat. No. 5,981,175. See further Taylor *et al.* (1992), Chen *et al.* (1993), Tuailon *et al.* (1993), Choi *et al.* (1993), Lonberg *et al.* (1994), Taylor *et al.* (1994), and Tuailon *et al.* (1995), Fishwild *et al.* (1996).

Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been introduced. See European Patent Application Nos. 773 288 and 843 961. Xenerex Biosciences is developing a technology for the potential generation of human antibodies. In this technology, SCID mice are reconstituted with human lymphatic cells, e.g., B and/or T cells. Mice are then immunized with an antigen and can generate an immune response against the antigen. See U.S. Pat. Nos. 5,476,996; 5,698,767; and 5,958,765.

Human anti-mouse antibody (HAMA) responses have led the industry to prepare chimeric or otherwise humanized antibodies. It is however expected that certain human anti-chimeric antibody (HACA) responses will be observed, particularly in chronic or multi-dose utilizations of the antibody. Thus, it would be desirable to provide antibody constructs comprising a human binding domain against CD70 and/or a human binding domain against CD3 in order to vitiate concerns and/or effects of HAMA or HACA response.

The CD70 binding domains of the bispecific antibody constructs that were generated in the context of the present invention were characterized for their epitope specificity, as described in Example 2. The binders were classified into different groups (I, II, III, IIIv, V, VI, VII and VIII – see Table 4), depending on the chimeric CD70 molecule for which a loss of binding was observed in the flow cytometry readout. Hence, according to a preferred embodiment, the first binding domain of the antibody construct of the invention binds to an epitope of CD70 which is comprised within the region denominated E3 (the region as depicted in SEQ ID NO: 745). As described in the following, the binding domain recognizing region E3 may recognize additional CD70 regions.

It is furthermore envisaged that the first binding domain of the antibody construct of the invention binds to an epitope of CD70 which is comprised within a combination of CD70 regions selected from the group consisting of:

- a) regions E2, E3, E4 and E6,
- b) regions E2, E3 and E4,
- c) regions E2, E3 and E6,
- d) regions E2 and E3,
- e) regions E3, E4 and E6,
- f) regions E3 and E4, and
- g) regions E3 and E6.

The epitope recognized by the anti-CD70 binding domain may be linear or conformational. The position of the above described regions E2, E3, E4 and E6 within the human CD70 protein as well as their sequence identifiers are described in Example 1.

In a further preferred embodiment, the first binding domain of the antibody construct of the invention does not bind to an epitope comprised within the region denominated E1. It is additionally or alternatively envisaged that the first binding domain of the antibody construct of the invention does not bind to an epitope comprised within the region denominated E7.

The terms “(specifically) binds to”, “(specifically) recognizes”, “is (specifically) directed to”, and “(specifically) reacts with” mean in accordance with this invention that a binding domain interacts or specifically interacts with a given epitope or a given target site on the target molecules (antigens), here: CD70 and CD3, respectively.

The term “epitope” refers to a site on an antigen to which a binding domain, an antibody or immunoglobulin, or a derivative, fragment or variant of an antibody or an immunoglobulin, specifically binds. An “epitope” is antigenic and thus the term epitope is sometimes also referred to herein as “antigenic structure” or “antigenic determinant”. Thus, the binding domain is an “antigen interaction site”. Said binding/interaction is also understood to define a “specific recognition”.

“Epitopes” can be formed both by contiguous amino acids or non-contiguous amino acids juxtaposed by tertiary folding of a protein. A “linear epitope” is an epitope where an amino acid primary sequence comprises the recognized epitope. A linear epitope typically includes at least 3 or at least 4, and more usually, at least 5 or at least 6 or at least 7, for example, about 8 to about 10 amino acids in a unique sequence.

A “conformational epitope”, in contrast to a linear epitope, is an epitope wherein the primary sequence of the amino acids comprising the epitope is not the sole defining component of the epitope recognized (e.g., an epitope wherein the primary sequence of amino acids is not necessarily recognized by the binding domain). Typically a conformational epitope comprises an increased number of amino acids relative to a linear epitope. With regard to recognition of conformational epitopes, the binding domain recognizes a three-dimensional structure of the antigen, preferably a peptide or protein or fragment thereof (in the context of the present

invention, the antigenic structure for the first binding domain is comprised within the CD70 protein). For example, when a protein molecule folds to form a three-dimensional structure, certain amino acids and/or the polypeptide backbone forming the conformational epitope become juxtaposed enabling the antibody to recognize the epitope. Methods of determining the conformation of epitopes include, but are not limited to, x-ray crystallography, two-dimensional nuclear magnetic resonance (2D-NMR) spectroscopy and site-directed spin labelling and electron paramagnetic resonance (EPR) spectroscopy.

A method for epitope mapping is described in the following: When a region (a contiguous amino acid stretch) in the human CD70 protein is exchanged / replaced with its corresponding region of a non-human and non-primate CD70 antigen (*e.g.*, mouse CD70, but others like chicken, rat, hamster, rabbit etc. might also be conceivable), a decrease in the binding of the binding domain is expected to occur, unless the binding domain is cross-reactive for the non-human, non-primate CD70 used. Said decrease is preferably at least 10%, 20%, 30%, 40%, or 50%; more preferably at least 60%, 70%, or 80%, and most preferably 90%, 95% or even 100% in comparison to the binding to the respective region in the human CD70 protein, whereby binding to the respective region in the human CD70 protein is set to be 100%. It is envisaged that the aforementioned human CD70 / non-human CD70 chimeras are expressed in CHO cells. It is also envisaged that at the C-terminus of the chimeric molecules a v5 tag is fused, *e.g.* via a GGGGS linker. The method is described in more detail in Examples 1 and 2.

In an alternative or additional method for epitope mapping, several truncated versions of the human CD70 extracellular domain can be generated in order to determine a specific region that is recognized by a binding domain. In these truncated versions, the different extracellular CD70 domains / sub-domains or regions are stepwise deleted, starting from the C-terminus. It is envisaged that the truncated CD70 versions are expressed in CHO cells. It is also envisaged that at the C-terminus of the truncated molecules a v5 tag is fused, *e.g.* via a GGGGS linker, which allows verifying their correct expression on the cell surface. A decrease or a loss of binding is expected to occur with those truncated CD70 versions which do not encompass any more the CD70 region that is recognized by the binding domain. The decrease of binding is preferably at least 10%, 20%, 30%, 40%, 50%; more preferably at least 60%, 70%, 80%, and most preferably 90%, 95% or even 100%, whereby binding to the entire human CD70 protein (or its extracellular region or domain) is set to be 100%.

A further method to determine the contribution of a specific residue of a target antigen to the recognition by an antibody construct or binding domain is alanine scanning (see e.g. Morrison KL & Weiss GA. *Cur Opin Chem Biol.* 2001 Jun;5(3):302-7), where each residue to be analyzed is replaced by alanine, e.g. via site-directed mutagenesis. Alanine is used because of its non-bulky, chemically inert, methyl functional group that nevertheless mimics the secondary structure references that many of the other amino acids possess. Sometimes bulky amino acids such as valine or leucine can be used in cases where conservation of the size of mutated residues is desired. Alanine scanning is a mature technology which has been used for a long period of time.

The interaction between the binding domain and the epitope or the region comprising the epitope implies that a binding domain exhibits appreciable affinity for the epitope / the region comprising the epitope on a particular protein or antigen (here: CD70 and CD3, respectively) and, generally, does not exhibit significant reactivity with proteins or antigens other than CD70 or CD3. "Appreciable affinity" includes binding with an affinity of about 10^{-6} M (KD) or stronger. Preferably, binding is considered specific when the binding affinity is about 10^{-12} to 10^{-8} M, 10^{-12} to 10^{-9} M, 10^{-12} to 10^{-10} M, 10^{-11} to 10^{-8} M, preferably of about 10^{-11} to 10^{-9} M. Whether a binding domain specifically reacts with or binds to a target can be tested readily by, *inter alia*, comparing the reaction of said binding domain with a target protein or antigen with the reaction of said binding domain with proteins or antigens other than CD70 or CD3. Preferably, a binding domain of the invention does not essentially or substantially bind to proteins or antigens other than CD70 or CD3 (*i.e.*, the first binding domain is not capable of binding to proteins other than CD70 and the second binding domain is not capable of binding to proteins other than CD3).

The term "does not essentially / substantially bind" or "is not capable of binding" means that a binding domain of the present invention does not bind a protein or antigen other than CD70 or CD3, *i.e.*, does not show reactivity of more than 30%, preferably not more than 20%, more preferably not more than 10%, particularly preferably not more than 9%, 8%, 7%, 6% or 5% with proteins or antigens other than CD70 or CD3, whereby binding to CD70 or CD3, respectively, is set to be 100%.

Specific binding is believed to be effected by specific motifs in the amino acid sequence of the binding domain and the antigen. Thus, binding is achieved as a result of their primary, secondary and/or tertiary structure as well as the result of secondary modifications of said structures. The specific interaction of the antigen-interaction-site with its specific antigen may

result in a simple binding of said site to the antigen. Moreover, the specific interaction of the antigen-interaction-site with its specific antigen may alternatively or additionally result in the initiation of a signal, e.g. due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc.

Preferably, the first binding domain of the bispecific antibody construct of the invention comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3, wherein said CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 are selected from the group consisting of those depicted in:

- | | |
|---------------------------|---------------------------|
| 1) SEQ ID NOs: 1-6; | 26) SEQ: ID NOs: 251-256; |
| 2) SEQ: ID NOs: 11-16; | 27) SEQ: ID NOs: 261-266; |
| 3) SEQ: ID NOs: 21-26; | 28) SEQ: ID NOs: 271-276; |
| 4) SEQ: ID NOs: 31-36; | 29) SEQ: ID NOs: 281-286; |
| 5) SEQ: ID NOs: 41-46; | 30) SEQ: ID NOs: 291-296; |
| 6) SEQ: ID NOs: 51-56; | 31) SEQ: ID NOs: 301-306; |
| 7) SEQ: ID NOs: 61-66; | 32) SEQ: ID NOs: 311-316; |
| 8) SEQ: ID NOs: 71-76; | 33) SEQ: ID NOs: 321-326; |
| 9) SEQ: ID NOs: 81-86; | 34) SEQ: ID NOs: 331-336; |
| 10) SEQ: ID NOs: 91-96; | 35) SEQ: ID NOs: 341-346; |
| 11) SEQ: ID NOs: 101-106; | 36) SEQ: ID NOs: 351-356; |
| 12) SEQ: ID NOs: 111-116; | 37) SEQ: ID NOs: 361-366; |
| 13) SEQ: ID NOs: 121-126; | 38) SEQ: ID NOs: 371-376; |
| 14) SEQ: ID NOs: 131-136; | 39) SEQ: ID NOs: 381-386; |
| 15) SEQ: ID NOs: 141-146; | 40) SEQ: ID NOs: 391-396; |
| 16) SEQ: ID NOs: 151-156; | 41) SEQ: ID NOs: 401-406; |
| 17) SEQ: ID NOs: 161-166; | 42) SEQ: ID NOs: 411-416; |
| 18) SEQ: ID NOs: 171-176; | 43) SEQ: ID NOs: 421-426; |
| 19) SEQ: ID NOs: 181-186; | 44) SEQ: ID NOs: 431-436; |
| 20) SEQ: ID NOs: 191-196; | 45) SEQ: ID NOs: 441-446; |
| 21) SEQ: ID NOs: 201-206; | 46) SEQ: ID NOs: 451-456; |
| 22) SEQ: ID NOs: 211-216; | 47) SEQ: ID NOs: 461-466; |
| 23) SEQ: ID NOs: 221-226; | 48) SEQ: ID NOs: 471-476; |
| 24) SEQ: ID NOs: 231-236; | 49) SEQ: ID NOs: 481-486; |
| 25) SEQ: ID NOs: 241-246; | 50) SEQ: ID NOs: 491-496; |

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|-----------------------------|------------------------------|
| 51) SEQ: ID NOs: 501-506; | 83) SEQ: ID NOs: 1156-1161; |
| 52) SEQ: ID NOs: 511-516; | 84) SEQ: ID NOs: 1170-1175; |
| 53) SEQ: ID NOs: 521-526; | 85) SEQ: ID NOs: 1184-1189; |
| 54) SEQ: ID NOs: 531-536; | 86) SEQ: ID NOs: 1198-1203; |
| 55) SEQ: ID NOs: 541-546; | 87) SEQ: ID NOs: 1212-1217; |
| 56) SEQ: ID NOs: 551-556; | 88) SEQ: ID NOs: 1226-1231; |
| 57) SEQ: ID NOs: 561-566; | 89) SEQ: ID NOs: 1240-1245; |
| 58) SEQ: ID NOs: 571-576; | 90) SEQ: ID NOs: 1254-1259; |
| 59) SEQ: ID NOs: 581-586; | 91) SEQ: ID NOs: 1268-1273; |
| 60) SEQ: ID NOs: 591-596; | 92) SEQ: ID NOs: 1282-1287; |
| 61) SEQ: ID NOs: 601-606; | 93) SEQ: ID NOs: 1296-1301; |
| 62) SEQ: ID NOs: 611-616; | 94) SEQ: ID NOs: 1310-1315; |
| 63) SEQ: ID NOs: 621-626; | 95) SEQ: ID NOs: 1324-1329; |
| 64) SEQ: ID NOs: 631-636; | 96) SEQ: ID NOs: 1338-1343; |
| 65) SEQ: ID NOs: 641-646; | 97) SEQ: ID NOs: 1352-1357; |
| 66) SEQ: ID NOs: 651-656; | 98) SEQ: ID NOs: 1366-1371; |
| 67) SEQ: ID NOs: 661-666; | 99) SEQ: ID NOs: 1380-1385; |
| 68) SEQ: ID NOs: 671-676; | 100) SEQ: ID NOs: 1394-1399; |
| 69) SEQ: ID NOs: 681-686; | 101) SEQ: ID NOs: 1408-1413; |
| 70) SEQ: ID NOs: 691-696; | 102) SEQ: ID NOs: 1422-1427; |
| 71) SEQ: ID NOs: 701-706; | 103) SEQ: ID NOs: 1436-1441; |
| 72) SEQ: ID NOs: 711-716; | 104) SEQ: ID NOs: 1450-1455; |
| 73) SEQ: ID NOs: 721-726; | 105) SEQ: ID NOs: 1464-1469; |
| 74) SEQ: ID NOs: 731-736; | 106) SEQ: ID NOs: 1478-1483; |
| 75) SEQ: ID NOs: 1044-1049; | 107) SEQ: ID NOs: 1492-1497; |
| 76) SEQ: ID NOs: 1058-1063; | 108) SEQ: ID NOs: 1506-1511; |
| 77) SEQ: ID NOs: 1072-1077; | 109) SEQ: ID NOs: 1520-1525; |
| 78) SEQ: ID NOs: 1086-1091; | 110) SEQ: ID NOs: 1534-1539; |
| 79) SEQ: ID NOs: 1100-1005; | 111) SEQ: ID NOs: 1548-1553; |
| 80) SEQ: ID NOs: 1114-1119; | and |
| 81) SEQ: ID NOs: 1128-1133; | 112) SEQ: ID NOs: 1562-1567. |
| 82) SEQ: ID NOs: 1142-1147; | |

Of the above defined antibody constructs, the following were found to have particularly beneficial characteristics, as determined in Examples 3-16: The bispecific antibody constructs comprising

a first binding domain which binds to human CD70 on the surface of a target cell and a second binding domain which binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3, wherein said CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 are selected from the group consisting of those depicted in:

- 1) SEQ: ID NOs: 1044-1049;
- 2) SEQ: ID NOs: 1086-1091;
- 3) SEQ: ID NOs: 1142-1147;
- 4) SEQ: ID NOs: 1170-1175;
- 5) SEQ: ID NOs: 1184-1189;
- 6) SEQ: ID NOs: 1212-1217;
- 7) SEQ: ID NOs: 1226-1231;
- 8) SEQ: ID NOs: 1240-1245;
- 9) SEQ: ID NOs: 1254-1259;
- 10) SEQ: ID NOs: 1268-1273;
- 11) SEQ: ID NOs: 1338-1343;
- 12) SEQ: ID NOs: 1352-1357;
- 13) SEQ: ID NOs: 1366-1371;
- 14) SEQ: ID NOs: 1422-1427; and
- 15) SEQ: ID NOs: 1436-1441.

These constructs are characterized e.g. by a particularly high affinity, high cytotoxic activity (low EC50 values), and beneficial interspecies affinity gap, as well as a high sequence identity of the VH and VL sequences to the human germline, low monomer to dimer conversion, high thermostability, high plasma stability, low turbidity, high protein homogeneity, and a beneficial monomer/dimer potency gap. In this context, it should be noted that these CDR amino acid sequences have a considerably high sequence similarity, which is outlined in the following Tables 1 and 2.

Table 1: VH-CDR sequences of a selection of CD70 binders

	VH-CDR1	VH-CDR2	VH-CDR3	SEQ ID NOs
CD70-13D_CC	SYAMS	VISGSGGRPNYAESVKG	VDYSNYLFFDY	1044-1046
CD70-16D_CC	SYAMS	AISGSGGRTFYAESVEG	HDYSNYPYFDY	1086-1088
CD70-21D_CC	TYAMS	AISGSGGRTFYAESVEG	HDYSNYPYFDY	1142-1144

CD70-24D_CC	SYAMS	AISGSGGSTFYAESVKG	HDYSNYPYFDY	1170-1172
CD70-25D_CC	SYAMS	AISGSGGRTFYAESVEG	HDYSNYPYFDY	1184-1186
CD70_1-G2D_CC	SYAMS	AISGSGGSTFYAESVQG	HDYSNYPYFDY	1212-1214
CD70-27D_CC	TYAMS	AISGSGGGTFYAESVKG	HDYSNYPYFDY	1226-1228
CD70-28D_CC	TYAMS	LISGSGGRTYYAESVKG	HDYSNYPYFDY	1240-1242
CD70-31D_CC	SYAMS	AISGSGGRAQYAESVQG	HDYSNYPYFDY	1254-1256
CD70-32D_CC	SYAMS	AISGSGGRTFYAESVEG	HDYSNYPYFDY	1268-1270
CD70-42D_CC	TYAMS	LISGSGGRTYYAESVKG	HDYSNYPYFDY	1338-1340
CD70-43D_CC	SYAMS	AISGSGGRTFYAESVEG	HDYSNYPYFDY	1352-1354
CD70-48D_CC	SYAMS	VISGSGGITDFAESVKG	HDYSNYFFFDY	1366-1368
CD70-62D_CC	YSMN	YISSSGGYIYYAESVKG	GDYSNYAYFDY	1422-1424
CD70-13D_CC	VYAMS	TISGSGGSTFYAESVKG	HDYSNYAYFDY	1436-1438

Table 2: VL-CDR sequences of a selection of CD70 binders

	VL-CDR1	VL-CDR2	VL-CDR3	SEQ ID NOs
CD70-13D_CC	RAGQSVRSSYL	GASSRAT	QQYGYSPPT	1047-1049
CD70-16D_CC	RASQSIRSSYL	GASSRAT	QQYGDLPFT	1089-1091
CD70-21D_CC	RASQSVRSTYL	GASSRAT	QQYGDLPFT	1145-1147
CD70-24D_CC	RASQSVRSSYL	GASSRAT	QQYGDLPFT	1173-1175
CD70-25D_CC	RASQSVRSNYL	GASSRAT	QQYGDLPFT	1187-1189
CD70_1-G2D_CC	RASQSVRGNYL	GASSRAT	QQYGYSPPT	1215-1217
CD70-27D_CC	RASQSIRSNYL	GASSRAT	QQYGSSPPT	1229-1231
CD70-28D_CC	RASQSVRSNYL	GASNRAT	QQYGISPPT	1243-1245
CD70-31D_CC	RASQSVSSN-LA	GSSSRAT	QQYGSSPPP	1257-1259
CD70-32D_CC	RASQGVRSDYL	GASSRAT	QQYGSTPPT	1271-1273
CD70-42D_CC	RASQGVRSSYL	GASSRAT	QQYGSSPPT	1341-1343
CD70-43D_CC	RASQSVRSNYL	GASSRAT	QQYGSSPPT	1355-1357
CD70-48D_CC	RASQGI-SNYL	AASILQS	QQYFAYPIT	1369-1371
CD70-62D_CC	RASQGI-SNYL	AASTLQS	QQYYSTPLT	1425-1427
CD70-13D_CC	RASQSVRSSYL	GASSRAT	QQYGDLPFT	1439-1441

This remarkable sequence similarity in the context of the common biological / biochemical characteristics of the antibody constructs allows for drafting a consensus sequence for the six VH and VL CDRs. These consensus sequences are identified in the following. Therefore, it is an object of the present invention to provide a bispecific antibody construct comprising a first binding domain which binds to human CD70 on the surface of a target cell and a second binding domain which binds to human CD3 on the surface of a T cell (and in one embodiment at least to macaque CD3), wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3, wherein

- said CDR-H1 has the amino acid sequence $X_1YX_2MX_3$ (SEQ ID NO: 1869), wherein X_1 is S, T or V, X_2 is A or S, and X_3 is S or N;
- said CDR-H2 has the amino acid sequence $X_1ISX_2SGGX_3X_4X_5X_6AESVX_7G$ (SEQ ID NO: 1870), wherein X_1 is A, Y, V, L, or T, X_2 is G or S, X_3 is R, Y, S, G or I, X_4 is T, I, P, or A, X_5 is F, Y, N, Q or D, X_6 is Y or F, and X_7 is E, K or Q;
- said CDR-H3 has the amino acid sequence $X_1DYSNYX_2X_3FDY$ (SEQ ID NO: 1871), wherein X_1 is H, G or V, X_2 is P, A, L or F, and X_3 is Y or F;
- said CDR-L1 has the amino acid sequence $RAX_1QX_2X_3X_4X_5X_6X_7LX_8$ (SEQ ID NO: 1872), wherein X_1 is S or G, X_2 is S or G, X_3 is I or V, X_4 is R, S or no amino acid, X_5 is S or G, X_6 is S, N, T or D, X_7 is Y or no amino acid, and X_8 is A or G;
- said CDR-L2 has the amino acid sequence $X_1X_2SX_3X_4X_5X_6$ (SEQ ID NO: 1873), wherein X_1 is G or A, X_2 is A or S, X_3 is S, T, N or I, X_4 is R or L, X_5 is A or Q, and X_6 is T or S; and
- said CDR-L3 has the amino acid sequence $QQYX_1X_2X_3PX_4X_5$ (SEQ ID NO: 1874), wherein X_1 is G, Y or F, X_2 is D, S, Y, I or A, X_3 is L, T, S or Y, X_4 is F, L, P or I, and X_5 is T or P.

It is furthermore envisaged that:

- said CDR-H1 has the amino acid sequence SYSMN (SEQ ID NO: 1422) or X_1YAMS (SEQ ID NO: 1875), wherein X_1 is S, T or V;
- said CDR-H2 has an amino acid sequence selected from the group consisting of YISSSGGYIYYAESVKG (SEQ ID NO: 1423), VISGSGGITDFAESVKG (SEQ ID NO: 1367) and $X_1ISGSGGX_2X_3X_4YAESVX_5G$ (SEQ ID NO: 1876), wherein X_1 is A, V, L or T, X_2 is R, S, or G, X_3 is T, P or A, X_4 is F, N, Y or Q, and X_5 is E, K, or Q;

- said CDR-H3 has an amino acid sequence selected from the group consisting of GDYSNYAYFDY (SEQ ID NO: 1424), HDYSNYFFFDY (SEQ ID NO: 1368), and X₁DYSNYX₂X₃FDY (SEQ ID NO: 1877), wherein X₁ is H or V, X₂ is P, L or A, and X₃ is Y or F;
- said CDR-L1 has the amino acid sequence RASQGISNYLA (SEQ ID NO: 1425) or RAX₁QX₂X₃X₄X₅X₆YLX₇ (SEQ ID NO: 1878), wherein X₁ is S or G, X₂ is S or G, X₃ is I or V, X₄ is R or S, X₅ is S or G, X₆ is S, T, N or D, and X₇ is A or G;
- said CDR-L2 has the amino acid sequence AASXLQS (SEQ ID NO: 1879), wherein X is T or I, or GX₁SX₂RAT (SEQ ID NO: 1880), wherein X₁ is A or S, and X₂ is S or N; and
- said CDR-L3 has an amino acid sequence selected from the group consisting of QQYYSTPLT (SEQ ID NO: 1427), QQYFAYPIT (SEQ ID NO: 1371) and QQYGX₁X₂PX₃X₄ (SEQ ID NO: 1881), wherein X₁ is D, Y, S or I, X₂ is L, S or T, X₃ is F or P, and X₄ is T or P.

It is furthermore envisaged that:

- said CDR-H1 has the amino acid sequence X₁YAMS (SEQ ID NO: 1875), wherein X₁ is S, T or V;
- said CDR-H2 has the amino acid sequence X₁ISGSGGX₂X₃X₄YAESVX₅G (SEQ ID NO: 1876), wherein X₁ is A, V, L or T, X₂ is R, S, or G, X₃ is T, P or A, X₄ is F, N, Y or Q, and X₅ is E, K, or Q;
- said CDR-H3 has the amino acid sequence X₁DYSNYX₂X₃FDY (SEQ ID NO: 1877), wherein X₁ is H or V, X₂ is P, L or A, and X₃ is Y or F;
- said CDR-L1 has the amino acid sequence RAX₁QX₂X₃X₄X₅X₆YLX₇ (SEQ ID NO: 1878), wherein X₁ is S or G, X₂ is S or G, X₃ is I or V, X₄ is R or S, X₅ is S or G, X₆ is S, T, N or D, and X₇ is A or G;
- said CDR-L2 has the amino acid sequence GX₁SX₂RAT (SEQ ID NO: 1880), wherein X₁ is A or S, and X₂ is S or N; and
- said CDR-L3 has the amino acid sequence QQYGX₁X₂PX₃X₄ (SEQ ID NO: 1881), wherein X₁ is D, Y, S or I, X₂ is L, S or T, X₃ is F or P, and X₄ is T or P.

It is furthermore envisaged that:

- said CDR-H1 has an amino acid sequence selected from the group consisting of SYAMS (SEQ ID NO: 1044), TYAMS (SEQ ID NO: 1142), VYAMS (SEQ ID NO: 1436) and SYSMN (SEQ ID NO: 1422);

- said CDR-H2 has an amino acid sequence selected from the group consisting of AISGSGGRTFYAESVEG (SEQ ID NO: 1087), VISGSGGRPNYAESVKG (SEQ ID NO: 1045), AISGSGGSTFYAESVKG (SEQ ID NO: 1171), AISGSGGSTFYAESVQG (SEQ ID NO: 1213), AISGSGGGTFYAESVKG (SEQ ID NO: 1227), LISGSGGRTYYAESVKG (SEQ ID NO: 1241), AISGSGGRAQYAESVQG (SEQ ID NO: 1255), TISGSGGSTFYAESVKG (SEQ ID NO: 1437), YISSSGGYIYYAESVKG (SEQ ID NO: 1423), and VISGSGGITDFAESVKG (SEQ ID NO: 1367);
- said CDR-H3 has an amino acid sequence selected from the group consisting of HDYSNYPYFDY (SEQ ID NO: 1088), VDYSNYLFFDY (SEQ ID NO: 1046), HDYSNYAYFDY (SEQ ID NO: 1438), GDYSNYAYFDY (SEQ ID NO: 1424), and HDYSNYFFFDY (SEQ ID NO: 1368);
- said CDR-L1 has an amino acid sequence selected from the group consisting of RASQSIRSSYLA (SEQ ID NO: 1089), RASQSVRSTYLA (SEQ ID NO: 1145), RAGQSVRSSYLG (SEQ ID NO: 1047), RASQSVRSSYLA (SEQ ID NO: 1173), RASQSVRSNYLA (SEQ ID NO: 1187), RASQSVRGNYLA (SEQ ID NO: 1215), RASQSIRSNYLA (SEQ ID NO: 1229), RASQSVSSNLA (SEQ ID NO: 1257), RASQGVRSDYLA (SEQ ID NO: 1271), RASQGVRSYLA (SEQ ID NO: 1341), and RASQGISNYLA (SEQ ID NO: 1369);
- said CDR-L2 has an amino acid sequence selected from the group consisting of GASSRAT (SEQ ID NO: 1048), GASNRAT (SEQ ID NO: 1244), GSSSRAT (SEQ ID NO: 1258), AASTLQS (SEQ ID NO: 1426) and AASILQS (SEQ ID NO: 1370); and
- said CDR-L3 has an amino acid sequence selected from the group consisting of QQYGDLPFT (SEQ ID NO: 1091); QQYGYSPPT (SEQ ID NO: 1049), QQYGYSPFT (SEQ ID NO: 1217), QQYGSSPFT (SEQ ID NO: 1231), QQYGISPPT (SEQ ID NO: 1245), QQYGSSPPP (SEQ ID NO: 1259), QQYGSTPPT (SEQ ID NO: 1273), QQYGSSPPT (SEQ ID NO: 1343), QQYYSTPLT (SEQ ID NO: 1427), and QQYFAYPIT (SEQ ID NO: 1371).

The term “variable” refers to the portions of the antibody or immunoglobulin domains that exhibit variability in their sequence and that are involved in determining the specificity and binding affinity of a particular antibody (i.e., the “variable domain(s)”). The pairing of a variable heavy chain (VH) and a variable light chain (VL) together forms a single antigen-binding site.

Variability is not evenly distributed throughout the variable domains of antibodies; it is concentrated in sub-domains of each of the heavy and light chain variable regions. These sub-

domains are called "hypervariable regions" or "complementarity determining regions" (CDRs). The more conserved (i.e., non-hypervariable) portions of the variable domains are called the "framework" regions (FRM or FR) and provide a scaffold for the six CDRs in three dimensional space to form an antigen-binding surface. The variable domains of naturally occurring heavy and light chains each comprise four FRM regions (FR1, FR2, FR3, and FR4), largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β -sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRM and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site (see Kabat *et al.*, *loc. cit.*).

The terms "CDR", and its plural "CDRs", refer to the complementarity determining region of which three make up the binding character of a light chain variable region (CDR-L1, CDR-L2 and CDR-L3) and three make up the binding character of a heavy chain variable region (CDR-H1, CDR-H2 and CDR-H3). CDRs contain most of the residues responsible for specific interactions of the antibody with the antigen and hence contribute to the functional activity of an antibody molecule: they are the main determinants of antigen specificity.

The exact definitional CDR boundaries and lengths are subject to different classification and numbering systems. CDRs may therefore be referred to by Kabat, Chothia, contact or any other boundary definitions, including the numbering system described herein. Despite differing boundaries, each of these systems has some degree of overlap in what constitutes the so called "hypervariable regions" within the variable sequences. CDR definitions according to these systems may therefore differ in length and boundary areas with respect to the adjacent framework region. See for example Kabat (an approach based on cross-species sequence variability), Chothia (an approach based on crystallographic studies of antigen-antibody complexes), and/or MacCallum (Kabat *et al.*, *loc. cit.*; Chothia *et al.*, J. Mol. Biol, 1987, 196: 901-917; and MacCallum *et al.*, J. Mol. Biol, 1996, 262: 732). Still another standard for characterizing the antigen binding site is the AbM definition used by Oxford Molecular's AbM antibody modeling software. See, e.g., Protein Sequence and Structure Analysis of Antibody Variable Domains. In: Antibody Engineering Lab Manual (Ed.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg). To the extent that two residue identification techniques define regions of overlapping, but not identical regions, they can be combined to define a hybrid CDR. However, the numbering in accordance with the so-called Kabat system is preferred.

Typically, CDRs form a loop structure that can be classified as a canonical structure. The term “canonical structure” refers to the main chain conformation that is adopted by the antigen binding (CDR) loops. From comparative structural studies, it has been found that five of the six antigen binding loops have only a limited repertoire of available conformations. Each canonical structure can be characterized by the torsion angles of the polypeptide backbone. Correspondent loops between antibodies may, therefore, have very similar three dimensional structures, despite high amino acid sequence variability in most parts of the loops (Chothia and Lesk, J. Mol. Biol., 1987, 196: 901; Chothia *et al.*, Nature, 1989, 342: 877; Martin and Thornton, J. Mol. Biol, 1996, 263: 800). Furthermore, there is a relationship between the adopted loop structure and the amino acid sequences surrounding it. The conformation of a particular canonical class is determined by the length of the loop and the amino acid residues residing at key positions within the loop, as well as within the conserved framework (*i.e.*, outside of the loop). Assignment to a particular canonical class can therefore be made based on the presence of these key amino acid residues.

The term “canonical structure” may also include considerations as to the linear sequence of the antibody, for example, as catalogued by Kabat (Kabat *et al.*, loc. cit.). The Kabat numbering scheme (system) is a widely adopted standard for numbering the amino acid residues of an antibody variable domain in a consistent manner and is the preferred scheme applied in the present invention as also mentioned elsewhere herein. Additional structural considerations can also be used to determine the canonical structure of an antibody. For example, those differences not fully reflected by Kabat numbering can be described by the numbering system of Chothia *et al.* and/or revealed by other techniques, for example, crystallography and two- or three-dimensional computational modeling. Accordingly, a given antibody sequence may be placed into a canonical class which allows for, among other things, identifying appropriate chassis sequences (*e.g.*, based on a desire to include a variety of canonical structures in a library). Kabat numbering of antibody amino acid sequences and structural considerations as described by Chothia *et al.*, loc. cit. and their implications for construing canonical aspects of antibody structure, are described in the literature. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known in the art. For a review of the antibody structure, see Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, eds. Harlow *et al.*, 1988.

The CDR3 of the light chain and, particularly, the CDR3 of the heavy chain may constitute the most important determinants in antigen binding within the light and heavy chain variable

regions. In some antibody constructs, the heavy chain CDR3 appears to constitute the major area of contact between the antigen and the antibody. *In vitro* selection schemes in which CDR3 alone is varied can be used to vary the binding properties of an antibody or determine which residues contribute to the binding of an antigen. Hence, CDR3 is typically the greatest source of molecular diversity within the antibody-binding site. H3, for example, can be as short as two amino acid residues or greater than 26 amino acids.

In a classical full-length antibody or immunoglobulin, each light (L) chain is linked to a heavy (H) chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. The CH domain most proximal to VH is usually designated as CH1. The constant ("C") domains are not directly involved in antigen binding, but exhibit various effector functions, such as antibody-dependent, cell-mediated cytotoxicity and complement activation. The Fc region of an antibody is comprised within the heavy chain constant domains and is for example able to interact with cell surface located Fc receptors.

The sequence of antibody genes after assembly and somatic mutation is highly varied, and these varied genes are estimated to encode 10^{10} different antibody molecules (Immunoglobulin Genes, 2nd ed., eds. Jonio et al., Academic Press, San Diego, CA, 1995). Accordingly, the immune system provides a repertoire of immunoglobulins. The term "repertoire" refers to at least one nucleotide sequence derived wholly or partially from at least one sequence encoding at least one immunoglobulin. The sequence(s) may be generated by rearrangement *in vivo* of the V, D, and J segments of heavy chains, and the V and J segments of light chains. Alternatively, the sequence(s) can be generated from a cell in response to which rearrangement occurs, e.g., *in vitro* stimulation. Alternatively, part or all of the sequence(s) may be obtained by DNA splicing, nucleotide synthesis, mutagenesis, and other methods, see, e.g., U.S. Patent 5,565,332. A repertoire may include only one sequence or may include a plurality of sequences, including ones in a genetically diverse collection.

A preferred antibody construct according to the invention can also be defined as a bispecific antibody construct comprising a first (preferably human) binding domain which binds to human CD70 on the surface of a target cell and a second binding domain which binds to human CD3 on the surface of a T cell, wherein the first binding domain binds to the same epitope on human CD70 as an antibody selected from the group consisting of CD70-1 to CD70-74 and those as depicted in items 75 to 112 below, *i.e.*, an antibody comprising a VH region comprising CDR-

H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3, wherein said CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 are selected from the group consisting of those depicted in:

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|---------------------------|---------------------------|
| 1) SEQ ID NOs: 1-6; | 32) SEQ: ID NOs: 311-316; |
| 2) SEQ: ID NOs: 11-16; | 33) SEQ: ID NOs: 321-326; |
| 3) SEQ: ID NOs: 21-26; | 34) SEQ: ID NOs: 331-336; |
| 4) SEQ: ID NOs: 31-36; | 35) SEQ: ID NOs: 341-346; |
| 5) SEQ: ID NOs: 41-46; | 36) SEQ: ID NOs: 351-356; |
| 6) SEQ: ID NOs: 51-56; | 37) SEQ: ID NOs: 361-366; |
| 7) SEQ: ID NOs: 61-66; | 38) SEQ: ID NOs: 371-376; |
| 8) SEQ: ID NOs: 71-76; | 39) SEQ: ID NOs: 381-386; |
| 9) SEQ: ID NOs: 81-86; | 40) SEQ: ID NOs: 391-396; |
| 10) SEQ: ID NOs: 91-96; | 41) SEQ: ID NOs: 401-406; |
| 11) SEQ: ID NOs: 101-106; | 42) SEQ: ID NOs: 411-416; |
| 12) SEQ: ID NOs: 111-116; | 43) SEQ: ID NOs: 421-426; |
| 13) SEQ: ID NOs: 121-126; | 44) SEQ: ID NOs: 431-436; |
| 14) SEQ: ID NOs: 131-136; | 45) SEQ: ID NOs: 441-446; |
| 15) SEQ: ID NOs: 141-146; | 46) SEQ: ID NOs: 451-456; |
| 16) SEQ: ID NOs: 151-156; | 47) SEQ: ID NOs: 461-466; |
| 17) SEQ: ID NOs: 161-166; | 48) SEQ: ID NOs: 471-476; |
| 18) SEQ: ID NOs: 171-176; | 49) SEQ: ID NOs: 481-486; |
| 19) SEQ: ID NOs: 181-186; | 50) SEQ: ID NOs: 491-496; |
| 20) SEQ: ID NOs: 191-196; | 51) SEQ: ID NOs: 501-506; |
| 21) SEQ: ID NOs: 201-206; | 52) SEQ: ID NOs: 511-516; |
| 22) SEQ: ID NOs: 211-216; | 53) SEQ: ID NOs: 521-526; |
| 23) SEQ: ID NOs: 221-226; | 54) SEQ: ID NOs: 531-536; |
| 24) SEQ: ID NOs: 231-236; | 55) SEQ: ID NOs: 541-546; |
| 25) SEQ: ID NOs: 241-246; | 56) SEQ: ID NOs: 551-556; |
| 26) SEQ: ID NOs: 251-256; | 57) SEQ: ID NOs: 561-566; |
| 27) SEQ: ID NOs: 261-266; | 58) SEQ: ID NOs: 571-576; |
| 28) SEQ: ID NOs: 271-276; | 59) SEQ: ID NOs: 581-586; |
| 29) SEQ: ID NOs: 281-286; | 60) SEQ: ID NOs: 591-596; |
| 30) SEQ: ID NOs: 291-296; | 61) SEQ: ID NOs: 601-606; |
| 31) SEQ: ID NOs: 301-306; | 62) SEQ: ID NOs: 611-616; |

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|-----------------------------|------------------------------|
| 63) SEQ: ID NOs: 621-626; | 89) SEQ: ID NOs: 1240-1245; |
| 64) SEQ: ID NOs: 631-636; | 90) SEQ: ID NOs: 1254-1259; |
| 65) SEQ: ID NOs: 641-646; | 91) SEQ: ID NOs: 1268-1273; |
| 66) SEQ: ID NOs: 651-656; | 92) SEQ: ID NOs: 1282-1287; |
| 67) SEQ: ID NOs: 661-666; | 93) SEQ: ID NOs: 1296-1301; |
| 68) SEQ: ID NOs: 671-676; | 94) SEQ: ID NOs: 1310-1315; |
| 69) SEQ: ID NOs: 681-686; | 95) SEQ: ID NOs: 1324-1329; |
| 70) SEQ: ID NOs: 691-696; | 96) SEQ: ID NOs: 1338-1343; |
| 71) SEQ: ID NOs: 701-706; | 97) SEQ: ID NOs: 1352-1357; |
| 72) SEQ: ID NOs: 711-716; | 98) SEQ: ID NOs: 1366-1371; |
| 73) SEQ: ID NOs: 721-726; | 99) SEQ: ID NOs: 1380-1385; |
| 74) SEQ: ID NOs: 731-736; | 100) SEQ: ID NOs: 1394-1399; |
| 75) SEQ: ID NOs: 1044-1049; | 101) SEQ: ID NOs: 1408-1413; |
| 76) SEQ: ID NOs: 1058-1063; | 102) SEQ: ID NOs: 1422-1427; |
| 77) SEQ: ID NOs: 1072-1077; | 103) SEQ: ID NOs: 1436-1441; |
| 78) SEQ: ID NOs: 1086-1091; | 104) SEQ: ID NOs: 1450-1455; |
| 79) SEQ: ID NOs: 1100-1005; | 105) SEQ: ID NOs: 1464-1469; |
| 80) SEQ: ID NOs: 1114-1119; | 106) SEQ: ID NOs: 1478-1483; |
| 81) SEQ: ID NOs: 1128-1133; | 107) SEQ: ID NOs: 1492-1497; |
| 82) SEQ: ID NOs: 1142-1147; | 108) SEQ: ID NOs: 1506-1511; |
| 83) SEQ: ID NOs: 1156-1161; | 109) SEQ: ID NOs: 1520-1525; |
| 84) SEQ: ID NOs: 1170-1175; | 110) SEQ: ID NOs: 1534-1539; |
| 85) SEQ: ID NOs: 1184-1189; | 111) SEQ: ID NOs: 1548-1553; |
| 86) SEQ: ID NOs: 1198-1203; | and |
| 87) SEQ: ID NOs: 1212-1217; | 112) SEQ: ID NOs: 1562-1567. |
| 88) SEQ: ID NOs: 1226-1231; | |

Whether or not an antibody construct binds to the same epitope of CD70 as another given antibody construct can be measured e.g. by epitope mapping with chimeric or truncated target molecules, e.g. as described herein above and in Example 2.

A preferred antibody construct according to the invention can also be defined as a bispecific antibody construct comprising a first (preferably human) binding domain which binds to human CD70 on the surface of a target cell and a second binding domain which binds to human CD3 on the surface of a T cell, wherein the first binding domain competes for binding with an

antibody selected from the group consisting of CD70-1 to CD70-74 and those as depicted in items 75 to 112 above, *i.e.*, an antibody comprising a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of those described in items 1) to 112) above.

Whether or not an antibody construct competes for binding with another given antibody construct can be measured in a competition assay such as a competitive ELISA or a cell-based competition assay. Avidin-coupled microparticles (beads) can also be used. Similar to an avidin-coated ELISA plate, when reacted with a biotinylated protein, each of these beads can be used as a substrate on which an assay can be performed. Antigen is coated onto a bead and then precoated with the first antibody. The second antibody is added and any additional binding is determined. Read-out occurs via flow cytometry. See Figure 2.

In one embodiment, the first binding domain of the antibody construct of the invention comprises a VH region selected from the group consisting of those depicted in SEQ ID NO: 7, SEQ ID NO: 17, SEQ ID NO: 27, SEQ ID NO: 37, SEQ ID NO: 47, SEQ ID NO: 57, SEQ ID NO: 67, SEQ ID NO: 77, SEQ ID NO: 87, SEQ ID NO: 97, SEQ ID NO: 107, SEQ ID NO: 117, SEQ ID NO: 127, SEQ ID NO: 137, SEQ ID NO: 147, SEQ ID NO: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547, SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737, SEQ ID NO: 920, SEQ ID NO: 924, SEQ ID NO: 928, SEQ ID NO: 932, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 944, SEQ ID NO: 948, SEQ ID NO: 952, SEQ ID NO: 956, SEQ ID NO: 960, SEQ ID NO: 964, SEQ ID NO: 968, SEQ ID NO: 972, SEQ ID NO: 976, SEQ ID NO: 980, SEQ ID NO: 984, SEQ ID NO: 988, SEQ ID NO: 992, SEQ ID NO: 996, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1008, SEQ ID NO: 1012, SEQ ID NO: 1016, SEQ ID NO: 1020, SEQ ID NO: 1024, SEQ ID NO: 1028,

SEQ ID NO: 1032, SEQ ID NO: 1036, SEQ ID NO: 1040, SEQ ID NO: 1050, SEQ ID NO: 1054, SEQ ID NO: 1064, SEQ ID NO: 1068, SEQ ID NO: 1078, SEQ ID NO: 1082, SEQ ID NO: 1092, SEQ ID NO: 1096, SEQ ID NO: 1106, SEQ ID NO: 1110, SEQ ID NO: 1120, SEQ ID NO: 1124, SEQ ID NO: 1134, SEQ ID NO: 1138, SEQ ID NO: 1148, SEQ ID NO: 1152, SEQ ID NO: 1162, SEQ ID NO: 1166, SEQ ID NO: 1176, SEQ ID NO: 1180, SEQ ID NO: 1190, SEQ ID NO: 1194, SEQ ID NO: 1204, SEQ ID NO: 1208, SEQ ID NO: 1218, SEQ ID NO: 1222, SEQ ID NO: 1232, SEQ ID NO: 1236, SEQ ID NO: 1246, SEQ ID NO: 1250, SEQ ID NO: 1260, SEQ ID NO: 1264, SEQ ID NO: 1274, SEQ ID NO: 1278, SEQ ID NO: 1288, SEQ ID NO: 1292, SEQ ID NO: 1302, SEQ ID NO: 1306, SEQ ID NO: 1316, SEQ ID NO: 1320, SEQ ID NO: 1330, SEQ ID NO: 1334, SEQ ID NO: 1344, SEQ ID NO: 1348, SEQ ID NO: 1358, SEQ ID NO: 1362, SEQ ID NO: 1372, SEQ ID NO: 1376, SEQ ID NO: 1386, SEQ ID NO: 1390, SEQ ID NO: 1400, SEQ ID NO: 1404, SEQ ID NO: 1414, SEQ ID NO: 1418, SEQ ID NO: 1428, SEQ ID NO: 1432, SEQ ID NO: 1442, SEQ ID NO: 1446, SEQ ID NO: 1456, SEQ ID NO: 1460, SEQ ID NO: 1470, SEQ ID NO: 1474, SEQ ID NO: 1484, SEQ ID NO: 1488, SEQ ID NO: 1498, SEQ ID NO: 1502, SEQ ID NO: 1512, SEQ ID NO: 1516, SEQ ID NO: 1526, SEQ ID NO: 1530, SEQ ID NO: 1540, SEQ ID NO: 1544, SEQ ID NO: 1554, SEQ ID NO: 1558, SEQ ID NO: 1568, and SEQ ID NO: 1572.

Preferred is when the the first binding domain of the antibody construct of the invention comprises a VH region selected from the group consisting of those depicted in SEQ ID NO: 1050, SEQ ID NO: 1092, SEQ ID NO: 1148, SEQ ID NO: 1176, SEQ ID NO: 1190, SEQ ID NO: 1218, SEQ ID NO: 1232, SEQ ID NO: 1246, SEQ ID NO: 1260, SEQ ID NO: 1274, SEQ ID NO: 1344, SEQ ID NO: 1358, SEQ ID NO: 1372, SEQ ID NO: 1428, and SEQ ID NO: 1442.

In a further embodiment, the first binding domain of the antibody construct of the invention comprises a VL region selected from the group consisting of those depicted in SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 28, SEQ ID NO: 38, SEQ ID NO: 48, SEQ ID NO: 58, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 98, SEQ ID NO: 108, SEQ ID NO: 118, SEQ ID NO: 128, SEQ ID NO: 138, SEQ ID NO: 148, SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508, SEQ ID NO: 518,

SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558, SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 921, SEQ ID NO: 925, SEQ ID NO: 929, SEQ ID NO: 933, SEQ ID NO: 937, SEQ ID NO: 941, SEQ ID NO: 945, SEQ ID NO: 949, SEQ ID NO: 953, SEQ ID NO: 957, SEQ ID NO: 961, SEQ ID NO: 965, SEQ ID NO: 969, SEQ ID NO: 973, SEQ ID NO: 977, SEQ ID NO: 981, SEQ ID NO: 985, SEQ ID NO: 989, SEQ ID NO: 993, SEQ ID NO: 997, SEQ ID NO: 1001, SEQ ID NO: 1005, SEQ ID NO: 1009, SEQ ID NO: 1013, SEQ ID NO: 1017, SEQ ID NO: 1021, SEQ ID NO: 1025, SEQ ID NO: 1029, SEQ ID NO: 1033, SEQ ID NO: 1037, SEQ ID NO: 1041, SEQ ID NO: 1051, SEQ ID NO: 1055, SEQ ID NO: 1065, SEQ ID NO: 1069, SEQ ID NO: 1079, SEQ ID NO: 1083, SEQ ID NO: 1093, SEQ ID NO: 1097, SEQ ID NO: 1107, SEQ ID NO: 1111, SEQ ID NO: 1121, SEQ ID NO: 1125, SEQ ID NO: 1135, SEQ ID NO: 1139, SEQ ID NO: 1149, SEQ ID NO: 1153, SEQ ID NO: 1163, SEQ ID NO: 1167, SEQ ID NO: 1177, SEQ ID NO: 1181, SEQ ID NO: 1191, SEQ ID NO: 1195, SEQ ID NO: 1205, SEQ ID NO: 1209, SEQ ID NO: 1219, SEQ ID NO: 1223, SEQ ID NO: 1233, SEQ ID NO: 1237, SEQ ID NO: 1247, SEQ ID NO: 1251, SEQ ID NO: 1261, SEQ ID NO: 1265, SEQ ID NO: 1275, SEQ ID NO: 1279, SEQ ID NO: 1289, SEQ ID NO: 1293, SEQ ID NO: 1303, SEQ ID NO: 1307, SEQ ID NO: 1317, SEQ ID NO: 1321, SEQ ID NO: 1331, SEQ ID NO: 1335, SEQ ID NO: 1345, SEQ ID NO: 1349, SEQ ID NO: 1359, SEQ ID NO: 1363, SEQ ID NO: 1373, SEQ ID NO: 1377, SEQ ID NO: 1387, SEQ ID NO: 1391, SEQ ID NO: 1401, SEQ ID NO: 1405, SEQ ID NO: 1415, SEQ ID NO: 1419, SEQ ID NO: 1429, SEQ ID NO: 1433, SEQ ID NO: 1443, SEQ ID NO: 1447, SEQ ID NO: 1457, SEQ ID NO: 1461, SEQ ID NO: 1471, SEQ ID NO: 1475, SEQ ID NO: 1485, SEQ ID NO: 1489, SEQ ID NO: 1499, SEQ ID NO: 1503, SEQ ID NO: 1513, SEQ ID NO: 1517, SEQ ID NO: 1527, SEQ ID NO: 1531, SEQ ID NO: 1541, SEQ ID NO: 1545, SEQ ID NO: 1555, SEQ ID NO: 1559, SEQ ID NO: 1569, and SEQ ID NO: 1573.

Preferred is when the the first binding domain of the antibody construct of the invention comprises a VL region selected from the group consisting of those depicted in SEQ ID NO: 1051, SEQ ID NO: 1093, SEQ ID NO: 1149, SEQ ID NO: 1177, SEQ ID NO: 1191, SEQ ID NO: 1219, SEQ ID NO: 1233, SEQ ID NO: 1247, SEQ ID NO: 1261, SEQ ID NO: 1275, SEQ ID NO: 1345, SEQ ID NO: 1359, SEQ ID NO: 1373, SEQ ID NO: 1429, and SEQ ID NO: 1443.

In another embodiment, the first binding domain of the antibody construct of the invention comprises a VH region and a VL region selected from the group consisting of pairs of a VH

region and a VL region as depicted in SEQ ID NOs: 7+8, SEQ ID NOs: 17+18, SEQ ID NOs: 27+28, SEQ ID NOs: 37+38, SEQ ID NOs: 47+48, SEQ ID NOs: 57+58, SEQ ID NOs: 67+68, SEQ ID NOs: 77+78, SEQ ID NOs: 87+88, SEQ ID NOs: 97+98, SEQ ID NOs: 107+108, SEQ ID NOs: 117+118, SEQ ID NOs: 127+128, SEQ ID NOs: 137+138, SEQ ID NOs: 147+148, SEQ ID NOs: 157+158, SEQ ID NOs: 167+168, SEQ ID NOs: 177+178, SEQ ID NOs: 187+188, SEQ ID NOs: 197+198, SEQ ID NOs: 207+208, SEQ ID NOs: 217+218, SEQ ID NOs: 227+228, SEQ ID NOs: 237+238, SEQ ID NOs: 247+248, SEQ ID NOs: 257+258, SEQ ID NOs: 267+268, SEQ ID NOs: 277+278, SEQ ID NOs: 287+288, SEQ ID NOs: 297+298, SEQ ID NOs: 307+308, SEQ ID NOs: 317+318, SEQ ID NOs: 327+328, SEQ ID NOs: 337+338, SEQ ID NOs: 347+348, SEQ ID NOs: 357+358, SEQ ID NOs: 367+368, SEQ ID NOs: 377+378, SEQ ID NOs: 387+388, SEQ ID NOs: 397+398, SEQ ID NOs: 407+408, SEQ ID NOs: 417+418, SEQ ID NOs: 427+428, SEQ ID NOs: 437+438, SEQ ID NOs: 447+448, SEQ ID NOs: 457+458, SEQ ID NOs: 467+468, SEQ ID NOs: 477+478, SEQ ID NOs: 487+488, SEQ ID NOs: 497+498, SEQ ID NOs: 507+508, SEQ ID NOs: 517+518, SEQ ID NOs: 527+528, SEQ ID NOs: 537+538, SEQ ID NOs: 547+548, SEQ ID NOs: 557+558, SEQ ID NOs: 567+568, SEQ ID NOs: 577+578, SEQ ID NOs: 587+588, SEQ ID NOs: 597+598, SEQ ID NOs: 607+608, SEQ ID NOs: 617+618, SEQ ID NOs: 627+628, SEQ ID NOs: 637+638, SEQ ID NOs: 647+648, SEQ ID NOs: 657+658, SEQ ID NOs: 667+668, SEQ ID NOs: 677+678, SEQ ID NOs: 687+688, SEQ ID NOs: 697+698, SEQ ID NOs: 707+708, SEQ ID NOs: 717+718, SEQ ID NOs: 727+728, SEQ ID NOs: 737+738, SEQ ID NOs: 920+921, SEQ ID NOs: 924+925, SEQ ID NOs: 928+929, SEQ ID NOs: 932+933, SEQ ID NOs: 936+937, SEQ ID NOs: 940+941, SEQ ID NOs: 944+945, SEQ ID NOs: 948+949, SEQ ID NOs: 952+953, SEQ ID NOs: 956+957, SEQ ID NOs: 960+961, SEQ ID NOs: 964+965, SEQ ID NOs: 968+969, SEQ ID NOs: 972+973, SEQ ID NOs: 976+977, SEQ ID NOs: 980+981, SEQ ID NOs: 984+985, SEQ ID NOs: 988+989, SEQ ID NOs: 992+993, SEQ ID NOs: 996+997, SEQ ID NOs: 1000+1001, SEQ ID NOs: 1004+1005, SEQ ID NOs: 1008+1009, SEQ ID NOs: 1012+1013, SEQ ID NOs: 1016+1017, SEQ ID NOs: 1020+1021, SEQ ID NOs: 1024+1025, SEQ ID NOs: 1028+1029, SEQ ID NOs: 1032+1033, SEQ ID NOs: 1036+1037, SEQ ID NOs: 1040+1041, SEQ ID NOs: 1050+1051, SEQ ID NOs: 1054+1055, SEQ ID NOs: 1064+1065, SEQ ID NOs: 1068+1069, SEQ ID NOs: 1078+1079, SEQ ID NOs: 1082+1083, SEQ ID NOs: 1092+1093, SEQ ID NOs: 1096+1097, SEQ ID NOs: 1106+1107, SEQ ID NOs: 1110+1111, SEQ ID NOs: 1120+1121, SEQ ID NOs: 1124+1125, SEQ ID NOs: 1134+1135, SEQ ID NOs: 1138+1139, SEQ ID NOs: 1148+1149, SEQ ID NOs: 1152+1153, SEQ ID

NOs: 1162+1163,	SEQ ID	NOs: 1166+1167,	SEQ ID	NOs: 1176+1177,	SEQ ID
NOs: 1180+1181,	SEQ ID	NOs: 1190+1191,	SEQ ID	NOs: 1194+1195,	SEQ ID
NOs: 1204+1205,	SEQ ID	NOs: 1208+1209,	SEQ ID	NOs: 1218+1219,	SEQ ID
NOs: 1222+1223,	SEQ ID	NOs: 1232+1233,	SEQ ID	NOs: 1236+1237,	SEQ ID
NOs: 1246+1247,	SEQ ID	NOs: 1250+1251,	SEQ ID	NOs: 1260+1261,	SEQ ID
NOs: 1264+1265,	SEQ ID	NOs: 1274+1275,	SEQ ID	NOs: 1278+1279,	SEQ ID
NOs: 1288+1289,	SEQ ID	NOs: 1292+1293,	SEQ ID	NOs: 1302+1303,	SEQ ID
NOs: 1306+1307,	SEQ ID	NOs: 1316+1317,	SEQ ID	NOs: 1320+1321,	SEQ ID
NOs: 1330+1331,	SEQ ID	NOs: 1334+1335,	SEQ ID	NOs: 1344+1345,	SEQ ID
NOs: 1348+1349,	SEQ ID	NOs: 1358+1359,	SEQ ID	NOs: 1362+1363,	SEQ ID
NOs: 1372+1373,	SEQ ID	NOs: 1376+1377,	SEQ ID	NOs: 1386+1387,	SEQ ID
NOs: 1390+1391,	SEQ ID	NOs: 1400+1401,	SEQ ID	NOs: 1404+1405,	SEQ ID
NOs: 1414+1415,	SEQ ID	NOs: 1418+1419,	SEQ ID	NOs: 1428+1429,	SEQ ID
NOs: 1432+1433,	SEQ ID	NOs: 1442+1443,	SEQ ID	NOs: 1446+1447,	SEQ ID
NOs: 1456+1457,	SEQ ID	NOs: 1460+1461,	SEQ ID	NOs: 1470+1471,	SEQ ID
NOs: 1474+1475,	SEQ ID	NOs: 1484+1485,	SEQ ID	NOs: 1488+1489,	SEQ ID
NOs: 1498+1499,	SEQ ID	NOs: 1502+1503,	SEQ ID	NOs: 1512+1513,	SEQ ID
NOs: 1516+1517,	SEQ ID	NOs: 1526+1527,	SEQ ID	NOs: 1530+1531,	SEQ ID
NOs: 1540+1541,	SEQ ID	NOs: 1544+1545,	SEQ ID	NOs: 1554+1555,	SEQ ID

NOs: 1558+1559, SEQ ID NOs: 1568+1569, and SEQ ID NOs: 1572+1573.

Preferred is when the first binding domain of the antibody construct of the invention comprises a VH region and a VL region selected from the group consisting of pairs of a VH region and a VL region as depicted in SEQ ID NOs: 1050+1051, SEQ ID NOs: 1092+1093, SEQ ID NOs: 1148+1149, SEQ ID NOs: 1176+1177, SEQ ID NOs: 1190+1191, SEQ ID NOs: 1218+1219, SEQ ID NOs: 1232+1233, SEQ ID NOs: 1246+1247, SEQ ID NOs: 1260+1261, SEQ ID NOs: 1274+1275, SEQ ID NOs: 1344+1345, SEQ ID NOs: 1358+1359, NOs: 1372+1373, SEQ ID NOs: 1428+1429, and SEQ ID NOs: 1442+1443.

In yet a further embodiment, the first binding domain of the antibody construct of the invention comprises a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 89, SEQ ID NO: 99, SEQ ID NO: 109, SEQ ID NO: 119, SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219,

SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 930, SEQ ID NO: 934, SEQ ID NO: 938, SEQ ID NO: 942, SEQ ID NO: 946, SEQ ID NO: 950, SEQ ID NO: 954, SEQ ID NO: 958, SEQ ID NO: 962, SEQ ID NO: 966, SEQ ID NO: 970, SEQ ID NO: 974, SEQ ID NO: 978, SEQ ID NO: 982, SEQ ID NO: 986, SEQ ID NO: 990, SEQ ID NO: 994, SEQ ID NO: 998, SEQ ID NO: 1002, SEQ ID NO: 1006, SEQ ID NO: 1010, SEQ ID NO: 1014, SEQ ID NO: 1018, SEQ ID NO: 1022, SEQ ID NO: 1026, SEQ ID NO: 1030, SEQ ID NO: 1034, SEQ ID NO: 1038, SEQ ID NO: 1042, SEQ ID NO: 1052, SEQ ID NO: 1056, SEQ ID NO: 1066, SEQ ID NO: 1070, SEQ ID NO: 1080, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1098, SEQ ID NO: 1108, SEQ ID NO: 1112, SEQ ID NO: 1122, SEQ ID NO: 1126, SEQ ID NO: 1136, SEQ ID NO: 1140, SEQ ID NO: 1150, SEQ ID NO: 1154, SEQ ID NO: 1164, SEQ ID NO: 1168, SEQ ID NO: 1178, SEQ ID NO: 1182, SEQ ID NO: 1192, SEQ ID NO: 1196, SEQ ID NO: 1206, SEQ ID NO: 1210, SEQ ID NO: 1220, SEQ ID NO: 1224, SEQ ID NO: 1234, SEQ ID NO: 1238, SEQ ID NO: 1248, SEQ ID NO: 1252, SEQ ID NO: 1262, SEQ ID NO: 1266, SEQ ID NO: 1276, SEQ ID NO: 1280, SEQ ID NO: 1290, SEQ ID NO: 1294, SEQ ID NO: 1304, SEQ ID NO: 1308, SEQ ID NO: 1318, SEQ ID NO: 1322, SEQ ID NO: 1332, SEQ ID NO: 1336, SEQ ID NO: 1346, SEQ ID NO: 1350, SEQ ID NO: 1360, SEQ ID NO: 1364, SEQ ID NO: 1374, SEQ ID NO: 1378, SEQ ID NO: 1388, SEQ ID NO: 1392, SEQ ID NO: 1402, SEQ ID NO: 1406, SEQ ID NO: 1416, SEQ ID NO: 1420, SEQ ID NO: 1430, SEQ ID NO: 1434, SEQ ID NO: 1444, SEQ ID NO: 1448, SEQ ID NO: 1458, SEQ ID NO: 1462, SEQ ID NO: 1472, SEQ ID NO: 1476, SEQ ID NO: 1486, SEQ ID NO: 1490, SEQ ID NO: 1500, SEQ ID NO: 1504, SEQ ID NO: 1514, SEQ ID NO: 1518, SEQ ID NO: 1528, SEQ ID NO: 1532, SEQ ID NO: 1542, SEQ ID NO: 1546, SEQ ID NO: 1556, SEQ ID NO: 1560, SEQ ID NO: 1570, and SEQ ID NO: 1574.

Preferred is when the first binding domain of the antibody construct of the invention comprises a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 1052, SEQ ID

NO: 1094, SEQ ID NO: 1150, SEQ ID NO: 1178, SEQ ID NO: 1192, SEQ ID NO: 1220, SEQ ID NO: 1234, SEQ ID NO: 1248, SEQ ID NO: 1262, SEQ ID NO: 1276, SEQ ID NO: 1346, SEQ ID NO: 1360, SEQ ID NO: 1374, SEQ ID NO: 1430, and SEQ ID NO: 1444.

The term “bispecific” as used herein refers to an antibody construct which is “at least bispecific”, *i.e.*, it comprises at least a first binding domain and a second binding domain, wherein the first binding domain binds to one antigen or target (here: CD70), and the second binding domain binds to another antigen or target (here: CD3). Accordingly, antibody constructs according to the invention comprise specificities for at least two different antigens or targets. The term “bispecific antibody construct” of the invention also encompasses multispecific antibody constructs such as trispecific antibody constructs, the latter ones including three binding domains, or constructs having more than three (e.g. four, five...) specificities.

Given that the antibody constructs according to the invention are (at least) bispecific, they do not occur naturally and they are markedly different from naturally occurring products. A “bispecific” antibody construct or immunoglobulin is hence an artificial hybrid antibody or immunoglobulin having at least two distinct binding sites with different specificities. Bispecific antibody constructs can be produced by a variety of methods including fusion of hybridomas or linking of Fab' fragments. See, *e.g.*, Songsivilai & Lachmann, Clin. Exp. Immunol. 79:315-321 (1990).

The at least two binding domains and the variable domains of the antibody construct of the present invention may or may not comprise peptide linkers (spacer peptides). The term “peptide linker” comprises in accordance with the present invention an amino acid sequence by which the amino acid sequences of one (variable and/or binding) domain and another (variable and/or binding) domain of the antibody construct of the invention are linked with each other. An essential technical feature of such peptide linker is that it does not comprise any polymerization activity. Among the suitable peptide linkers are those described in U.S. Patents 4,751,180 and 4,935,233 or WO 88/09344. The peptide linkers can also be used to attach other domains or modules or regions (such as half-life extending domains) to the antibody construct of the invention.

In the event that a linker is used, this linker is preferably of a length and sequence sufficient to ensure that each of the first and second domains can, independently from one another, retain their differential binding specificities. For peptide linkers which connect the at least two binding

domains (or two variable domains) in the antibody construct of the invention, those peptide linkers are preferred which comprise only a few number of amino acid residues, *e.g.* 12 amino acid residues or less. Thus, peptide linkers of 12, 11, 10, 9, 8, 7, 6 or 5 amino acid residues are preferred. An envisaged peptide linker with less than 5 amino acids comprises 4, 3, 2 or one amino acid(s), wherein Gly-rich linkers are preferred. A particularly preferred “single” amino acid in the context of said “peptide linker” is Gly. Accordingly, said peptide linker may consist of the single amino acid Gly. Another preferred embodiment of a peptide linker is characterized by the amino acid sequence Gly-Gly-Gly-Gly-Ser, *i.e.* Gly₄Ser (SEQ ID NO: 771), or polymers thereof, *i.e.* (Gly₄Ser)_x, where x is an integer of 1 or greater (*e.g.* 2 or 3). Preferred linkers are depicted in SEQ ID NOs: 770-778. The characteristics of said peptide linker, which comprise the absence of the promotion of secondary structures, are known in the art and are described *e.g.* in Dall’Acqua *et al.* (Biochem. (1998) 37, 9266-9273), Cheadle *et al.* (Mol Immunol (1992) 29, 21-30) and Raag and Whitlow (FASEB (1995) 9(1), 73-80). Peptide linkers which furthermore do not promote any secondary structures are preferred. The linkage of said domains to each other can be provided, *e.g.*, by genetic engineering, as described in the examples. Methods for preparing fused and operatively linked bispecific single chain constructs and expressing them in mammalian cells or bacteria are well-known in the art (*e.g.* WO 99/54440 or Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2001).

As described herein above, the invention provides a preferred embodiment wherein the antibody construct is in a format selected from the group consisting of (scFv)₂, scFv-single domain mAb, diabodies and oligomers of any of the aforementioned formats. The term “is in a format” does not exclude that the construct can be further modified by attachment or fusion to other moieties, as described herein.

According to a particularly preferred embodiment, and as documented in the appended examples, the antibody construct of the invention is a “bispecific single chain antibody construct”, more preferably a bispecific “single chain Fv” (scFv). Although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker – as described hereinbefore – that enables them to be made as a single protein chain in which the VL and VH regions pair to form a monovalent molecule; see *e.g.*, Huston *et al.* (1988) Proc. Natl. Acad. Sci USA 85:5879-5883). These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are evaluated for function in the same manner as are whole or full-length

antibodies. A single-chain variable fragment (scFv) is hence a fusion protein of the variable region of the heavy chain (VH) and of the light chain (VL) of immunoglobulins, usually connected with a short linker peptide of about ten to about 25 amino acids, preferably about 15 to 20 amino acids. The linker is usually rich in glycine for flexibility, as well as serine or threonine for solubility, and can either connect the N-terminus of the VH with the C-terminus of the VL, or *vice versa*. This protein retains the specificity of the original immunoglobulin, despite removal of the constant regions and introduction of the linker.

Bispecific single chain molecules are known in the art and are described in WO 99/54440, Mack, J. Immunol. (1997), 158, 3965-3970, Mack, PNAS, (1995), 92, 7021-7025, Kufer, Cancer Immunol. Immunother., (1997), 45, 193-197, Löffler, Blood, (2000), 95, 6, 2098-2103, Brühl, Immunol., (2001), 166, 2420-2426, Kipriyanov, J. Mol. Biol., (1999), 293, 41-56. Techniques described for the production of single chain antibodies (see, *inter alia*, US Patent 4,946,778, Kontermann and Dübel (2010), *loc. cit.* and Little (2009), *loc. cit.*) can be adapted to produce single chain antibody constructs specifically recognizing (an) elected target(s).

Bivalent (also called divalent) or bispecific single-chain variable fragments (bi-scFvs or di-scFvs having the format (scFv)₂) can be engineered by linking two scFv molecules (e.g. with linkers as described hereinbefore). If these two scFv molecules have the same binding specificity, the resulting (scFv)₂ molecule will preferably be called bivalent (*i.e.* it has two valences for the same target epitope). If the two scFv molecules have different binding specificities, the resulting (scFv)₂ molecule will preferably be called bispecific. The linking can be done by producing a single peptide chain with two VH regions and two VL regions, yielding tandem scFvs (see e.g. Kufer P. *et al.*, (2004) Trends in Biotechnology 22(5):238-244). Another possibility is the creation of scFv molecules with linker peptides that are too short for the two variable regions to fold together (e.g. about five amino acids), forcing the scFvs to dimerize. This type is known as diabodies (see e.g. Hollinger, Philipp *et al.*, (July 1993) Proceedings of the National Academy of Sciences of the United States of America 90 (14): 6444-8.).

According to a further preferred embodiment of the antibody construct of the invention the heavy chain (VH) and the light chain (VL) of a binding domain (binding either to the target antigen CD70 or to CD3) are not directly connected via a peptide linker as described above, but the binding domains are formed as described for the diabody. Thus, the VH of the CD3 binding domain may be fused to the VL of the CD70 binding domain via a peptide linker, and the VH of the CD70 binding domain is fused to the VL of the CD3 binding domain via such peptide linker.

Single domain antibodies comprise merely one (monomeric) antibody variable domain which is able to bind selectively to a specific antigen, independently of other V regions or domains. The first single domain antibodies were engineered from heavy chain antibodies found in camelids, and these are called V_{HH} fragments. Cartilaginous fishes also have heavy chain antibodies (IgNAR) from which single domain antibodies called V_{NAR} fragments can be obtained. An alternative approach is to split the dimeric variable domains from common immunoglobulins e.g. from humans or rodents into monomers, hence obtaining VH or VL as a single domain Ab. Although most research into single domain antibodies is currently based on heavy chain variable domains, nanobodies derived from light chains have also been shown to bind specifically to target epitopes. Examples of single domain antibodies are called sdAb, nanobodies or single variable domain antibodies.

A (single domain mAb)₂ is hence a monoclonal antibody construct composed of (at least) two single domain monoclonal antibodies, which are individually selected from the group comprising VH, VL, V_{HH} and V_{NAR} . The linker is preferably in the form of a peptide linker. Similarly, an “scFv-single domain mAb” is a monoclonal antibody construct composed of at least one single domain antibody as described above and one scFv molecule as described above. Again, the linker is preferably in the form of a peptide linker.

It is also envisaged that the antibody construct of the invention has, in addition to its function to bind to the target molecules CD70 and CD3, a further function. In this format, the antibody construct is a trifunctional or multifunctional antibody construct by targeting target cells through binding to CD70, mediating cytotoxic T cell activity through CD3 binding and providing a further function such as a fully functional Fc constant domain mediating antibody-dependent cellular cytotoxicity through recruitment of effector cells like NK cells, a label (fluorescent etc.), a therapeutic agent such as a toxin or radionuclide, and/or means to enhance serum half-life, etc.

Examples for means to extend serum half-life of the antibody constructs of the invention include peptides, proteins or domains of proteins, which are fused or otherwise attached to the antibody constructs. The group of peptides, proteins or protein domains includes peptides binding to other proteins with preferred pharmacokinetic profile in the human body such as serum albumin (see WO 2009/127691). An alternative concept of such half-life extending peptides includes peptides binding to the neonatal Fc receptor (FcRn, see WO 2007/098420), which can also be used in the constructs of the present invention. The concept of attaching larger domains of

proteins or complete proteins includes e.g. the fusion of human serum albumin, variants or mutants of human serum albumin (see WO 2011/051489, WO 2012/059486, WO 2012/150319, WO 2013/135896, WO 2014/072481, WO 2013/075066) or domains thereof as well as the fusion of constant region of immunoglobulins (Fc domains) and variants thereof. Such variants of Fc domains may be optimized / modified in order to allow the desired pairing of dimers or multimers, to abolish Fc receptor binding (e.g. the Fc γ receptor) or for other reasons. A further concept known in the art to extend the half-life of small protein compounds in the human body is the pegylation of those compounds such as the antibody construct of the present invention.

In a preferred embodiment, the bispecific antibody constructs according to the invention may be linked (e.g. via peptide bond) with a fusion partner (such as a protein or polypeptide or peptide), e.g. for the purpose of extending the construct's serum half-life. These fusion partners can be selected from human serum albumin ("HSA" or "HALB") as well as sequence variants thereof, peptides binding to HSA, peptides binding to FcRn ("FcRn BP"), or constructs comprising an (antibody derived) Fc region. Exemplary sequences of these fusion partners are depicted in SEQ ID NOs: 780-826. In general, the fusion partners may be linked to the N-terminus or to the C-terminus of the bispecific antibody constructs according to the invention, either directly (e.g. via peptide bond) or through a peptide linker such as (GGGGS)_n (wherein "n" is an integer of 2 or greater, e.g. 2 or 3 or 4). Suitable peptide linkers are depicted in SEQ ID NOs: 770-778.

Hence, a preferred antibody construct according to the present invention comprises:

(a) a polypeptide comprising in the following order starting from the N-terminus:

- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 89, SEQ ID NO: 99, SEQ ID NO: 109, SEQ ID NO: 119, SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID

NO: 509, SEQ ID NO: 519, SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 930, SEQ ID NO: 934, SEQ ID NO: 938, SEQ ID NO: 942, SEQ ID NO: 946, SEQ ID NO: 950, SEQ ID NO: 954, SEQ ID NO: 958, SEQ ID NO: 962, SEQ ID NO: 966, SEQ ID NO: 970, SEQ ID NO: 974, SEQ ID NO: 978, SEQ ID NO: 982, SEQ ID NO: 986, SEQ ID NO: 990, SEQ ID NO: 994, SEQ ID NO: 998, SEQ ID NO: 1002, SEQ ID NO: 1006, SEQ ID NO: 1010, SEQ ID NO: 1014, SEQ ID NO: 1018, SEQ ID NO: 1022, SEQ ID NO: 1026, SEQ ID NO: 1030, SEQ ID NO: 1034, SEQ ID NO: 1038, SEQ ID NO: 1042, SEQ ID NO: 1052, SEQ ID NO: 1056, SEQ ID NO: 1066, SEQ ID NO: 1070, SEQ ID NO: 1080, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1098, SEQ ID NO: 1108, SEQ ID NO: 1112, SEQ ID NO: 1122, SEQ ID NO: 1126, SEQ ID NO: 1136, SEQ ID NO: 1140, SEQ ID NO: 1150, SEQ ID NO: 1154, SEQ ID NO: 1164, SEQ ID NO: 1168, SEQ ID NO: 1178, SEQ ID NO: 1182, SEQ ID NO: 1192, SEQ ID NO: 1196, SEQ ID NO: 1206, SEQ ID NO: 1210, SEQ ID NO: 1220, SEQ ID NO: 1224, SEQ ID NO: 1234, SEQ ID NO: 1238, SEQ ID NO: 1248, SEQ ID NO: 1252, SEQ ID NO: 1262, SEQ ID NO: 1266, SEQ ID NO: 1276, SEQ ID NO: 1280, SEQ ID NO: 1290, SEQ ID NO: 1294, SEQ ID NO: 1304, SEQ ID NO: 1308, SEQ ID NO: 1318, SEQ ID NO: 1322, SEQ ID NO: 1332, SEQ ID NO: 1336, SEQ ID NO: 1346, SEQ ID NO: 1350, SEQ ID NO: 1360, SEQ ID NO: 1364, SEQ ID NO: 1374, SEQ ID NO: 1378, SEQ ID NO: 1388, SEQ ID NO: 1392, SEQ ID NO: 1402, SEQ ID NO: 1406, SEQ ID NO: 1416, SEQ ID NO: 1420, SEQ ID NO: 1430, SEQ ID NO: 1434, SEQ ID NO: 1444, SEQ ID NO: 1448, SEQ ID NO: 1458, SEQ ID NO: 1462, SEQ ID NO: 1472, SEQ ID NO: 1476, SEQ ID NO: 1486, SEQ ID NO: 1490, SEQ ID NO: 1500, SEQ ID NO: 1504, SEQ ID NO: 1514, SEQ ID NO: 1518, SEQ ID NO: 1528, SEQ ID NO: 1532, SEQ ID NO: 1542, SEQ ID NO: 1546, SEQ ID NO: 1556, SEQ ID NO: 1560, SEQ ID NO: 1570, and SEQ ID NO: 1574;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 770-778; and
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 835, SEQ ID NO: 844, SEQ ID NO: 853, SEQ ID NO: 862, SEQ ID

NO: 871, SEQ ID NO: 880, SEQ ID NO: 889, SEQ ID NO: 898, SEQ ID NO: 907, SEQ ID NO: 916, and SEQ ID NO: 919; and

- optionally a His-tag, such as the one depicted in SEQ ID NO 779;

(b) a polypeptide comprising in the following order starting from the N-terminus:

- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 89, SEQ ID NO: 99, SEQ ID NO: 109, SEQ ID NO: 119, SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 930, SEQ ID NO: 934, SEQ ID NO: 938, SEQ ID NO: 942, SEQ ID NO: 946, SEQ ID NO: 950, SEQ ID NO: 954, SEQ ID NO: 958, SEQ ID NO: 962, SEQ ID NO: 966, SEQ ID NO: 970, SEQ ID NO: 974, SEQ ID NO: 978, SEQ ID NO: 982, SEQ ID NO: 986, SEQ ID NO: 990, SEQ ID NO: 994, SEQ ID NO: 998, SEQ ID NO: 1002, SEQ ID NO: 1006, SEQ ID NO: 1010, SEQ ID NO: 1014, SEQ ID NO: 1018, SEQ ID NO: 1022, SEQ ID NO: 1026, SEQ ID NO: 1030, SEQ ID NO: 1034, SEQ ID NO: 1038, SEQ ID NO: 1042, SEQ ID NO: 1052, SEQ ID NO: 1056, SEQ ID NO: 1066, SEQ ID NO: 1070, SEQ ID NO: 1080, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1098, SEQ ID NO: 1108, SEQ ID NO: 1112, SEQ ID NO: 1122, SEQ ID NO: 1126, SEQ ID NO: 1136, SEQ ID NO: 1140, SEQ ID NO: 1150, SEQ ID NO: 1154, SEQ ID NO: 1164, SEQ ID NO: 1168, SEQ ID NO: 1178, SEQ ID NO: 1182, SEQ ID NO: 1192, SEQ ID NO: 1196, SEQ ID NO: 1206, SEQ ID NO: 1210, SEQ ID NO: 1220, SEQ ID NO: 1224, SEQ ID

NO: 1234, SEQ ID NO: 1238, SEQ ID NO: 1248, SEQ ID NO: 1252, SEQ ID NO: 1262, SEQ ID NO: 1266, SEQ ID NO: 1276, SEQ ID NO: 1280, SEQ ID NO: 1290, SEQ ID NO: 1294, SEQ ID NO: 1304, SEQ ID NO: 1308, SEQ ID NO: 1318, SEQ ID NO: 1322, SEQ ID NO: 1332, SEQ ID NO: 1336, SEQ ID NO: 1346, SEQ ID NO: 1350, SEQ ID NO: 1360, SEQ ID NO: 1364, SEQ ID NO: 1374, SEQ ID NO: 1378, SEQ ID NO: 1388, SEQ ID NO: 1392, SEQ ID NO: 1402, SEQ ID NO: 1406, SEQ ID NO: 1416, SEQ ID NO: 1420, SEQ ID NO: 1430, SEQ ID NO: 1434, SEQ ID NO: 1444, SEQ ID NO: 1448, SEQ ID NO: 1458, SEQ ID NO: 1462, SEQ ID NO: 1472, SEQ ID NO: 1476, SEQ ID NO: 1486, SEQ ID NO: 1490, SEQ ID NO: 1500, SEQ ID NO: 1504, SEQ ID NO: 1514, SEQ ID NO: 1518, SEQ ID NO: 1528, SEQ ID NO: 1532, SEQ ID NO: 1542, SEQ ID NO: 1546, SEQ ID NO: 1556, SEQ ID NO: 1560, SEQ ID NO: 1570, and SEQ ID NO: 1574;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 770-778;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 835, SEQ ID NO: 844, SEQ ID NO: 853, SEQ ID NO: 862, SEQ ID NO: 871, SEQ ID NO: 880, SEQ ID NO: 889, SEQ ID NO: 898, SEQ ID NO: 907, SEQ ID NO: 916, and SEQ ID NO: 919;
 - optionally a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 770-778;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOs: 780 and 786-815; and
 - optionally a His-tag, such as the one depicted in SEQ ID NO 779;
- (c) a polypeptide comprising in the following order starting from the N-terminus:
- a polypeptide having the amino acid sequence QRFVTGHFGGLX₁PANG (SEQ ID NO: 781) wherein X₁ is Y or H; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 89, SEQ ID NO: 99, SEQ ID NO: 109, SEQ ID NO: 119, SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID

NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 930, SEQ ID NO: 934, SEQ ID NO: 938, SEQ ID NO: 942, SEQ ID NO: 946, SEQ ID NO: 950, SEQ ID NO: 954, SEQ ID NO: 958, SEQ ID NO: 962, SEQ ID NO: 966, SEQ ID NO: 970, SEQ ID NO: 974, SEQ ID NO: 978, SEQ ID NO: 982, SEQ ID NO: 986, SEQ ID NO: 990, SEQ ID NO: 994, SEQ ID NO: 998, SEQ ID NO: 1002, SEQ ID NO: 1006, SEQ ID NO: 1010, SEQ ID NO: 1014, SEQ ID NO: 1018, SEQ ID NO: 1022, SEQ ID NO: 1026, SEQ ID NO: 1030, SEQ ID NO: 1034, SEQ ID NO: 1038, SEQ ID NO: 1042, SEQ ID NO: 1052, SEQ ID NO: 1056, SEQ ID NO: 1066, SEQ ID NO: 1070, SEQ ID NO: 1080, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1098, SEQ ID NO: 1108, SEQ ID NO: 1112, SEQ ID NO: 1122, SEQ ID NO: 1126, SEQ ID NO: 1136, SEQ ID NO: 1140, SEQ ID NO: 1150, SEQ ID NO: 1154, SEQ ID NO: 1164, SEQ ID NO: 1168, SEQ ID NO: 1178, SEQ ID NO: 1182, SEQ ID NO: 1192, SEQ ID NO: 1196, SEQ ID NO: 1206, SEQ ID NO: 1210, SEQ ID NO: 1220, SEQ ID NO: 1224, SEQ ID NO: 1234, SEQ ID NO: 1238, SEQ ID NO: 1248, SEQ ID NO: 1252, SEQ ID NO: 1262, SEQ ID NO: 1266, SEQ ID NO: 1276, SEQ ID NO: 1280, SEQ ID NO: 1290, SEQ ID NO: 1294, SEQ ID NO: 1304, SEQ ID NO: 1308, SEQ ID NO: 1318, SEQ ID NO: 1322, SEQ ID NO: 1332, SEQ ID NO: 1336, SEQ ID NO: 1346, SEQ ID NO: 1350, SEQ ID NO: 1360, SEQ ID NO: 1364, SEQ ID NO: 1374, SEQ ID NO: 1378, SEQ ID NO: 1388, SEQ ID NO: 1392, SEQ ID NO: 1402, SEQ ID NO: 1406, SEQ ID NO: 1416, SEQ ID NO: 1420, SEQ ID NO: 1430, SEQ ID NO: 1434, SEQ ID NO: 1444, SEQ ID NO: 1448, SEQ ID NO: 1458, SEQ ID NO: 1462, SEQ ID NO: 1472, SEQ ID NO: 1476, SEQ ID NO: 1486, SEQ ID NO: 1490, SEQ ID NO: 1500, SEQ ID NO: 1504, SEQ ID NO: 1514, SEQ ID NO: 1518, SEQ ID NO: 1528, SEQ ID NO: 1532, SEQ ID NO: 1542, SEQ ID NO: 1546, SEQ ID NO: 1556, SEQ ID NO: 1560, SEQ ID NO: 1570, and SEQ ID NO: 1574;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 770-778;
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 835, SEQ ID NO: 844, SEQ ID NO: 853, SEQ ID NO: 862, SEQ ID NO: 871, SEQ ID NO: 880, SEQ ID NO: 889, SEQ ID NO: 898, SEQ ID NO: 907, SEQ ID NO: 916, and SEQ ID NO: 919;
- a polypeptide having the amino acid sequence QRFVTGHFGGLHPANG (SEQ ID NO: 783) or QRFCTGHFGGLHPCNG (SEQ ID NO: 785); and
- optionally a His-tag, such as the one depicted in SEQ ID NO 779;

(d) a polypeptide comprising in the following order starting from the N-terminus

- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 833, SEQ ID NO: 842, SEQ ID NO: 851, SEQ ID NO: 860, SEQ ID NO: 869, SEQ ID NO: 878, SEQ ID NO: 887, SEQ ID NO: 896, SEQ ID NO: 905, SEQ ID NO: 914, and SEQ ID NO: 917;
- a peptide linker having the amino acid sequence depicted in SEQ ID NO: 777;
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 28, SEQ ID NO: 38, SEQ ID NO: 48, SEQ ID NO: 58, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 98, SEQ ID NO: 108, SEQ ID NO: 118, SEQ ID NO: 128, SEQ ID NO: 138, SEQ ID NO: 148, SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508, SEQ ID NO: 518, SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558, SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 921, SEQ ID NO: 925, SEQ ID NO: 929, SEQ ID NO: 933, SEQ ID NO: 937, SEQ ID NO: 941, SEQ ID NO: 945, SEQ ID NO: 949,

SEQ ID NO: 953, SEQ ID NO: 957, SEQ ID NO: 961, SEQ ID NO: 965, SEQ ID NO: 969, SEQ ID NO: 973, SEQ ID NO: 977, SEQ ID NO: 981, SEQ ID NO: 985, SEQ ID NO: 989, SEQ ID NO: 993, SEQ ID NO: 997, SEQ ID NO: 1001, SEQ ID NO: 1005, SEQ ID NO: 1009, SEQ ID NO: 1013, SEQ ID NO: 1017, SEQ ID NO: 1021, SEQ ID NO: 1025, SEQ ID NO: 1029, SEQ ID NO: 1033, SEQ ID NO: 1037, SEQ ID NO: 1041, SEQ ID NO: 1051, SEQ ID NO: 1055, SEQ ID NO: 1065, SEQ ID NO: 1069, SEQ ID NO: 1079, SEQ ID NO: 1083, SEQ ID NO: 1093, SEQ ID NO: 1097, SEQ ID NO: 1107, SEQ ID NO: 1111, SEQ ID NO: 1121, SEQ ID NO: 1125, SEQ ID NO: 1135, SEQ ID NO: 1139, SEQ ID NO: 1149, SEQ ID NO: 1153, SEQ ID NO: 1163, SEQ ID NO: 1167, SEQ ID NO: 1177, SEQ ID NO: 1181, SEQ ID NO: 1191, SEQ ID NO: 1195, SEQ ID NO: 1205, SEQ ID NO: 1209, SEQ ID NO: 1219, SEQ ID NO: 1223, SEQ ID NO: 1233, SEQ ID NO: 1237, SEQ ID NO: 1247, SEQ ID NO: 1251, SEQ ID NO: 1261, SEQ ID NO: 1265, SEQ ID NO: 1275, SEQ ID NO: 1279, SEQ ID NO: 1289, SEQ ID NO: 1293, SEQ ID NO: 1303, SEQ ID NO: 1307, SEQ ID NO: 1317, SEQ ID NO: 1321, SEQ ID NO: 1331, SEQ ID NO: 1335, SEQ ID NO: 1345, SEQ ID NO: 1349, SEQ ID NO: 1359, SEQ ID NO: 1363, SEQ ID NO: 1373, SEQ ID NO: 1377, SEQ ID NO: 1387, SEQ ID NO: 1391, SEQ ID NO: 1401, SEQ ID NO: 1405, SEQ ID NO: 1415, SEQ ID NO: 1419, SEQ ID NO: 1429, SEQ ID NO: 1433, SEQ ID NO: 1443, SEQ ID NO: 1447, SEQ ID NO: 1457, SEQ ID NO: 1461, SEQ ID NO: 1471, SEQ ID NO: 1475, SEQ ID NO: 1485, SEQ ID NO: 1489, SEQ ID NO: 1499, SEQ ID NO: 1503, SEQ ID NO: 1513, SEQ ID NO: 1517, SEQ ID NO: 1527, SEQ ID NO: 1531, SEQ ID NO: 1541, SEQ ID NO: 1545, SEQ ID NO: 1555, SEQ ID NO: 1559, SEQ ID NO: 1569, and SEQ ID NO: 1573, followed by a serine residue at the C-terminus;

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 816; and
- a polypeptide comprising in the following order starting from the N-terminus:
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 17, SEQ ID NO: 27, SEQ ID NO: 37, SEQ ID NO: 47, SEQ ID NO: 57, SEQ ID NO: 67, SEQ ID NO: 77, SEQ ID NO: 87, SEQ ID NO: 97, SEQ ID NO: 107, SEQ ID NO: 117, SEQ ID NO: 127, SEQ ID NO: 137, SEQ ID NO: 147, SEQ ID NO: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID

NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547, SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637, SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737; SEQ ID NO: 920, SEQ ID NO: 924, SEQ ID NO: 928, SEQ ID NO: 932, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 944, SEQ ID NO: 948, SEQ ID NO: 952, SEQ ID NO: 956, SEQ ID NO: 960, SEQ ID NO: 964, SEQ ID NO: 968, SEQ ID NO: 972, SEQ ID NO: 976, SEQ ID NO: 980, SEQ ID NO: 984, SEQ ID NO: 988, SEQ ID NO: 992, SEQ ID NO: 996, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1008, SEQ ID NO: 1012, SEQ ID NO: 1016, SEQ ID NO: 1020, SEQ ID NO: 1024, SEQ ID NO: 1028, SEQ ID NO: 1032, SEQ ID NO: 1036, SEQ ID NO: 1040, SEQ ID NO: 1050, SEQ ID NO: 1054, SEQ ID NO: 1064, SEQ ID NO: 1068, SEQ ID NO: 1078, SEQ ID NO: 1082, SEQ ID NO: 1092, SEQ ID NO: 1096, SEQ ID NO: 1106, SEQ ID NO: 1110, SEQ ID NO: 1120, SEQ ID NO: 1124, SEQ ID NO: 1134, SEQ ID NO: 1138, SEQ ID NO: 1148, SEQ ID NO: 1152, SEQ ID NO: 1162, SEQ ID NO: 1166, SEQ ID NO: 1176, SEQ ID NO: 1180, SEQ ID NO: 1190, SEQ ID NO: 1194, SEQ ID NO: 1204, SEQ ID NO: 1208, SEQ ID NO: 1218, SEQ ID NO: 1222, SEQ ID NO: 1232, SEQ ID NO: 1236, SEQ ID NO: 1246, SEQ ID NO: 1250, SEQ ID NO: 1260, SEQ ID NO: 1264, SEQ ID NO: 1274, SEQ ID NO: 1278, SEQ ID NO: 1288, SEQ ID NO: 1292, SEQ ID NO: 1302, SEQ ID NO: 1306, SEQ ID NO: 1316, SEQ ID NO: 1320, SEQ ID NO: 1330, SEQ ID NO: 1334, SEQ ID NO: 1344, SEQ ID NO: 1348, SEQ ID NO: 1358, SEQ ID NO: 1362, SEQ ID NO: 1372, SEQ ID NO: 1376, SEQ ID NO: 1386, SEQ ID NO: 1390, SEQ ID NO: 1400, SEQ ID NO: 1404, SEQ ID NO: 1414, SEQ ID NO: 1418, SEQ ID NO: 1428, SEQ ID NO: 1432, SEQ ID NO: 1442, SEQ ID NO: 1446, SEQ ID NO: 1456, SEQ ID NO: 1460, SEQ ID NO: 1470, SEQ ID NO: 1474, SEQ ID NO: 1484, SEQ ID NO: 1488, SEQ ID NO: 1498, SEQ ID NO: 1502, SEQ ID NO: 1512, SEQ ID NO: 1516, SEQ ID NO: 1526, SEQ ID NO: 1530, SEQ ID NO: 1540, SEQ ID NO: 1544, SEQ ID NO: 1554, SEQ ID NO: 1558, SEQ ID NO: 1568, and SEQ ID NO: 1572;

- a peptide linker having the amino acid sequence depicted in SEQ ID NO: 777;
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 834, SEQ ID NO: 843, SEQ ID NO: 852, SEQ ID NO: 861, SEQ ID

NO: 870, SEQ ID NO: 879, SEQ ID NO: 888, SEQ ID NO: 897, SEQ ID NO: 906, SEQ ID NO: 915, and SEQ ID NO: 918 followed by a serine residue at the C-terminus; and

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 817;

(e) a polypeptide comprising in the following order starting from the N-terminus:

- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 833, SEQ ID NO: 842, SEQ ID NO: 851, SEQ ID NO: 860, SEQ ID NO: 869, SEQ ID NO: 878, SEQ ID NO: 887, SEQ ID NO: 896, SEQ ID NO: 905, SEQ ID NO: 914, and SEQ ID NO: 917;
- a peptide linker having the amino acid sequence depicted in SEQ ID NO: 777;
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 28, SEQ ID NO: 38, SEQ ID NO: 48, SEQ ID NO: 58, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 88, SEQ ID NO: 98, SEQ ID NO: 108, SEQ ID NO: 118, SEQ ID NO: 128, SEQ ID NO: 138, SEQ ID NO: 148, SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 178, SEQ ID NO: 188, SEQ ID NO: 198, SEQ ID NO: 208, SEQ ID NO: 218, SEQ ID NO: 228, SEQ ID NO: 238, SEQ ID NO: 248, SEQ ID NO: 258, SEQ ID NO: 268, SEQ ID NO: 278, SEQ ID NO: 288, SEQ ID NO: 298, SEQ ID NO: 308, SEQ ID NO: 318, SEQ ID NO: 328, SEQ ID NO: 338, SEQ ID NO: 348, SEQ ID NO: 358, SEQ ID NO: 368, SEQ ID NO: 378, SEQ ID NO: 388, SEQ ID NO: 398, SEQ ID NO: 408, SEQ ID NO: 418, SEQ ID NO: 428, SEQ ID NO: 438, SEQ ID NO: 448, SEQ ID NO: 458, SEQ ID NO: 468, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 498, SEQ ID NO: 508, SEQ ID NO: 518, SEQ ID NO: 528, SEQ ID NO: 538, SEQ ID NO: 548, SEQ ID NO: 558, SEQ ID NO: 568, SEQ ID NO: 578, SEQ ID NO: 588, SEQ ID NO: 598, SEQ ID NO: 608, SEQ ID NO: 618, SEQ ID NO: 628, SEQ ID NO: 638, SEQ ID NO: 648, SEQ ID NO: 658, SEQ ID NO: 668, SEQ ID NO: 678, SEQ ID NO: 688, SEQ ID NO: 698, SEQ ID NO: 708, SEQ ID NO: 718, SEQ ID NO: 728, SEQ ID NO: 738, SEQ ID NO: 921, SEQ ID NO: 925, SEQ ID NO: 929, SEQ ID NO: 933, SEQ ID NO: 937, SEQ ID NO: 941, SEQ ID NO: 945, SEQ ID NO: 949, SEQ ID NO: 953, SEQ ID NO: 957, SEQ ID NO: 961, SEQ ID NO: 965, SEQ ID NO: 969, SEQ ID NO: 973, SEQ ID NO: 977, SEQ ID NO: 981, SEQ ID NO: 985, SEQ ID NO: 989, SEQ ID NO: 993, SEQ ID NO: 997, SEQ ID NO: 1001, SEQ ID NO: 1005, SEQ ID NO: 1009, SEQ ID NO: 1013, SEQ ID NO: 1017, SEQ ID NO: 1021, SEQ ID NO: 1025, SEQ ID NO: 1029, SEQ ID NO: 1033, SEQ ID NO: 1037, SEQ ID

NO: 1041, SEQ ID NO: 1051, SEQ ID NO: 1055, SEQ ID NO: 1065, SEQ ID NO: 1069, SEQ ID NO: 1079, SEQ ID NO: 1083, SEQ ID NO: 1093, SEQ ID NO: 1097, SEQ ID NO: 1107, SEQ ID NO: 1111, SEQ ID NO: 1121, SEQ ID NO: 1125, SEQ ID NO: 1135, SEQ ID NO: 1139, SEQ ID NO: 1149, SEQ ID NO: 1153, SEQ ID NO: 1163, SEQ ID NO: 1167, SEQ ID NO: 1177, SEQ ID NO: 1181, SEQ ID NO: 1191, SEQ ID NO: 1195, SEQ ID NO: 1205, SEQ ID NO: 1209, SEQ ID NO: 1219, SEQ ID NO: 1223, SEQ ID NO: 1233, SEQ ID NO: 1237, SEQ ID NO: 1247, SEQ ID NO: 1251, SEQ ID NO: 1261, SEQ ID NO: 1265, SEQ ID NO: 1275, SEQ ID NO: 1279, SEQ ID NO: 1289, SEQ ID NO: 1293, SEQ ID NO: 1303, SEQ ID NO: 1307, SEQ ID NO: 1317, SEQ ID NO: 1321, SEQ ID NO: 1331, SEQ ID NO: 1335, SEQ ID NO: 1345, SEQ ID NO: 1349, SEQ ID NO: 1359, SEQ ID NO: 1363, SEQ ID NO: 1373, SEQ ID NO: 1377, SEQ ID NO: 1387, SEQ ID NO: 1391, SEQ ID NO: 1401, SEQ ID NO: 1405, SEQ ID NO: 1415, SEQ ID NO: 1419, SEQ ID NO: 1429, SEQ ID NO: 1433, SEQ ID NO: 1443, SEQ ID NO: 1447, SEQ ID NO: 1457, SEQ ID NO: 1461, SEQ ID NO: 1471, SEQ ID NO: 1475, SEQ ID NO: 1485, SEQ ID NO: 1489, SEQ ID NO: 1499, SEQ ID NO: 1503, SEQ ID NO: 1513, SEQ ID NO: 1517, SEQ ID NO: 1527, SEQ ID NO: 1531, SEQ ID NO: 1541, SEQ ID NO: 1545, SEQ ID NO: 1555, SEQ ID NO: 1559, SEQ ID NO: 1569, and SEQ ID NO: 1573; and

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 818; and
- a polypeptide comprising in the following order starting from the N-terminus:
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 17, SEQ ID NO: 27, SEQ ID NO: 37, SEQ ID NO: 47, SEQ ID NO: 57, SEQ ID NO: 67, SEQ ID NO: 77, SEQ ID NO: 87, SEQ ID NO: 97, SEQ ID NO: 107, SEQ ID NO: 117, SEQ ID NO: 127, SEQ ID NO: 137, SEQ ID NO: 147, SEQ ID NO: 157, SEQ ID NO: 167, SEQ ID NO: 177, SEQ ID NO: 187, SEQ ID NO: 197, SEQ ID NO: 207, SEQ ID NO: 217, SEQ ID NO: 227, SEQ ID NO: 237, SEQ ID NO: 247, SEQ ID NO: 257, SEQ ID NO: 267, SEQ ID NO: 277, SEQ ID NO: 287, SEQ ID NO: 297, SEQ ID NO: 307, SEQ ID NO: 317, SEQ ID NO: 327, SEQ ID NO: 337, SEQ ID NO: 347, SEQ ID NO: 357, SEQ ID NO: 367, SEQ ID NO: 377, SEQ ID NO: 387, SEQ ID NO: 397, SEQ ID NO: 407, SEQ ID NO: 417, SEQ ID NO: 427, SEQ ID NO: 437, SEQ ID NO: 447, SEQ ID NO: 457, SEQ ID NO: 467, SEQ ID NO: 477, SEQ ID NO: 487, SEQ ID NO: 497, SEQ ID NO: 507, SEQ ID NO: 517, SEQ ID NO: 527, SEQ ID NO: 537, SEQ ID NO: 547, SEQ ID NO: 557, SEQ ID NO: 567, SEQ ID NO: 577, SEQ ID NO: 587, SEQ ID NO: 597, SEQ ID NO: 607, SEQ ID NO: 617, SEQ ID NO: 627, SEQ ID NO: 637,

SEQ ID NO: 647, SEQ ID NO: 657, SEQ ID NO: 667, SEQ ID NO: 677, SEQ ID NO: 687, SEQ ID NO: 697, SEQ ID NO: 707, SEQ ID NO: 717, SEQ ID NO: 727, SEQ ID NO: 737; SEQ ID NO: 920, SEQ ID NO: 924, SEQ ID NO: 928, SEQ ID NO: 932, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 944, SEQ ID NO: 948, SEQ ID NO: 952, SEQ ID NO: 956, SEQ ID NO: 960, SEQ ID NO: 964, SEQ ID NO: 968, SEQ ID NO: 972, SEQ ID NO: 976, SEQ ID NO: 980, SEQ ID NO: 984, SEQ ID NO: 988, SEQ ID NO: 992, SEQ ID NO: 996, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1008, SEQ ID NO: 1012, SEQ ID NO: 1016, SEQ ID NO: 1020, SEQ ID NO: 1024, SEQ ID NO: 1028, SEQ ID NO: 1032, SEQ ID NO: 1036, SEQ ID NO: 1040, SEQ ID NO: 1050, SEQ ID NO: 1054, SEQ ID NO: 1064, SEQ ID NO: 1068, SEQ ID NO: 1078, SEQ ID NO: 1082, SEQ ID NO: 1092, SEQ ID NO: 1096, SEQ ID NO: 1106, SEQ ID NO: 1110, SEQ ID NO: 1120, SEQ ID NO: 1124, SEQ ID NO: 1134, SEQ ID NO: 1138, SEQ ID NO: 1148, SEQ ID NO: 1152, SEQ ID NO: 1162, SEQ ID NO: 1166, SEQ ID NO: 1176, SEQ ID NO: 1180, SEQ ID NO: 1190, SEQ ID NO: 1194, SEQ ID NO: 1204, SEQ ID NO: 1208, SEQ ID NO: 1218, SEQ ID NO: 1222, SEQ ID NO: 1232, SEQ ID NO: 1236, SEQ ID NO: 1246, SEQ ID NO: 1250, SEQ ID NO: 1260, SEQ ID NO: 1264, SEQ ID NO: 1274, SEQ ID NO: 1278, SEQ ID NO: 1288, SEQ ID NO: 1292, SEQ ID NO: 1302, SEQ ID NO: 1306, SEQ ID NO: 1316, SEQ ID NO: 1320, SEQ ID NO: 1330, SEQ ID NO: 1334, SEQ ID NO: 1344, SEQ ID NO: 1348, SEQ ID NO: 1358, SEQ ID NO: 1362, SEQ ID NO: 1372, SEQ ID NO: 1376, SEQ ID NO: 1386, SEQ ID NO: 1390, SEQ ID NO: 1400, SEQ ID NO: 1404, SEQ ID NO: 1414, SEQ ID NO: 1418, SEQ ID NO: 1428, SEQ ID NO: 1432, SEQ ID NO: 1442, SEQ ID NO: 1446, SEQ ID NO: 1456, SEQ ID NO: 1460, SEQ ID NO: 1470, SEQ ID NO: 1474, SEQ ID NO: 1484, SEQ ID NO: 1488, SEQ ID NO: 1498, SEQ ID NO: 1502, SEQ ID NO: 1512, SEQ ID NO: 1516, SEQ ID NO: 1526, SEQ ID NO: 1530, SEQ ID NO: 1540, SEQ ID NO: 1544, SEQ ID NO: 1554, SEQ ID NO: 1558, SEQ ID NO: 1568, and SEQ ID NO: 1572;

- a peptide linker having the amino acid sequence depicted in SEQ ID NO: 777;
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 834, SEQ ID NO: 843, SEQ ID NO: 852, SEQ ID NO: 861, SEQ ID NO: 870, SEQ ID NO: 879, SEQ ID NO: 888, SEQ ID NO: 897, SEQ ID NO: 906, SEQ ID NO: 915, and SEQ ID NO: 918 followed by a serine residue at the C-terminus; and
- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 819;

(f) a polypeptide comprising in the following order starting from the N-terminus:

- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 89, SEQ ID NO: 99, SEQ ID NO: 109, SEQ ID NO: 119, SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 930, SEQ ID NO: 934, SEQ ID NO: 938, SEQ ID NO: 942, SEQ ID NO: 946, SEQ ID NO: 950, SEQ ID NO: 954, SEQ ID NO: 958, SEQ ID NO: 962, SEQ ID NO: 966, SEQ ID NO: 970, SEQ ID NO: 974, SEQ ID NO: 978, SEQ ID NO: 982, SEQ ID NO: 986, SEQ ID NO: 990, SEQ ID NO: 994, SEQ ID NO: 998, SEQ ID NO: 1002, SEQ ID NO: 1006, SEQ ID NO: 1010, SEQ ID NO: 1014, SEQ ID NO: 1018, SEQ ID NO: 1022, SEQ ID NO: 1026, SEQ ID NO: 1030, SEQ ID NO: 1034, SEQ ID NO: 1038, SEQ ID NO: 1042, SEQ ID NO: 1052, SEQ ID NO: 1056, SEQ ID NO: 1066, SEQ ID NO: 1070, SEQ ID NO: 1080, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1098, SEQ ID NO: 1108, SEQ ID NO: 1112, SEQ ID NO: 1122, SEQ ID NO: 1126, SEQ ID NO: 1136, SEQ ID NO: 1140, SEQ ID NO: 1150, SEQ ID NO: 1154, SEQ ID NO: 1164, SEQ ID NO: 1168, SEQ ID NO: 1178, SEQ ID NO: 1182, SEQ ID NO: 1192, SEQ ID NO: 1196, SEQ ID NO: 1206, SEQ ID NO: 1210, SEQ ID NO: 1220, SEQ ID NO: 1224, SEQ ID NO: 1234, SEQ ID NO: 1238, SEQ ID NO: 1248, SEQ ID NO: 1252, SEQ ID NO: 1262, SEQ ID NO: 1266, SEQ ID NO: 1276, SEQ ID NO: 1280, SEQ ID NO: 1290, SEQ ID NO: 1294, SEQ ID NO: 1304, SEQ ID NO: 1308, SEQ ID NO: 1318, SEQ ID NO: 1322, SEQ ID NO: 1332, SEQ ID NO: 1336, SEQ ID NO: 1346, SEQ ID NO: 1350, SEQ ID

NO: 1360, SEQ ID NO: 1364, SEQ ID NO: 1374, SEQ ID NO: 1378, SEQ ID NO: 1388, SEQ ID NO: 1392, SEQ ID NO: 1402, SEQ ID NO: 1406, SEQ ID NO: 1416, SEQ ID NO: 1420, SEQ ID NO: 1430, SEQ ID NO: 1434, SEQ ID NO: 1444, SEQ ID NO: 1448, SEQ ID NO: 1458, SEQ ID NO: 1462, SEQ ID NO: 1472, SEQ ID NO: 1476, SEQ ID NO: 1486, SEQ ID NO: 1490, SEQ ID NO: 1500, SEQ ID NO: 1504, SEQ ID NO: 1514, SEQ ID NO: 1518, SEQ ID NO: 1528, SEQ ID NO: 1532, SEQ ID NO: 1542, SEQ ID NO: 1546, SEQ ID NO: 1556, SEQ ID NO: 1560, SEQ ID NO: 1570, and SEQ ID NO: 1574;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 770-778;
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 835, SEQ ID NO: 844, SEQ ID NO: 853, SEQ ID NO: 862, SEQ ID NO: 871, SEQ ID NO: 880, SEQ ID NO: 889, SEQ ID NO: 898, SEQ ID NO: 907, SEQ ID NO: 916, and SEQ ID NO: 919;
- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 820; and
a polypeptide having the amino acid sequence depicted in SEQ ID NO: 821;

(g) a polypeptide comprising in the following order starting from the N-terminus:

- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 89, SEQ ID NO: 99, SEQ ID NO: 109, SEQ ID NO: 119, SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729,

SEQ ID NO: 739, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 930, SEQ ID NO: 934, SEQ ID NO: 938, SEQ ID NO: 942, SEQ ID NO: 946, SEQ ID NO: 950, SEQ ID NO: 954, SEQ ID NO: 958, SEQ ID NO: 962, SEQ ID NO: 966, SEQ ID NO: 970, SEQ ID NO: 974, SEQ ID NO: 978, SEQ ID NO: 982, SEQ ID NO: 986, SEQ ID NO: 990, SEQ ID NO: 994, SEQ ID NO: 998, SEQ ID NO: 1002, SEQ ID NO: 1006, SEQ ID NO: 1010, SEQ ID NO: 1014, SEQ ID NO: 1018, SEQ ID NO: 1022, SEQ ID NO: 1026, SEQ ID NO: 1030, SEQ ID NO: 1034, SEQ ID NO: 1038, SEQ ID NO: 1042, SEQ ID NO: 1052, SEQ ID NO: 1056, SEQ ID NO: 1066, SEQ ID NO: 1070, SEQ ID NO: 1080, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1098, SEQ ID NO: 1108, SEQ ID NO: 1112, SEQ ID NO: 1122, SEQ ID NO: 1126, SEQ ID NO: 1136, SEQ ID NO: 1140, SEQ ID NO: 1150, SEQ ID NO: 1154, SEQ ID NO: 1164, SEQ ID NO: 1168, SEQ ID NO: 1178, SEQ ID NO: 1182, SEQ ID NO: 1192, SEQ ID NO: 1196, SEQ ID NO: 1206, SEQ ID NO: 1210, SEQ ID NO: 1220, SEQ ID NO: 1224, SEQ ID NO: 1234, SEQ ID NO: 1238, SEQ ID NO: 1248, SEQ ID NO: 1252, SEQ ID NO: 1262, SEQ ID NO: 1266, SEQ ID NO: 1276, SEQ ID NO: 1280, SEQ ID NO: 1290, SEQ ID NO: 1294, SEQ ID NO: 1304, SEQ ID NO: 1308, SEQ ID NO: 1318, SEQ ID NO: 1322, SEQ ID NO: 1332, SEQ ID NO: 1336, SEQ ID NO: 1346, SEQ ID NO: 1350, SEQ ID NO: 1360, SEQ ID NO: 1364, SEQ ID NO: 1374, SEQ ID NO: 1378, SEQ ID NO: 1388, SEQ ID NO: 1392, SEQ ID NO: 1402, SEQ ID NO: 1406, SEQ ID NO: 1416, SEQ ID NO: 1420, SEQ ID NO: 1430, SEQ ID NO: 1434, SEQ ID NO: 1444, SEQ ID NO: 1448, SEQ ID NO: 1458, SEQ ID NO: 1462, SEQ ID NO: 1472, SEQ ID NO: 1476, SEQ ID NO: 1486, SEQ ID NO: 1490, SEQ ID NO: 1500, SEQ ID NO: 1504, SEQ ID NO: 1514, SEQ ID NO: 1518, SEQ ID NO: 1528, SEQ ID NO: 1532, SEQ ID NO: 1542, SEQ ID NO: 1546, SEQ ID NO: 1556, SEQ ID NO: 1560, SEQ ID NO: 1570, and SEQ ID NO: 1574; and

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 822; and
- a polypeptide comprising in the following order starting from the N-terminus:
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 835, SEQ ID NO: 844, SEQ ID NO: 853, SEQ ID NO: 862, SEQ ID NO: 871, SEQ ID NO: 880, SEQ ID NO: 889, SEQ ID NO: 898, SEQ ID NO: 907, SEQ ID NO: 916, and SEQ ID NO: 919; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 823;

(h) a polypeptide comprising in the following order starting from the N-terminus:

- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 89, SEQ ID NO: 99, SEQ ID NO: 109, SEQ ID NO: 119, SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 930, SEQ ID NO: 934, SEQ ID NO: 938, SEQ ID NO: 942, SEQ ID NO: 946, SEQ ID NO: 950, SEQ ID NO: 954, SEQ ID NO: 958, SEQ ID NO: 962, SEQ ID NO: 966, SEQ ID NO: 970, SEQ ID NO: 974, SEQ ID NO: 978, SEQ ID NO: 982, SEQ ID NO: 986, SEQ ID NO: 990, SEQ ID NO: 994, SEQ ID NO: 998, SEQ ID NO: 1002, SEQ ID NO: 1006, SEQ ID NO: 1010, SEQ ID NO: 1014, SEQ ID NO: 1018, SEQ ID NO: 1022, SEQ ID NO: 1026, SEQ ID NO: 1030, SEQ ID NO: 1034, SEQ ID NO: 1038, SEQ ID NO: 1042, SEQ ID NO: 1052, SEQ ID NO: 1056, SEQ ID NO: 1066, SEQ ID NO: 1070, SEQ ID NO: 1080, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1098, SEQ ID NO: 1108, SEQ ID NO: 1112, SEQ ID NO: 1122, SEQ ID NO: 1126, SEQ ID NO: 1136, SEQ ID NO: 1140, SEQ ID NO: 1150, SEQ ID NO: 1154, SEQ ID NO: 1164, SEQ ID NO: 1168, SEQ ID NO: 1178, SEQ ID NO: 1182, SEQ ID NO: 1192, SEQ ID NO: 1196, SEQ ID NO: 1206, SEQ ID NO: 1210, SEQ ID NO: 1220, SEQ ID NO: 1224, SEQ ID NO: 1234, SEQ ID NO: 1238, SEQ ID NO: 1248, SEQ ID NO: 1252, SEQ ID NO: 1262, SEQ ID NO: 1266, SEQ ID NO: 1276, SEQ ID NO: 1280, SEQ ID NO: 1290, SEQ ID NO: 1294, SEQ ID NO: 1304, SEQ ID NO: 1308, SEQ ID NO: 1318, SEQ ID NO: 1322, SEQ ID NO: 1332, SEQ ID NO: 1336, SEQ ID NO: 1346, SEQ ID NO: 1350, SEQ ID NO: 1360, SEQ ID NO: 1364, SEQ ID NO: 1374, SEQ ID NO: 1378, SEQ ID NO: 1388,

SEQ ID NO: 1392, SEQ ID NO: 1402, SEQ ID NO: 1406, SEQ ID NO: 1416, SEQ ID NO: 1420, SEQ ID NO: 1430, SEQ ID NO: 1434, SEQ ID NO: 1444, SEQ ID NO: 1448, SEQ ID NO: 1458, SEQ ID NO: 1462, SEQ ID NO: 1472, SEQ ID NO: 1476, SEQ ID NO: 1486, SEQ ID NO: 1490, SEQ ID NO: 1500, SEQ ID NO: 1504, SEQ ID NO: 1514, SEQ ID NO: 1518, SEQ ID NO: 1528, SEQ ID NO: 1532, SEQ ID NO: 1542, SEQ ID NO: 1546, SEQ ID NO: 1556, SEQ ID NO: 1560, SEQ ID NO: 1570, and SEQ ID NO: 1574; and

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 824; and
- a polypeptide comprising in the following order starting from the N-terminus:
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 835, SEQ ID NO: 844, SEQ ID NO: 853, SEQ ID NO: 862, SEQ ID NO: 871, SEQ ID NO: 880, SEQ ID NO: 889, SEQ ID NO: 898, SEQ ID NO: 907, SEQ ID NO: 916, and SEQ ID NO: 919; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 825; or
- (i) a polypeptide comprising in the following order starting from the N-terminus:
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 89, SEQ ID NO: 99, SEQ ID NO: 109, SEQ ID NO: 119, SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 930, SEQ ID NO: 934, SEQ ID NO: 938, SEQ ID NO: 942, SEQ ID NO: 946, SEQ ID NO: 950,

SEQ ID NO: 954, SEQ ID NO: 958, SEQ ID NO: 962, SEQ ID NO: 966, SEQ ID NO: 970, SEQ ID NO: 974, SEQ ID NO: 978, SEQ ID NO: 982, SEQ ID NO: 986, SEQ ID NO: 990, SEQ ID NO: 994, SEQ ID NO: 998, SEQ ID NO: 1002, SEQ ID NO: 1006, SEQ ID NO: 1010, SEQ ID NO: 1014, SEQ ID NO: 1018, SEQ ID NO: 1022, SEQ ID NO: 1026, SEQ ID NO: 1030, SEQ ID NO: 1034, SEQ ID NO: 1038, SEQ ID NO: 1042, SEQ ID NO: 1052, SEQ ID NO: 1056, SEQ ID NO: 1066, SEQ ID NO: 1070, SEQ ID NO: 1080, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1098, SEQ ID NO: 1108, SEQ ID NO: 1112, SEQ ID NO: 1122, SEQ ID NO: 1126, SEQ ID NO: 1136, SEQ ID NO: 1140, SEQ ID NO: 1150, SEQ ID NO: 1154, SEQ ID NO: 1164, SEQ ID NO: 1168, SEQ ID NO: 1178, SEQ ID NO: 1182, SEQ ID NO: 1192, SEQ ID NO: 1196, SEQ ID NO: 1206, SEQ ID NO: 1210, SEQ ID NO: 1220, SEQ ID NO: 1224, SEQ ID NO: 1234, SEQ ID NO: 1238, SEQ ID NO: 1248, SEQ ID NO: 1252, SEQ ID NO: 1262, SEQ ID NO: 1266, SEQ ID NO: 1276, SEQ ID NO: 1280, SEQ ID NO: 1290, SEQ ID NO: 1294, SEQ ID NO: 1304, SEQ ID NO: 1308, SEQ ID NO: 1318, SEQ ID NO: 1322, SEQ ID NO: 1332, SEQ ID NO: 1336, SEQ ID NO: 1346, SEQ ID NO: 1350, SEQ ID NO: 1360, SEQ ID NO: 1364, SEQ ID NO: 1374, SEQ ID NO: 1378, SEQ ID NO: 1388, SEQ ID NO: 1392, SEQ ID NO: 1402, SEQ ID NO: 1406, SEQ ID NO: 1416, SEQ ID NO: 1420, SEQ ID NO: 1430, SEQ ID NO: 1434, SEQ ID NO: 1444, SEQ ID NO: 1448, SEQ ID NO: 1458, SEQ ID NO: 1462, SEQ ID NO: 1472, SEQ ID NO: 1476, SEQ ID NO: 1486, SEQ ID NO: 1490, SEQ ID NO: 1500, SEQ ID NO: 1504, SEQ ID NO: 1514, SEQ ID NO: 1518, SEQ ID NO: 1528, SEQ ID NO: 1532, SEQ ID NO: 1542, SEQ ID NO: 1546, SEQ ID NO: 1556, SEQ ID NO: 1560, SEQ ID NO: 1570, and SEQ ID NO: 1574;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 770-778;
- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 835, SEQ ID NO: 844, SEQ ID NO: 853, SEQ ID NO: 862, SEQ ID NO: 871, SEQ ID NO: 880, SEQ ID NO: 889, SEQ ID NO: 898, SEQ ID NO: 907, SEQ ID NO: 916, and SEQ ID NO: 919; and
- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 826.

As described above, several preferred antibody constructs of the invention are modified by fusion with another moiety such as albumin or albumin variants. If these fusion constructs are characterized for their properties, such as in particular their target affinity or cytotoxic activity, the skilled person will be aware that similar fusion constructs or unmodified bispecific antibody

constructs can be expected to have similar (or possibly even better) properties. For example, if a bispecific antibody construct fused with albumin has an appreciable or desirable cytotoxic activity or target affinity, it can be expected that the same / similar or even a higher cytotoxic activity / target affinity will be observed for the same construct w/o albumin.

According to another preferred embodiment, the bispecific antibody construct of the invention comprises (in addition to the two binding domains) a third domain which comprises two polypeptide monomers, each comprising a hinge, a CH2 and a CH3 domain, wherein said two polypeptides (or polypeptide monomers) are fused to each other via a peptide linker. Preferably, said third domain comprises in an N- to C-terminal order: hinge-CH2-CH3-linker-hinge-CH2-CH3. Preferred amino acid sequences for said third domain are depicted in SEQ ID NOs: 1856-1863. Each of said polypeptide monomers preferably has an amino acid sequence that is selected from the group consisting of SEQ ID NOs: 1848-1855, or that is at least 90% identical to those sequences. In another preferred embodiment, the first and second binding domains of the bispecific antibody construct of the invention are fused to the third domain via a peptide linker which is for example selected from the group consisting of SEQ ID NOs: 770, 771, 773, 774, 775, 777 and 778.

In line with the present invention, a "hinge" is an IgG hinge region. This region can be identified by analogy using the Kabat numbering, see Kabat positions 223-243. In line with the above, the minimal requirement for a "hinge" are the amino acid residues corresponding to the IgG₁ sequence stretch of D231 to P243 according to the Kabat numbering. The terms CH2 and CH3 refer to the immunoglobulin heavy chain constant regions 2 and 3. These regions can as well be identified by analogy using the Kabat numbering, see Kabat positions 244-360 for CH2 and Kabat positions 361-478 for CH3. It is understood that there is some variation between the immunoglobulins in terms of their IgG₁ Fc region, IgG₂ Fc region, IgG₃ Fc region, IgG₄ Fc region, IgM Fc region, IgA Fc region, IgD Fc region and IgE Fc region (see, e.g., Padlan, *Molecular Immunology*, 31(3), 169-217 (1993)). The term Fc monomer refers to the last two heavy chain constant regions of IgA, IgD, and IgG, and the last three heavy chain constant regions of IgE and IgM. The Fc monomer can also include the flexible hinge N-terminal to these domains. For IgA and IgM, the Fc monomer may include the J chain. For IgG, the Fc portion comprises immunoglobulin domains CH2 and CH3 and the hinge between the first two domains and CH2. Although the boundaries of the Fc portion of an immunoglobulin may vary, an example for a human IgG heavy chain Fc portion comprising a functional hinge, CH2 and CH3 domain can be defined e.g. to comprise residues D231 (of the hinge domain) to P476 (of the C-

terminus of the CH3 domain), or D231 to L476, respectively, for IgG₄, wherein the numbering is according to Kabat.

The antibody construct of the invention may hence comprise in an N- to C-terminal order:

- (a) the first binding domain;
- (b) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 771, 777, and 778;
- (c) the second binding domain;
- (d) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 770, 771, 773, 774, 775, 777 and 778;
- (e) the first polypeptide monomer of the third domain (comprising a hinge, a CH2 and a CH3 domain);
- (f) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1865, 1866, 1867, and 1868; and
- (g) the second polypeptide monomer of the third domain (comprising a hinge, a CH2 and a CH3 domain).

It is also preferred that the antibody construct of the invention comprises in an N- to C-terminal order:

- the first binding domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 9, SEQ ID NO: 19, SEQ ID NO: 29, SEQ ID NO: 39, SEQ ID NO: 49, SEQ ID NO: 59, SEQ ID NO: 69, SEQ ID NO: 79, SEQ ID NO: 89, SEQ ID NO: 99, SEQ ID NO: 109, SEQ ID NO: 119, SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 179, SEQ ID NO: 189, SEQ ID NO: 199, SEQ ID NO: 209, SEQ ID NO: 219, SEQ ID NO: 229, SEQ ID NO: 239, SEQ ID NO: 249, SEQ ID NO: 259, SEQ ID NO: 269, SEQ ID NO: 279, SEQ ID NO: 289, SEQ ID NO: 299, SEQ ID NO: 309, SEQ ID NO: 319, SEQ ID NO: 329, SEQ ID NO: 339, SEQ ID NO: 349, SEQ ID NO: 359, SEQ ID NO: 369, SEQ ID NO: 379, SEQ ID NO: 389, SEQ ID NO: 399, SEQ ID NO: 409, SEQ ID NO: 419, SEQ ID NO: 429, SEQ ID NO: 439, SEQ ID NO: 449, SEQ ID NO: 459, SEQ ID NO: 469, SEQ ID NO: 479, SEQ ID NO: 489, SEQ ID NO: 499, SEQ ID NO: 509, SEQ ID NO: 519, SEQ ID NO: 529, SEQ ID NO: 539, SEQ ID NO: 549, SEQ ID NO: 559, SEQ ID NO: 569, SEQ ID NO: 579, SEQ ID NO: 589, SEQ ID NO: 599, SEQ ID NO: 609, SEQ ID NO: 619, SEQ ID NO: 629, SEQ ID NO: 639, SEQ ID NO: 649, SEQ ID NO: 659, SEQ ID NO: 669, SEQ ID NO: 679, SEQ ID

NO: 689, SEQ ID NO: 699, SEQ ID NO: 709, SEQ ID NO: 719, SEQ ID NO: 729, SEQ ID NO: 739, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 930, SEQ ID NO: 934, SEQ ID NO: 938, SEQ ID NO: 942, SEQ ID NO: 946, SEQ ID NO: 950, SEQ ID NO: 954, SEQ ID NO: 958, SEQ ID NO: 962, SEQ ID NO: 966, SEQ ID NO: 970, SEQ ID NO: 974, SEQ ID NO: 978, SEQ ID NO: 982, SEQ ID NO: 986, SEQ ID NO: 990, SEQ ID NO: 994, SEQ ID NO: 998, SEQ ID NO: 1002, SEQ ID NO: 1006, SEQ ID NO: 1010, SEQ ID NO: 1014, SEQ ID NO: 1018, SEQ ID NO: 1022, SEQ ID NO: 1026, SEQ ID NO: 1030, SEQ ID NO: 1034, SEQ ID NO: 1038, SEQ ID NO: 1042, SEQ ID NO: 1052, SEQ ID NO: 1056, SEQ ID NO: 1066, SEQ ID NO: 1070, SEQ ID NO: 1080, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1098, SEQ ID NO: 1108, SEQ ID NO: 1112, SEQ ID NO: 1122, SEQ ID NO: 1126, SEQ ID NO: 1136, SEQ ID NO: 1140, SEQ ID NO: 1150, SEQ ID NO: 1154, SEQ ID NO: 1164, SEQ ID NO: 1168, SEQ ID NO: 1178, SEQ ID NO: 1182, SEQ ID NO: 1192, SEQ ID NO: 1196, SEQ ID NO: 1206, SEQ ID NO: 1210, SEQ ID NO: 1220, SEQ ID NO: 1224, SEQ ID NO: 1234, SEQ ID NO: 1238, SEQ ID NO: 1248, SEQ ID NO: 1252, SEQ ID NO: 1262, SEQ ID NO: 1266, SEQ ID NO: 1276, SEQ ID NO: 1280, SEQ ID NO: 1290, SEQ ID NO: 1294, SEQ ID NO: 1304, SEQ ID NO: 1308, SEQ ID NO: 1318, SEQ ID NO: 1322, SEQ ID NO: 1332, SEQ ID NO: 1336, SEQ ID NO: 1346, SEQ ID NO: 1350, SEQ ID NO: 1360, SEQ ID NO: 1364, SEQ ID NO: 1374, SEQ ID NO: 1378, SEQ ID NO: 1388, SEQ ID NO: 1392, SEQ ID NO: 1402, SEQ ID NO: 1406, SEQ ID NO: 1416, SEQ ID NO: 1420, SEQ ID NO: 1430, SEQ ID NO: 1434, SEQ ID NO: 1444, SEQ ID NO: 1448, SEQ ID NO: 1458, SEQ ID NO: 1462, SEQ ID NO: 1472, SEQ ID NO: 1476, SEQ ID NO: 1486, SEQ ID NO: 1490, SEQ ID NO: 1500, SEQ ID NO: 1504, SEQ ID NO: 1514, SEQ ID NO: 1518, SEQ ID NO: 1528, SEQ ID NO: 1532, SEQ ID NO: 1542, SEQ ID NO: 1546, SEQ ID NO: 1556, SEQ ID NO: 1560, SEQ ID NO: 1570, and SEQ ID NO: 1574;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 771, 777, and 778;
- the second binding domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 835, SEQ ID NO: 844, SEQ ID NO: 853, SEQ ID NO: 862, SEQ ID NO: 871, SEQ ID NO: 880, SEQ ID NO: 889, SEQ ID NO: 898, SEQ ID NO: 907, SEQ ID NO: 916, and SEQ ID NO: 919;
- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 770, 771, 773, 774, 775, 777 and 778; and

- the third domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1856-1863.

Hence, in a preferred embodiment, the antibody construct of the present invention comprises or consists of a polypeptide selected from the group consisting of those depicted in SEQ ID NOs: 1576-1847. Preferred are those polypeptides selected from the group consisting of those depicted in SEQ ID NO: 1696, SEQ ID NO: 1702, SEQ ID NO: 1710, SEQ ID NO: 1714, SEQ ID NO: 1716, SEQ ID NO: 1720, SEQ ID NO: 1722, SEQ ID NO: 1724, SEQ ID NO: 1726, SEQ ID NO: 1728, SEQ ID NO: 1738, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1750, and SEQ ID NO: 1752.

Covalent modifications of the antibody constructs are also included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the antibody construct are introduced into the molecule by reacting specific amino acid residues of the antibody construct with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

Cysteinyl residues most commonly are reacted with α -haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues also are derivatized by reaction with bromotrifluoroacetone, α -bromo- β -(5-imidazolyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1 M sodium cacodylate at pH 6.0. Lysiny and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysiny residues. Other suitable reagents for derivatizing α -amino-containing residues include imidoesters such as methyl picolinimide; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidazole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using ^{125}I or ^{131}I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides ($\text{R}'\text{—N}=\text{C}=\text{N}\text{—R}'$), where R and R' are optionally different alkyl groups, such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

Derivatization with bifunctional agents is useful for crosslinking the antibody constructs of the present invention to a water-insoluble support matrix or surface for use in a variety of methods. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimide yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates as described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, *Proteins: Structure and Molecular Properties*, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the antibody constructs included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (e.g., the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed below.

Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

Addition of glycosylation sites to the antibody construct is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the amino acid sequence of an antibody construct is preferably altered through changes at the DNA level, particularly by mutating the DNA encoding the polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the antibody construct is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode

used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330, and in Aplin and Wriston, 1981, CRC Crit. Rev. Biochem., pp. 259-306.

Removal of carbohydrate moieties present on the starting antibody construct may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin *et al.*, 1987, *Arch. Biochem. Biophys.* 259:52 and by Edge *et al.*, 1981, *Anal. Biochem.* 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, 1987, *Meth. Enzymol.* 138:350. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin *et al.*, 1982, *J. Biol. Chem.* 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

Other modifications of the antibody construct are also contemplated herein. For example, another type of covalent modification of the antibody construct comprises linking the antibody construct to various non-proteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antibody construct, e.g. in order to facilitate the addition of polymers such as PEG.

In some embodiments, the covalent modification of the antibody constructs of the invention comprises the addition of one or more labels. The labelling group may be coupled to the antibody construct *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and can be used in performing the present invention. The term "label" or "labelling group" refers to any detectable label. In general, labels fall into a variety of classes, depending on the assay in which they are to be detected – the following examples include, but are not limited to:

- a) isotopic labels, which may be radioactive or heavy isotopes, such as radioisotopes or radionuclides (e.g., ^3H , ^{14}C , ^{15}N , ^{35}S , ^{89}Zr , ^{90}Y , ^{99}Tc , ^{111}In , ^{125}I , ^{131}I)
- b) magnetic labels (e.g., magnetic particles)
- c) redox active moieties
- d) optical dyes (including, but not limited to, chromophores, phosphors and fluorophores) such as fluorescent groups (e.g., FITC, rhodamine, lanthanide phosphors), chemiluminescent groups, and fluorophores which can be either “small molecule” fluoeres or proteinaceous fluoeres
- e) enzymatic groups (e.g. horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase)
- f) biotinylated groups
- g) predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.)

By “fluorescent label” is meant any molecule that may be detected *via* its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland.

Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie *et al.*, 1994, *Science* 263:802-805), EGFP (Clontech Laboratories, Inc., Genbank Accession Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998, *Biotechniques* 24:462-471; Heim *et al.*, 1996, *Curr. Biol.* 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki *et al.*, 1993, *J. Immunol.* 150:5408-5417), β galactosidase (Nolan *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:2603-2607) and Renilla

(WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, U.S. Patent Nos. 5,292,658; 5,418,155; 5,683,888; 5,741,668; 5,777,079; 5,804,387; 5,874,304; 5,876,995; 5,925,558).

Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz *et al.*, 1988, *Science* 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe *et al.*, 1994, *FEBS Letters* 344:191. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow *et al.*, 1994, *Semin. Immunol.* 6:267-78. In one approach, recombinant fusion proteins comprising a CD70 antibody fragment or derivative fused to a leucine zipper peptide are expressed in suitable host cells, and the soluble oligomeric CD70 antibody fragments or derivatives that form are recovered from the culture supernatant.

The antibody construct of the invention may also comprise additional domains, which are e.g. helpful in the isolation of the molecule or relate to an adapted pharmacokinetic profile of the molecule. Domains helpful for the isolation of an antibody construct may be selected from peptide motives or secondarily introduced moieties, which can be captured in an isolation method, e.g. an isolation column. Non-limiting embodiments of such additional domains comprise peptide motives known as Myc-tag, HAT-tag, HA-tag, TAP-tag, GST-tag, chitin binding domain (CBD-tag), maltose binding protein (MBP-tag), Flag-tag, Strep-tag and variants thereof (e.g. StrepII-tag) and His-tag. All herein disclosed antibody constructs characterized by the identified CDRs are preferred to comprise a His-tag domain, which is generally known as a repeat of consecutive His residues in the amino acid sequence of a molecule, preferably of five, and more preferably of six His residues (hexa-histidine). The His-tag may be located e.g. at the N- or C-terminus of the antibody construct, preferably it is located at the C-terminus. Most preferably, a hexa-histidine tag (HHHHHH, see SEQ ID NO: 779) is linked via peptide bond to the C-terminus of the antibody construct according to the invention.

The first binding domain of the antibody construct of the present invention binds to human CD70 on the surface of a target cell. The preferred amino acid sequence of human CD70 is

represented by SEQ ID NO: 741. It is understood that the term “on the surface”, in the context of the present invention, means that the binding domain specifically binds to an epitope comprised within the CD70 extracellular domain (CD70 ECD). The first binding domain according to the invention hence preferably binds to CD70 when it is expressed by naturally expressing cells or cell lines, and/or by cells or cell lines transformed or (stably / transiently) transfected with CD70. In a preferred embodiment the first binding domain also binds to CD70 when CD70 is used as a “target” or “ligand” molecule in an *in vitro* binding assay such as BIAcore or Scatchard. The “target cell” can be any prokaryotic or eukaryotic cell expressing CD70 on its surface; preferably the target cell is a cell that is part of the human or animal body, such as a specific cancer cell being selected e.g. from the group consisting of renal, lung, pancreatic, ovarian, breast, colon, or head and neck cancer, melanoma, Kaposi's Sarcoma, embryonal carcinoma, brain tumor, leukemia or lymphoma.

The term “CD70 ECD” refers to a form of CD70 which is essentially free of transmembrane and cytoplasmic domains of CD70. It will be understood by the skilled artisan that the transmembrane domain identified for the CD70 polypeptide of the present invention is identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain specifically mentioned herein. A preferred human CD70 ECD is shown in SEQ ID NO: 742.

The affinity of the first binding domain for human CD70 is preferably ≤ 20 nM or ≤ 15 nM, more preferably ≤ 10 nM, even more preferably ≤ 5 nM, even more preferably ≤ 2 nM, even more preferably ≤ 1 nM, even more preferably ≤ 0.6 nM, even more preferably ≤ 0.5 nM, and most preferably ≤ 0.4 nM. The affinity can be measured for example in a BIAcore assay or in a Scatchard assay, e.g. as described in the Examples. Other methods of determining the affinity are also well-known to the skilled person.

T cells or T lymphocytes are a type of lymphocyte (itself a type of white blood cell) that play a central role in cell-mediated immunity. There are several subsets of T cells, each with a distinct function. T cells can be distinguished from other lymphocytes, such as B cells and NK cells, by the presence of a T cell receptor (TCR) on the cell surface. The TCR is responsible for recognizing antigens bound to major histocompatibility complex (MHC) molecules and is composed of two different protein chains. In 95% of the T cells, the TCR consists of an alpha (α) and beta (β) chain. When the TCR engages with antigenic peptide and MHC (peptide / MHC

complex), the T lymphocyte is activated through a series of biochemical events mediated by associated enzymes, co-receptors, specialized adaptor molecules, and activated or released transcription factors

The CD3 receptor complex is a protein complex and is composed of four chains. In mammals, the complex contains a CD3 γ (gamma) chain, a CD3 δ (delta) chain, and two CD3 ϵ (epsilon) chains. These chains associate with the T cell receptor (TCR) and the so-called ζ (zeta) chain to form the T cell receptor CD3 complex and to generate an activation signal in T lymphocytes. The CD3 γ (gamma), CD3 δ (delta), and CD3 ϵ (epsilon) chains are highly related cell-surface proteins of the immunoglobulin superfamily containing a single extracellular immunoglobulin domain. The intracellular tails of the CD3 molecules contain a single conserved motif known as an immunoreceptor tyrosine-based activation motif or ITAM for short, which is essential for the signaling capacity of the TCR. The CD3 epsilon molecule is a polypeptide which in humans is encoded by the *CD3E* gene which resides on chromosome 11. The most preferred epitope of CD3 epsilon is comprised within amino acid residues 1-27 of the human CD3 epsilon extracellular domain.

The redirected lysis of target cells via the recruitment of T cells by a multispecific, at least bispecific, antibody construct involves cytolytic synapse formation and delivery of perforin and granzymes. The engaged T cells are capable of serial target cell lysis, and are not affected by immune escape mechanisms interfering with peptide antigen processing and presentation, or clonal T cell differentiation; see, for example, WO 2007/042261.

Cytotoxicity mediated by CD70xCD3 bispecific antibody constructs can be measured in various ways. See Examples 8.1 to 8.7. Effector cells can be e.g. stimulated enriched (human) CD8 positive T cells or unstimulated (human) peripheral blood mononuclear cells (PBMC). If the target cells are of macaque origin or express or are transfected with macaque CD70, the effector cells should also be of macaque origin such as a macaque T cell line, e.g. 4119LnPx. The target cells should express (at least the extracellular domain of) CD70, e.g. human or macaque CD70. Target cells can be a cell line (such as CHO) which is stably or transiently transfected with CD70, e.g. human or macaque CD70. Alternatively, the target cells can be a CD70 positive natural expresser cell line, such as the human ovarian carcinoma cell line OVCAR 8. Usually EC50 values are expected to be lower with target cell lines expressing higher levels of CD70 on the cell surface. The effector to target cell (E:T) ratio is usually about 10:1, but can also vary. Cytotoxic activity of CD70xCD3 bispecific antibody constructs can be

measured in a 51-chromium release assay (incubation time of about 18 hours) or in a FACS-based cytotoxicity assay (incubation time of about 48 hours). Modifications of the assay incubation time (cytotoxic reaction) are also possible. Other methods of measuring cytotoxicity are well-known to the skilled person and comprise MTT or MTS assays, ATP-based assays including bioluminescent assays, the sulforhodamine B (SRB) assay, WST assay, clonogenic assay and the ECIS technology.

The cytotoxic activity mediated by CD70xCD3 bispecific antibody constructs of the present invention is preferably measured in a cell-based cytotoxicity assay. It may also be measured in a 51-chromium release assay. It is represented by the EC_{50} value, which corresponds to the half maximal effective concentration (concentration of the antibody construct which induces a cytotoxic response halfway between the baseline and maximum). Preferably, the EC_{50} value of the CD70xCD3 bispecific antibody constructs is ≤ 10.000 pM or ≤ 5000 pM, more preferably ≤ 4000 pM or ≤ 3000 pM, even more preferably ≤ 2000 pM or ≤ 1000 pM, even more preferably ≤ 500 pM or ≤ 400 pM, even more preferably ≤ 300 pM or ≤ 200 pM, even more preferably ≤ 100 pM or ≤ 50 pM, even more preferably ≤ 20 pM or ≤ 10 pM, and most preferably ≤ 5 pM or ≤ 2 pM or ≤ 1 pM, or even ≤ 0.5 pM or ≤ 0.2 pM or ≤ 0.1 pM.

The above given EC_{50} values can be measured in different assays. The skilled person is aware that an EC_{50} value can be expected to be lower when stimulated / enriched CD8⁺ T cells are used as effector cells, compared with unstimulated PBMC. It can furthermore be expected that the EC_{50} values are lower when the target cells express a high number of the target antigen compared with a low target expression rat. For example, when stimulated / enriched human CD8⁺ T cells are used as effector cells (and either CD70 transfected cells such as CHO cells or a CD70 positive cell line are used as target cells), the EC_{50} value of the CD70 xCD3 bispecific antibody construct is preferably ≤ 1000 pM, more preferably ≤ 500 pM, even more preferably ≤ 250 pM, even more preferably ≤ 100 pM, even more preferably ≤ 50 pM, even more preferably ≤ 10 pM, and most preferably ≤ 5 pM or ≤ 2 pM or ≤ 1 pM. When human PBMCs are used as effector cells, the EC_{50} value of the CD70xCD3 bispecific antibody construct is preferably ≤ 10.000 pM or ≤ 5000 pM or ≤ 4000 pM (in particular when the target cells are a CD70 positive cell line), more preferably ≤ 2000 pM (in particular when the target cells are CD70 transfected cells such as CHO cells), more preferably ≤ 1000 pM or ≤ 500 pM, even more preferably ≤ 200 pM, even more preferably ≤ 150 pM, even more preferably ≤ 100 pM, and most preferably ≤ 50 pM or ≤ 20 pM, or lower. When a macaque T cell line such as LnPx4119 is used as effector cells, and a macaque CD70 transfected cell line such as CHO cells is used as target cell line,

the EC₅₀ value of the CD70 xCD3 bispecific antibody construct is preferably ≤ 2000 pM or ≤ 1500 pM, more preferably ≤ 1000 pM or ≤ 500 pM, even more preferably ≤ 300 pM or ≤ 250 pM, even more preferably ≤ 100 pM, and most preferably ≤ 50 pM or ≤ 20 pM, or lower, such as ≤ 10 pM, ≤ 5 pM, ≤ 1 pM, or ≤ 0.5 pM.

Preferably, the CD70xCD3 bispecific antibody constructs of the present invention do not induce / mediate lysis or do not essentially induce / mediate lysis of CD70 negative cells such as CHO cells. The term “do not induce lysis”, “do not essentially induce lysis”, “do not mediate lysis” or “do not essentially mediate lysis” means that an antibody construct of the present invention does not induce or mediate lysis of more than 30%, preferably not more than 20%, more preferably not more than 10%, particularly preferably not more than 9%, 8%, 7%, 6% or 5% of CD70 negative cells, whereby lysis of a CD70 positive cell line (see above) is set to be 100%. This usually applies for concentrations of the antibody construct of up to 500 nM. The skilled person knows how to measure cell lysis without further ado. Moreover, the present specification teaches specific instructions how to measure cell lysis.

The difference in cytotoxic activity between the monomeric and the dimeric isoform of individual CD70xCD3 bispecific antibody constructs is referred to as “potency gap”. This potency gap can e.g. be calculated as ratio between EC₅₀ values of the molecule’s monomeric and dimeric form, see Example 15. Potency gaps of the CD70xCD3 bispecific antibody constructs of the present invention are preferably ≤ 5 , more preferably ≤ 4 , even more preferably ≤ 3 , even more preferably ≤ 2 or ≤ 1.5 , and most preferably ≤ 1 .

The first and/or the second (or any further) binding domain(s) of the antibody construct of the invention is/are preferably cross-species specific for members of the mammalian order of primates. Cross-species specific CD3 binding domains are, for example, described in WO 2008/119567. According to one embodiment, the first and/or second binding domain, in addition to binding to human CD70 and human CD3, respectively, will also bind to CD70 / CD3 of primates including (but not limited to) new world primates (such as *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus*), old world primates (such as baboons and macaques), gibbons, orangutans, and non-human *homininae*. It is envisaged that the first binding domain of the antibody construct of the invention which binds to human CD70 on the surface of a target cell also binds at least to macaque CD70, and/or the second binding domain which binds to human CD3 on the surface of a T cell also binds at least to macaque CD3. A preferred macaque is *Macaca fascicularis*. *Macaca mulatta* (Rhesus) is also envisaged.

A preferred bispecific antibody construct of the invention comprises a first binding domain which binds to human CD70 on the surface of a target cell and a second binding domain which binds to human CD3 on the surface of a T cell and at least macaque CD3.

In one aspect of the invention, the first binding domain binds to human CD70 and further binds to macaque CD70, such as CD70 of *Macaca fascicularis*, and more preferably, to macaque CD70 ECD. A preferred *Macaca fascicularis* CD70 is depicted in SEQ ID NO: 755. A preferred macaque CD70 ECD is depicted in SEQ ID NO: 756. The affinity of the first binding domain for macaque CD70 is preferably ≤ 50 or ≤ 40 nM, more preferably ≤ 30 nM or ≤ 20 nM or ≤ 15 nM, more preferably ≤ 10 nM or ≤ 5 nM, even more preferably ≤ 2 nM or ≤ 1 nM, even more preferably ≤ 0.5 nM or ≤ 0.2 nM, and most preferably ≤ 0.1 nM.

Preferably the affinity gap of the antibody constructs according to the invention for binding macaque CD70 versus human CD70 [ma CD70:hu CD70] (as determined e.g. by BiaCore or by Scatchard analysis) is between 0.1 and 10, more preferably between 0.2 and 5 or between 0.2 and 2, even more preferably between 0.3 and 4, even more preferably between 0.5 and 3 or between 0.5 and 2.5, and most preferably between 0.5 and 2 or between 0.6 and 2. See Examples 3 and 4.

In one embodiment of the antibody construct of the invention, the second binding domain binds to human CD3 epsilon and to *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus* CD3 epsilon. Preferably, the second binding domain binds to an extracellular epitope of these CD3 epsilon chains. It is also envisaged that the second binding domain binds to an extracellular epitope of the human and the *Macaca* CD3 epsilon chain. The most preferred epitope of CD3 epsilon is comprised within amino acid residues 1-27 of the human CD3 epsilon extracellular domain. Even more specifically, the epitope comprises at least the amino acid sequence Gln-Asp-Gly-Asn-Glu. *Callithrix jacchus* and *Saguinus oedipus* are both new world primate belonging to the family of *Callitrichidae*, while *Saimiri sciureus* is a new world primate belonging to the family of *Cebidae*.

It is particularly preferred for the antibody construct of the present invention that the second binding domain which binds to human CD3 on the surface of a T cell comprises a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from:

- (a) CDR-L1 as depicted in SEQ ID NO: 27 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 28 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 29 of WO 2008/119567;
- (b) CDR-L1 as depicted in SEQ ID NO: 117 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 118 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 119 of WO 2008/119567; and
- (c) CDR-L1 as depicted in SEQ ID NO: 153 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 154 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 155 of WO 2008/119567.

In an alternatively preferred embodiment of the antibody construct of the present invention, the second binding domain which binds to human CD3 on the surface of a T cell comprises a VH region comprising CDR-H 1, CDR-H2 and CDR-H3 selected from:

- (a) CDR-H1 as depicted in SEQ ID NO: 12 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 13 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 14 of WO 2008/119567;
- (b) CDR-H1 as depicted in SEQ ID NO: 30 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 31 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 32 of WO 2008/119567;
- (c) CDR-H1 as depicted in SEQ ID NO: 48 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 49 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 50 of WO 2008/119567;
- (d) CDR-H1 as depicted in SEQ ID NO: 66 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 67 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 68 of WO 2008/119567;
- (e) CDR-H1 as depicted in SEQ ID NO: 84 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 85 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 86 of WO 2008/119567;
- (f) CDR-H1 as depicted in SEQ ID NO: 102 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 103 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 104 of WO 2008/119567;
- (g) CDR-H1 as depicted in SEQ ID NO: 120 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 121 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 122 of WO 2008/119567;

- (h) CDR-H1 as depicted in SEQ ID NO: 138 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 139 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 140 of WO 2008/119567;
- (i) CDR-H1 as depicted in SEQ ID NO: 156 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 157 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 158 of WO 2008/119567; and
- (j) CDR-H1 as depicted in SEQ ID NO: 174 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 175 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 176 of WO 2008/119567.

It is further preferred for the antibody construct of the present invention that the second binding domain which binds to human CD3 on the surface of a T cell comprises a VL region selected from the group consisting of a VL region as depicted in SEQ ID NO: 35, 39, 125, 129, 161 or 165 of WO 2008/119567.

It is alternatively preferred that the second binding domain which binds to human CD3 on the surface of a T cell comprises a VH region selected from the group consisting of a VH region as depicted in SEQ ID NO: 15, 19, 33, 37, 51, 55, 69, 73, 87, 91, 105, 109, 123, 127, 141, 145, 159, 163, 177 or 181 of WO 2008/119567.

More preferably, the antibody construct of the present invention is characterized by the second binding domain which binds to human CD3 on the surface of a T cell comprising a VL region and a VH region selected from the group consisting of:

- (a) a VL region as depicted in SEQ ID NO: 17 or 21 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 15 or 19 of WO 2008/119567;
- (b) a VL region as depicted in SEQ ID NO: 35 or 39 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 33 or 37 of WO 2008/119567;
- (c) a VL region as depicted in SEQ ID NO: 53 or 57 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 51 or 55 of WO 2008/119567;
- (d) a VL region as depicted in SEQ ID NO: 71 or 75 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 69 or 73 of WO 2008/119567;
- (e) a VL region as depicted in SEQ ID NO: 89 or 93 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 87 or 91 of WO 2008/119567;
- (f) a VL region as depicted in SEQ ID NO: 107 or 111 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 105 or 109 of WO 2008/119567;

- (g) a VL region as depicted in SEQ ID NO: 125 or 129 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 123 or 127 of WO 2008/119567;
- (h) a VL region as depicted in SEQ ID NO: 143 or 147 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 141 or 145 of WO 2008/119567;
- (i) a VL region as depicted in SEQ ID NO: 161 or 165 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 159 or 163 of WO 2008/119567; and
- (j) a VL region as depicted in SEQ ID NO: 179 or 183 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 177 or 181 of WO 2008/119567.

According to a preferred embodiment of the antibody construct of the present invention, the binding domains and in particular the second binding domain (which binds to human CD3 on the surface of a T cell) have the following format: The pairs of VH regions and VL regions are in the format of a single chain antibody (scFv). The VH and VL regions are arranged in the order VH-VL or VL-VH. It is preferred that the VH-region is positioned N-terminally of a linker sequence, and the VL-region is positioned C-terminally of the linker sequence.

A preferred embodiment of the above described antibody construct of the present invention is characterized by the second binding domain which binds to human CD3 on the surface of a T cell comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 23, 25, 41, 43, 59, 61, 77, 79, 95, 97, 113, 115, 131, 133, 149, 151, 167, 169, 185 or 187 of WO 2008/119567.

Hence, in one embodiment, the antibody construct of the invention comprises a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 10, SEQ ID NO: 20, SEQ ID NO: 30, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 60, SEQ ID NO: 70, SEQ ID NO: 80, SEQ ID NO: 90, SEQ ID NO: 100, SEQ ID NO: 110, SEQ ID NO: 120, SEQ ID NO: 130, SEQ ID NO: 140, SEQ ID NO: 150, SEQ ID NO: 160, SEQ ID NO: 170, SEQ ID NO: 180, SEQ ID NO: 190, SEQ ID NO: 200, SEQ ID NO: 210, SEQ ID NO: 220, SEQ ID NO: 230, SEQ ID NO: 240, SEQ ID NO: 250, SEQ ID NO: 260, SEQ ID NO: 270, SEQ ID NO: 280, SEQ ID NO: 290, SEQ ID NO: 300, SEQ ID NO: 310, SEQ ID NO: 320, SEQ ID NO: 330, SEQ ID NO: 340, SEQ ID NO: 350, SEQ ID NO: 360, SEQ ID NO: 370, SEQ ID NO: 380, SEQ ID NO: 390, SEQ ID NO: 400, SEQ ID NO: 410, SEQ ID NO: 420, SEQ ID NO: 430, SEQ ID NO: 440, SEQ ID NO: 450, SEQ ID NO: 460, SEQ ID NO: 470, SEQ ID NO: 480, SEQ ID NO: 490, SEQ ID NO: 500, SEQ ID NO: 510, SEQ ID NO: 520, SEQ ID NO: 530, SEQ ID NO: 540, SEQ ID NO: 550, SEQ ID NO: 560, SEQ ID NO: 570, SEQ ID

NO: 580, SEQ ID NO: 590, SEQ ID NO: 600, SEQ ID NO: 610, SEQ ID NO: 620, SEQ ID NO: 630, SEQ ID NO: 640, SEQ ID NO: 650, SEQ ID NO: 660, SEQ ID NO: 670, SEQ ID NO: 680, SEQ ID NO: 690, SEQ ID NO: 700, SEQ ID NO: 710, SEQ ID NO: 720, SEQ ID NO: 730, SEQ ID NO: 740, SEQ ID NO: 923, SEQ ID NO: 927, SEQ ID NO: 931, SEQ ID NO: 935, SEQ ID NO: 939, SEQ ID NO: 943, SEQ ID NO: 947, SEQ ID NO: 951, SEQ ID NO: 955, SEQ ID NO: 959, SEQ ID NO: 963, SEQ ID NO: 967, SEQ ID NO: 971, SEQ ID NO: 975, SEQ ID NO: 979, SEQ ID NO: 983, SEQ ID NO: 987, SEQ ID NO: 991, SEQ ID NO: 995, SEQ ID NO: 999, SEQ ID NO: 1003, SEQ ID NO: 1007, SEQ ID NO: 1011, SEQ ID NO: 1015, SEQ ID NO: 1019, SEQ ID NO: 1023, SEQ ID NO: 1027, SEQ ID NO: 1031, SEQ ID NO: 1035, SEQ ID NO: 1039, SEQ ID NO: 1043, SEQ ID NO: 1053, SEQ ID NO: 1057, SEQ ID NO: 1067, SEQ ID NO: 1071, SEQ ID NO: 1081, SEQ ID NO: 1085, SEQ ID NO: 1095, SEQ ID NO: 1099, SEQ ID NO: 1109, SEQ ID NO: 1113, SEQ ID NO: 1123, SEQ ID NO: 1127, SEQ ID NO: 1137, SEQ ID NO: 1141, SEQ ID NO: 1151, SEQ ID NO: 1155, SEQ ID NO: 1165, SEQ ID NO: 1169, SEQ ID NO: 1179, SEQ ID NO: 1183, SEQ ID NO: 1193, SEQ ID NO: 1197, SEQ ID NO: 1207, SEQ ID NO: 1211, SEQ ID NO: 1221, SEQ ID NO: 1225, SEQ ID NO: 1235, SEQ ID NO: 1239, SEQ ID NO: 1249, SEQ ID NO: 1253, SEQ ID NO: 1263, SEQ ID NO: 1267, SEQ ID NO: 1277, SEQ ID NO: 1281, SEQ ID NO: 1291, SEQ ID NO: 1295, SEQ ID NO: 1305, SEQ ID NO: 1309, SEQ ID NO: 1319, SEQ ID NO: 1323, SEQ ID NO: 1333, SEQ ID NO: 1337, SEQ ID NO: 1347, SEQ ID NO: 1351, SEQ ID NO: 1361, SEQ ID NO: 1365, SEQ ID NO: 1375, SEQ ID NO: 1379, SEQ ID NO: 1389, SEQ ID NO: 1393, SEQ ID NO: 1403, SEQ ID NO: 1407, SEQ ID NO: 1417, SEQ ID NO: 1421, SEQ ID NO: 1431, SEQ ID NO: 1435, SEQ ID NO: 1445, SEQ ID NO: 1449, SEQ ID NO: 1459, SEQ ID NO: 1463, SEQ ID NO: 1473, SEQ ID NO: 1477, SEQ ID NO: 1487, SEQ ID NO: 1491, SEQ ID NO: 1501, SEQ ID NO: 1505, SEQ ID NO: 1515, SEQ ID NO: 1519, SEQ ID NO: 1529, SEQ ID NO: 1533, SEQ ID NO: 1543, SEQ ID NO: 1547, SEQ ID NO: 1557, SEQ ID NO: 1561, SEQ ID NO: 1571, and SEQ ID NO: 1575.

Preferred is when the antibody construct of the invention comprises a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 1053, SEQ ID NO: 1095, SEQ ID NO: 1151, SEQ ID NO: 1179, SEQ ID NO: 1193, SEQ ID NO: 1221, SEQ ID NO: 1235, SEQ ID NO: 1249, SEQ ID NO: 1263, SEQ ID NO: 1277, SEQ ID NO: 1347, SEQ ID NO: 1361, SEQ ID NO: 1375, SEQ ID NO: 1431, and SEQ ID NO: 1445.

Amino acid sequence modifications of the antibody constructs described herein are also contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody construct. Amino acid sequence variants of the antibody

constructs are prepared by introducing appropriate nucleotide changes into the antibody constructs nucleic acid, or by peptide synthesis. All of the below described amino acid sequence modifications should result in an antibody construct which still retains the desired biological activity (binding to CD70 and to CD3) of the unmodified parental molecule.

The term “amino acid” or “amino acid residue” typically refers to an amino acid having its art recognized definition such as an amino acid selected from the group consisting of: alanine (Ala or A); arginine (Arg or R); asparagine (Asn or N); aspartic acid (Asp or D); cysteine (Cys or C); glutamine (Gln or Q); glutamic acid (Glu or E); glycine (Gly or G); histidine (His or H); isoleucine (Ile or I); leucine (Leu or L); lysine (Lys or K); methionine (Met or M); phenylalanine (Phe or F); proline (Pro or P); serine (Ser or S); threonine (Thr or T); tryptophan (Trp or W); tyrosine (Tyr or Y); and valine (Val or V), although modified, synthetic, or rare amino acids may be used as desired. Generally, amino acids can be grouped as having a nonpolar side chain (e.g., Ala, Cys, Ile, Leu, Met, Phe, Pro, Val); a negatively charged side chain (e.g., Asp, Glu); a positively charged side chain (e.g., Arg, His, Lys); or an uncharged polar side chain (e.g., Asn, Cys, Gln, Gly, His, Met, Phe, Ser, Thr, Trp, and Tyr).

Amino acid modifications include, for example, deletions from, and/or insertions into, and/or substitutions of, residues within the amino acid sequences of the antibody constructs. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the antibody constructs, such as changing the number or position of glycosylation sites.

For example, 1, 2, 3, 4, 5, or 6 amino acids may be inserted or deleted in each of the CDRs (of course, dependent on their length), while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 amino acids may be inserted or deleted in each of the FRs. Preferably, amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 residues to polypeptides containing a hundred or more residues, as well as intra-sequence insertions of single or multiple amino acid residues. An insertional variant of the antibody construct of the invention includes the fusion to the N-terminus or to the C-terminus of the antibody construct of an enzyme or the fusion to a polypeptide which increases the serum half-life of the antibody construct.

The sites of greatest interest for substitutional mutagenesis include the CDRs of the heavy and/or light chain, in particular the hypervariable regions, but FR alterations in the heavy and/or light chain are also contemplated. The substitutions are preferably conservative substitutions as described herein. Preferably, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids may be substituted in a CDR, while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 amino acids may be substituted in the framework regions (FRs), depending on the length of the CDR or FR. For example, if a CDR sequence encompasses 6 amino acids, it is envisaged that one, two or three of these amino acids are substituted. Similarly, if a CDR sequence encompasses 15 amino acids it is envisaged that one, two, three, four, five or six of these amino acids are substituted.

A useful method for identification of certain residues or regions of the antibody constructs that are preferred locations for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells in *Science*, 244: 1081-1085 (1989). Here, a residue or group of target residues within the antibody construct is/are identified (e.g. charged residues such as arg, asp, his, lys, and glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids with the epitope.

Those amino acid locations demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at, or for, the sites of substitution. Thus, while the site or region for introducing an amino acid sequence variation is predetermined, the nature of the mutation *per se* needs not to be predetermined. For example, to analyze or optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at a target codon or region, and the expressed antibody construct variants are screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in the DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of antigen binding activities, such as CD70 or CD3 binding.

Generally, if amino acids are substituted in one or more or all of the CDRs of the heavy and/or light chain, it is preferred that the then-obtained "substituted" sequence is at least 60% or 65%, more preferably 70% or 75%, even more preferably 80% or 85%, and particularly preferably 90% or 95% identical to the "original" CDR sequence. This means that it is dependent of the length of the CDR to which degree it is identical to the "substituted" sequence. For example, a CDR having 5 amino acids is preferably 80% identical to its substituted sequence in order to

have at least one amino acid substituted. Accordingly, the CDRs of the antibody construct may have different degrees of identity to their substituted sequences, e.g., CDRL1 may have 80%, while CDRL3 may have 90%.

Preferred substitutions (or replacements) are conservative substitutions. However, any substitution (including non-conservative substitution or one or more from the "exemplary substitutions" listed in Table 3, below) is envisaged as long as the antibody construct retains its capability to bind to CD70 via the first binding domain and to CD3 or CD3 epsilon via the second binding domain and/or its CDRs have an identity to the then substituted sequence (at least 60% or 65%, more preferably 70% or 75%, even more preferably 80% or 85%, and particularly preferably 90% or 95% identical to the "original" CDR sequence).

Conservative substitutions are shown in Table 3 under the heading of "preferred substitutions". If such substitutions result in a change in biological activity, then more substantial changes, denominated "exemplary substitutions" in Table 3, or as further described below in reference to amino acid classes, may be introduced and the products screened for a desired characteristic.

Table 3: Amino acid substitutions

Original	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val, leu, ile	val
Arg (R)	lys, gln, asn	lys
Asn (N)	gln, his, asp, lys, arg	gln
Asp (D)	glu, asn	glu
Cys (C)	ser, ala	ser
Gln (Q)	asn, glu	asn
Glu (E)	asp, gln	asp
Gly (G)	Ala	ala
His (H)	asn, gln, lys, arg	arg
Ile (I)	leu, val, met, ala, phe	leu
Leu (L)	norleucine, ile, val, met, ala	ile
Lys (K)	arg, gln, asn	arg
Met (M)	leu, phe, ile	leu
Phe (F)	leu, val, ile, ala, tyr	tyr
Pro (P)	Ala	ala

Ser (S)	Thr	thr
Thr (T)	Ser	ser
Trp (W)	tyr, phe	tyr
Tyr (Y)	trp, phe, thr, ser	phe
Val (V)	ile, leu, met, phe, ala	leu

Substantial modifications in the biological properties of the antibody construct of the present invention are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties: (1) hydrophobic: norleucine, met, ala, val, leu, ile; (2) neutral hydrophilic: cys, ser, thr; (3) acidic: asp, glu; (4) basic: asn, gin, his, lys, arg; (5) residues that influence chain orientation: gly, pro; and (6) aromatic : trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Any cysteine residue not involved in maintaining the proper conformation of the antibody construct may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the antibody to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

For amino acid sequences, sequence identity and/or similarity is determined by using standard techniques known in the art, including, but not limited to, the local sequence identity algorithm of Smith and Waterman, 1981, *Adv. Appl. Math.* 2:482, the sequence identity alignment algorithm of Needleman and Wunsch, 1970, *J. Mol. Biol.* 48:443, the search for similarity method of Pearson and Lipman, 1988, *Proc. Nat. Acad. Sci. U.S.A.* 85:2444, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.), the Best Fit sequence program described by Devereux *et al.*, 1984, *Nucl. Acid Res.* 12:387-395, preferably using the default settings, or by inspection. Preferably, percent identity is calculated by FastDB based upon the following parameters: mismatch penalty of 1; gap penalty of 1; gap size penalty of 0.33; and joining penalty of 30, "Current Methods in Sequence Comparison and

Analysis," *Macromolecule Sequencing and Synthesis, Selected Methods and Applications*, pp 127-149 (1988), Alan R. Liss, Inc.

An example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, 1987, *J. Mol. Evol.* 35:351-360; the method is similar to that described by Higgins and Sharp, 1989, *CABIOS* 5:151-153. Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in: Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1997, *Nucleic Acids Res.* 25:3389-3402; and Karin *et al.*, 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90:5873-5787. A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul *et al.*, 1996, *Methods in Enzymology* 266:460-480. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity.

An additional useful algorithm is gapped BLAST as reported by Altschul *et al.*, 1993, *Nucl. Acids Res.* 25:3389-3402. Gapped BLAST uses BLOSUM-62 substitution scores; threshold T parameter set to 9; the two-hit method to trigger ungapped extensions, charges gap lengths of k a cost of 10+k; Xu set to 16, and Xg set to 40 for database search stage and to 67 for the output stage of the algorithms. Gapped alignments are triggered by a score corresponding to about 22 bits.

Generally, the amino acid homology, similarity, or identity between individual variant CDRs are at least 60% to the sequences depicted herein, and more typically with preferably increasing homologies or identities of at least 65% or 70%, more preferably at least 75% or 80%, even more preferably at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, and almost 100%. In a similar manner, "percent (%) nucleic acid sequence identity" with respect to the nucleic acid sequence of the binding proteins identified herein is defined as the percentage

of nucleotide residues in a candidate sequence that are identical with the nucleotide residues in the coding sequence of the antibody construct. A specific method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

Generally, the nucleic acid sequence homology, similarity, or identity between the nucleotide sequences encoding individual variant CDRs and the nucleotide sequences depicted herein are at least 60%, and more typically with preferably increasing homologies or identities of at least 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, and almost 100%. Thus, a “variant CDR” is one with the specified homology, similarity, or identity to the parent CDR of the invention, and shares biological function, including, but not limited to, at least 60%, 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the specificity and/or activity of the parent CDR.

In one embodiment, the percentage of identity to human germline of the antibody constructs according to the invention is $\geq 70\%$ or $\geq 75\%$, more preferably $\geq 80\%$ or $\geq 85\%$, even more preferably $\geq 90\%$, and most preferably $\geq 91\%$, $\geq 92\%$, $\geq 93\%$, $\geq 94\%$, $\geq 95\%$ or even $\geq 96\%$, $\geq 97\%$ or $\geq 98\%$. See Example 7. Identity to human antibody germline gene products is thought to be an important feature to reduce the risk of therapeutic proteins to elicit an immune response against the drug in the patient during treatment. Hwang & Foote (“Immunogenicity of engineered antibodies”; Methods 36 (2005) 3-10) demonstrate that the reduction of non-human portions of drug antibody constructs leads to a decrease of risk to induce anti-drug antibodies in the patients during treatment. By comparing an exhaustive number of clinically evaluated antibody drugs and the respective immunogenicity data, the trend is shown that humanization of the V-regions of antibodies makes the protein less immunogenic (average 5.1 % of patients) than antibodies carrying unaltered non-human V regions (average 23.59 % of patients). A higher degree of identity to human sequences is hence desirable for V-region based protein therapeutics in the form of antibody constructs. For this purpose of determining the germline identity, the V-regions of VL can be aligned with the amino acid sequences of human germline V segments and J segments (<http://vbase.mrc-cpe.cam.ac.uk/>) using Vector NTI software and the amino acid sequence calculated by dividing the identical amino acid residues by the total number of amino acid residues of the VL in percent. The same can be done for the VH segments (<http://vbase.mrc-cpe.cam.ac.uk/>) with the exception that the VH CDR3 may be excluded due to its high diversity and a lack of existing human germline VH CDR3 alignment

partners. Recombinant techniques can then be used to increase sequence identity to human antibody germline genes.

In a further embodiment, the bispecific antibody constructs of the present invention exhibit high monomer yields under standard research scale conditions, *e.g.*, in a standard two-step purification process. Preferably the monomer yield of the antibody constructs according to the invention is ≥ 0.25 mg/L supernatant, more preferably ≥ 0.5 mg/L, even more preferably ≥ 1 mg/L, and most preferably ≥ 2.5 mg/L supernatant.

Likewise, the yield of the dimeric antibody construct isoforms and hence the monomer percentage (*i.e.*, monomer : (monomer+dimer)) of the antibody constructs can be determined. The productivity of monomeric and dimeric antibody constructs and the calculated monomer percentage can *e.g.* be obtained in the SEC purification step of culture supernatant from standardized research-scale production in roller bottles. In one embodiment, the monomer percentage of the antibody constructs is $\geq 80\%$, more preferably $\geq 85\%$, even more preferably $\geq 90\%$, and most preferably $\geq 95\%$.

In one embodiment, the antibody constructs have a preferred plasma stability (ratio of EC50 with plasma to EC50 w/o plasma) of ≤ 8 or ≤ 7 or ≤ 6 , more preferably ≤ 5 or ≤ 4 , more preferably ≤ 3.5 or ≤ 3 , even more preferably ≤ 2.5 or ≤ 2 , and most preferably ≤ 1.5 or ≤ 1 . The plasma stability of an antibody construct can be tested by incubation of the construct in human plasma at 37°C for 24 hours followed by EC50 determination in a 51-chromium release cytotoxicity assay. The effector cells in the cytotoxicity assay can be stimulated enriched human CD8 positive T cells. Target cells can *e.g.* be CHO cells transfected with human CD70. The effector to target cell (E:T) ratio can be chosen as 10:1. The human plasma pool used for this purpose is derived from the blood of healthy donors collected by EDTA coated syringes. Cellular components are removed by centrifugation and the upper plasma phase is collected and subsequently pooled. As control, antibody constructs are diluted immediately prior to the cytotoxicity assay in RPMI-1640 medium. The plasma stability is calculated as ratio of EC50 (after plasma incubation) to EC50 (control). See Example 11.

It is furthermore preferred that the monomer to dimer conversion of antibody constructs of the invention is low. The conversion can be measured under different conditions and analyzed by high performance size exclusion chromatography. See Example 9. For example, incubation of the monomeric isoforms of the antibody constructs can be carried out for 7 days at 37°C and

concentrations of e.g. 100 µg/ml or 250 µg/ml in an incubator. Under these conditions, it is preferred that the antibody constructs of the invention show a dimer percentage that is $\leq 5\%$, more preferably $\leq 4\%$, even more preferably $\leq 3\%$, even more preferably $\leq 2.5\%$, even more preferably $\leq 2\%$, even more preferably $\leq 1.5\%$, and most preferably $\leq 1\%$, $\leq 0.6\%$, or $\leq 0.5\%$, $\leq 0.3\%$ or even 0% .

It is also preferred that the bispecific antibody constructs of the present invention present with very low dimer conversion after a number of freeze/thaw cycles. For example, the antibody construct monomer is adjusted to a concentration of 250 µg/ml e.g. in generic formulation buffer and subjected to three freeze/thaw cycles (freezing at -80°C for 30 min followed by thawing for 30 min at room temperature), followed by high performance SEC to determine the percentage of initially monomeric antibody construct, which had been converted into dimeric antibody construct. Preferably the dimer percentages of the bispecific antibody constructs are $\leq 5\%$, more preferably $\leq 4\%$, even more preferably $\leq 3\%$, even more preferably $\leq 2.5\%$, even more preferably $\leq 2\%$, even more preferably $\leq 1.5\%$, and most preferably $\leq 1\%$ or even $\leq 0.5\%$ or 0% , for example after three freeze/thaw cycles.

The bispecific antibody constructs of the present invention preferably show a favorable thermostability with aggregation temperatures $\geq 45^{\circ}\text{C}$ or $\geq 50^{\circ}\text{C}$, more preferably $\geq 52^{\circ}\text{C}$ or $\geq 54^{\circ}\text{C}$, even more preferably $\geq 56^{\circ}\text{C}$ or $\geq 57^{\circ}\text{C}$, and most preferably $\geq 58^{\circ}\text{C}$ or $\geq 59^{\circ}\text{C}$ or $\geq 60^{\circ}\text{C}$. The thermostability parameter can be determined in terms of antibody aggregation temperature as follows: Antibody solution at a concentration 250 µg/ml is transferred into a single use cuvette and placed in a Dynamic Light Scattering (DLS) device. The sample is heated from 40°C to 70°C at a heating rate of $0.5^{\circ}\text{C}/\text{min}$ with constant acquisition of the measured radius. Increase of radius indicating melting of the protein and aggregation is used to calculate the aggregation temperature of the antibody. See Example 10.

Alternatively, temperature melting curves can be determined by Differential Scanning Calorimetry (DSC) to determine intrinsic biophysical protein stabilities of the antibody constructs. These experiments are performed using a MicroCal LLC (Northampton, MA, U.S.A) VP-DSC device. The energy uptake of a sample containing an antibody construct is recorded from 20°C to 90°C compared to a sample containing only the formulation buffer. The antibody constructs are adjusted to a final concentration of 250 µg/ml e.g. in SEC running buffer. For recording of the respective melting curve, the overall sample temperature is increased stepwise. At each temperature T energy uptake of the sample and the formulation buffer reference is

recorded. The difference in energy uptake C_p (kcal/mole/°C) of the sample minus the reference is plotted against the respective temperature. The melting temperature is defined as the temperature at the first maximum of energy uptake.

It is furthermore envisaged that the CD70xCD3 bispecific antibody constructs of the invention do not cross-react with (*i.e.*, do not essentially bind to) the human CD70 paralogue CD40L. Furthermore, it is envisaged that the CD70xCD3 bispecific antibody constructs of the invention do not cross-react with (*i.e.*, do not essentially bind to) the macaque / cyno CD70 paralogue CD40L. See Example 6.

It is furthermore envisaged that the binding of the first binding domain of the antibody constructs of the invention to human CD70 is reduced by the presence of soluble CD27 by $\leq 25\%$, preferably $\leq 20\%$, more preferably $\leq 15\%$, more preferably $\leq 10\%$, even more preferably $\leq 5\%$, and most preferably $\leq 2\%$. It is envisaged that the concentration of CD27 in this context is physiological, *e.g.*, between about 100 and about 500 pg/ml, or even higher, *e.g.*, up to 1 $\mu\text{g/ml}$. For details of the assay see Example 16.

The CD70xCD3 bispecific antibody constructs of the invention are also envisaged to have a turbidity (as measured by OD340 after concentration of purified monomeric antibody construct to 2.5 mg/ml and over night incubation) of ≤ 0.2 , preferably of ≤ 0.15 , more preferably of ≤ 0.12 , even more preferably of ≤ 0.1 , and most preferably of ≤ 0.08 or ≤ 0.05 . See Example 12.

The CD70xCD3 bispecific antibody constructs of the invention are also envisaged to not be internalized or to not undergo significant internalization by the target cell. Changes in the potency of the CD70xCD3 bispecific antibody construct as a function of preincubation of the construct on the target cells in the absence of T cells can be measured. If the antibody construct is internalized, it should undergo lysosomal degradation. The effective concentration should decrease with time, and thus the apparent potency should decrease as well. The effect is observed with other targets, for which this is a known phenomenon.

The rate of internalization can be assayed *e.g.* as follows: T cells are counted and diluted to a concentration of 1×10^5 / ml in assay media. CD70 positive (*e.g.* natural expresser) cells are counted and plated at 2500 cells per well (cpw). The antibody construct is diluted serially 1:2, at a starting concentration of 100 nM. The antibody construct is added to the culture assay plates to allow for 0 hours, 1 hour or 2 hours of incubation prior to addition of the T cells. Then the

T cells are plated at 25000 cpw, and the assay is incubated for 48 hours at 37°C. Target cell survival is analyzed e.g. with the Steady-Glo® system (25 µl/well). Preferably, the internalization rate is $\leq 20\%$ after a 2 hour (pre-)incubation of the antibody construct with the target cell, more preferably $\leq 15\%$, even more preferably $\leq 10\%$, and most preferably $\leq 5\%$.

In a further embodiment the antibody construct according to the invention is stable at acidic pH. The more tolerant the antibody construct behaves at unphysiologic pH such as pH 5.5 (a pH which is required to run e.g. a cation exchange chromatography), the higher is the recovery of the antibody construct eluted from an ion exchange column relative to the total amount of loaded protein. Recovery of the antibody construct from an ion (e.g., cation) exchange column at pH 5.5 is preferably $\geq 50\%$, more preferably $\geq 60\%$ or $\geq 65\%$, even more preferably $\geq 70\%$ or $\geq 72\%$ or $\geq 74\%$ or $\geq 76\%$ or $\geq 78\%$, even more preferably $\geq 80\%$, even more preferably $\geq 90\%$, even more preferably $\geq 95\%$, and most preferably $\geq 99\%$. See Example 13.

It is furthermore envisaged that the bispecific antibody constructs of the present invention exhibit therapeutic efficacy or anti-tumor activity. This can e.g. be assessed in a study as disclosed in the following example of an advanced stage human tumor xenograft model:

On day 1 of the study, 5×10^6 cells of a human CD70 positive cancer cell line are subcutaneously injected in the right dorsal flank of female NOD/SCID mice. When the mean tumor volume reaches about 100 mm^3 , in vitro expanded human CD3 positive T cells are transplanted into the mice by injection of about 2×10^7 cells into the peritoneal cavity of the animals. Mice of vehicle control group 1 do not receive effector cells and are used as an untransplanted control for comparison with vehicle control group 2 (receiving effector cells) to monitor the impact of T cells alone on tumor growth. The antibody treatment starts when the mean tumor volume reaches about 200 mm^3 . The mean tumor size of each treatment group on the day of treatment start should not be statistically different from any other group (analysis of variance). Mice are treated with 0.5 mg/kg/day of a CD70xCD3 bispecific antibody construct by intravenous bolus injection for about 15 to 20 days. Tumors are measured by caliper during the study and progress evaluated by intergroup comparison of tumor volumes (TV). The tumor growth inhibition T/C [%] is determined by calculating TV as $T/C\% = 100 \times (\text{median TV of analyzed group}) / (\text{median TV of control group 2})$.

The skilled person knows how to modify or adapt certain parameters of this study, such as the number of injected tumor cells, the site of injection, the number of transplanted human T cells,

the amount of bispecific antibody constructs to be administered, and the timelines, while still arriving at a meaningful and reproducible result. Preferably, the tumor growth inhibition T/C [%] is ≤ 70 or ≤ 60 , more preferably ≤ 50 or ≤ 40 , even more preferably ≤ 30 or ≤ 20 and most preferably ≤ 10 or ≤ 5 or even ≤ 2.5 .

The invention further provides a polynucleotide / nucleic acid molecule encoding an antibody construct of the invention.

A polynucleotide is a biopolymer composed of 13 or more nucleotide monomers covalently bonded in a chain. DNA (such as cDNA) and RNA (such as mRNA) are examples of polynucleotides with distinct biological function. Nucleotides are organic molecules that serve as the monomers or subunits of nucleic acid molecules like DNA or RNA. The nucleic acid molecule or polynucleotide can be double stranded and single stranded, linear and circular. It is preferably comprised in a vector which is preferably comprised in a host cell. Said host cell is, *e.g.* after transformation or transfection with the vector or the polynucleotide of the invention, capable of expressing the antibody construct. For that purpose the polynucleotide or nucleic acid molecule is operatively linked with control sequences.

The genetic code is the set of rules by which information encoded within genetic material (nucleic acids) is translated into proteins. Biological decoding in living cells is accomplished by the ribosome which links amino acids in an order specified by mRNA, using tRNA molecules to carry amino acids and to read the mRNA three nucleotides at a time. The code defines how sequences of these nucleotide triplets, called codons, specify which amino acid will be added next during protein synthesis. With some exceptions, a three-nucleotide codon in a nucleic acid sequence specifies a single amino acid. Because the vast majority of genes are encoded with exactly the same code, this particular code is often referred to as the canonical or standard genetic code. While the genetic code determines the protein sequence for a given coding region, other genomic regions can influence when and where these proteins are produced.

Furthermore, the invention provides a vector comprising a polynucleotide / nucleic acid molecule of the invention.

A vector is a nucleic acid molecule used as a vehicle to transfer (foreign) genetic material into a cell. The term “vector” encompasses – but is not restricted to – plasmids, viruses, cosmids and artificial chromosomes. In general, engineered vectors comprise an origin of replication, a

multicloning site and a selectable marker. The vector itself is generally a nucleotide sequence, commonly a DNA sequence, that comprises an insert (transgene) and a larger sequence that serves as the “backbone” of the vector. Modern vectors may encompass additional features besides the transgene insert and a backbone: promoter, genetic marker, antibiotic resistance, reporter gene, targeting sequence, protein purification tag. Vectors called expression vectors (expression constructs) specifically are for the expression of the transgene in the target cell, and generally have control sequences.

The term “control sequences” refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

A nucleic acid is “operably linked” when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, “operably linked” means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

“Transfection” is the process of deliberately introducing nucleic acid molecules or polynucleotides (including vectors) into target cells. The term is mostly used for non-viral methods in eukaryotic cells. Transduction is often used to describe virus-mediated transfer of nucleic acid molecules or polynucleotides. Transfection of animal cells typically involves opening transient pores or “holes” in the cell membrane, to allow the uptake of material. Transfection can be carried out using calcium phosphate, by electroporation, by cell squeezing or by mixing a cationic lipid with the material to produce liposomes, which fuse with the cell membrane and deposit their cargo inside.

The term “transformation” is used to describe non-viral transfer of nucleic acid molecules or polynucleotides (including vectors) into bacteria, and also into non-animal eukaryotic cells, including plant cells. Transformation is hence the genetic alteration of a bacterial or non-animal eukaryotic cell resulting from the direct uptake through the cell membrane(s) from its surroundings and subsequent incorporation of exogenous genetic material (nucleic acid molecules). Transformation can be effected by artificial means. For transformation to happen, cells or bacteria must be in a state of competence, which might occur as a time-limited response to environmental conditions such as starvation and cell density.

Moreover, the invention provides a host cell transformed or transfected with the polynucleotide / nucleic acid molecule or with the vector of the invention.

As used herein, the terms “host cell” or “recipient cell” are intended to include any individual cell or cell culture that can be or has/have been recipients of vectors, exogenous nucleic acid molecules, and polynucleotides encoding the antibody construct of the present invention; and/or recipients of the antibody construct itself. The introduction of the respective material into the cell is carried out by way of transformation, transfection and the like. The term “host cell” is also intended to include progeny or potential progeny of a single cell. Because certain modifications may occur in succeeding generations due to either natural, accidental, or deliberate mutation or due to environmental influences, such progeny may not, in fact, be completely identical (in morphology or in genomic or total DNA complement) to the parent cell, but is still included within the scope of the term as used herein. Suitable host cells include prokaryotic or eukaryotic cells, and also include but are not limited to bacteria, yeast cells, fungi cells, plant cells, and animal cells such as insect cells and mammalian cells, e.g., murine, rat, macaque or human.

The antibody construct of the invention can be produced in bacteria. After expression, the antibody construct of the invention is isolated from the *E. coli* cell paste in a soluble fraction and can be purified through, e.g., affinity chromatography and/or size exclusion. Final purification can be carried out similar to the process for purifying antibody expressed e.g., in CHO cells.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for the antibody construct of the invention. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Schizosaccharomyces pombe*, Kluyveromyces hosts such

as *K. lactis*, *K. fragilis* (ATCC 12424), *K. bulgaricus* (ATCC 16045), *K. wickerhamii* (ATCC 24178), *K. waltii* (ATCC 56500), *K. drosophilae* (ATCC 36906), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402 226); *Pichia pastoris* (EP 183 070); *Candida*; *Trichoderma reesei* (EP 244 234); *Neurospora crassa*; *Schwanniomyces* such as *Schwanniomyces occidentalis*; and filamentous fungi such as *Neurospora*, *Penicillium*, *Tolypocladium*, and *Aspergillus* hosts such as *A. nidulans* and *A. niger*.

Suitable host cells for the expression of glycosylated antibody construct of the invention are derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruit fly), and *Bombyx mori* have been identified. A variety of viral strains for transfection are publicly available, e.g., the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

Plant cell cultures of cotton, corn, potato, soybean, petunia, tomato, *Arabidopsis* and tobacco can also be used as hosts. Cloning and expression vectors useful in the production of proteins in plant cell culture are known to those of skill in the art. See e.g. Hiatt *et al.*, *Nature* (1989) 342: 76-78, Owen *et al.* (1992) *Bio/Technology* 10: 790-794, Artsaenko *et al.* (1995) *The Plant J* 8: 745-750, and Fecker *et al.* (1996) *Plant Mol Biol* 32: 979-986.

However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham *et al.*, *J. Gen Virol.* 36 : 59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub *et al.*, *Proc. Natl. Acad. Sci. USA* 77: 4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.* 23: 243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, 1413 8065); mouse mammary tumor (MMT 060562, ATCC CCL5 1);

TRI cells (Mather *et al.*, Annals N. Y Acad. Sci. (1982) 383: 44-68); MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

In a further embodiment the invention provides a process for the production of an antibody construct of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the antibody construct of the invention and recovering the produced antibody construct from the culture.

As used herein, the term “culturing” refers to the *in vitro* maintenance, differentiation, growth, proliferation and/or propagation of cells under suitable conditions in a medium. The term “expression” includes any step involved in the production of an antibody construct of the invention including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

When using recombinant techniques, the antibody construct can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody construct is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter *et al.*, Bio/Technology 10: 163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation. Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

The antibody construct of the invention prepared from the host cells can be recovered or purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE™, chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered. Where the

antibody construct of the invention comprises a CH3 domain, the Bakerbond ABX resin (J.T. Baker, Phillipsburg, NJ) is useful for purification.

Affinity chromatography is a preferred purification technique. The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly (styrenedivinyl) benzene allow for faster flow rates and shorter processing times than can be achieved with agarose.

Moreover, the invention provides a pharmaceutical composition comprising an antibody construct of the invention or an antibody construct produced according to the process of the invention.

As used herein, the term "pharmaceutical composition" relates to a composition which is suitable for administration to a patient, preferably a human patient. The particularly preferred pharmaceutical composition of this invention comprises one or a plurality of the antibody construct(s) of the invention, preferably in a therapeutically effective amount. Preferably, the pharmaceutical composition further comprises suitable formulations of one or more (pharmaceutically effective) carriers, stabilizers, excipients, diluents, solubilizers, surfactants, emulsifiers, preservatives and/or adjuvants. Acceptable constituents of the composition are preferably nontoxic to recipients at the dosages and concentrations employed. Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions.

The inventive compositions may comprise a pharmaceutically acceptable carrier. In general, as used herein, "pharmaceutically acceptable carrier" means any and all aqueous and non-aqueous solutions, sterile solutions, solvents, buffers, e.g. phosphate buffered saline (PBS) solutions, water, suspensions, emulsions, such as oil/water emulsions, various types of wetting agents, liposomes, dispersion media and coatings, which are compatible with pharmaceutical administration, in particular with parenteral administration. The use of such media and agents in pharmaceutical compositions is well known in the art, and the compositions comprising such carriers can be formulated by well-known conventional methods.

Certain embodiments provide pharmaceutical compositions comprising the antibody construct of the invention and further one or more excipients such as those illustratively described in this section and elsewhere herein. Excipients can be used in the invention in this regard for a wide

variety of purposes, such as adjusting physical, chemical, or biological properties of formulations, such as adjustment of viscosity, and or processes of the invention to improve effectiveness and or to stabilize such formulations and processes against degradation and spoilage due to, for instance, stresses that occur during manufacturing, shipping, storage, pre-use preparation, administration, and thereafter.

In certain embodiments, the pharmaceutical composition may contain formulation materials for the purpose of modifying, maintaining or preserving, *e.g.*, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition (see, REMINGTON'S PHARMACEUTICAL SCIENCES, 18th Edition, (A.R. Genrmo, ed.), 1990, Mack Publishing Company). In such embodiments, suitable formulation materials may include, but are not limited to:

- amino acids such as glycine, alanine, glutamine, asparagine, threonine, proline, 2-phenylalanine, including charged amino acids, preferably lysine, lysine acetate, arginine, glutamate and/or histidine
- antimicrobials such as antibacterial and antifungal agents
- antioxidants such as ascorbic acid, methionine, sodium sulfite or sodium hydrogen-sulfite;
- buffers, buffer systems and buffering agents which are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8 or 9; examples of buffers are borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids, succinate, phosphate, histidine and acetate; for example Tris buffer of about pH 7.0-8.5, or acetate buffer of about pH 4.0-5.5;
- non-aqueous solvents such as propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate;
- aqueous carriers including water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media;
- biodegradable polymers such as polyesters;
- bulking agents such as mannitol or glycine;
- chelating agents such as ethylenediamine tetraacetic acid (EDTA);
- isotonic and absorption delaying agents;
- complexing agents such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin)
- fillers;

- monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrans); carbohydrates may be non-reducing sugars, preferably trehalose, sucrose, octasulfate, sorbitol or xylitol;
- (low molecular weight) proteins, polypeptides or proteinaceous carriers such as human or bovine serum albumin, gelatin or immunoglobulins, preferably of human origin;
- coloring and flavouring agents;
- sulfur containing reducing agents, such as glutathione, thioctic acid, sodium thioglycolate, thioglycerol, [alpha]-monothioglycerol, and sodium thio sulfate
- diluting agents;
- emulsifying agents;
- hydrophilic polymers such as polyvinylpyrrolidone)
- salt-forming counter-ions such as sodium;
- preservatives such as antimicrobials, anti-oxidants, chelating agents, inert gases and the like; examples are: benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide);
- metal complexes such as Zn-protein complexes;
- solvents and co-solvents (such as glycerin, propylene glycol or polyethylene glycol);
- sugars and sugar alcohols, such as trehalose, sucrose, octasulfate, mannitol, sorbitol or xylitol stachyose, mannose, sorbose, xylose, ribose, myoinisitose, galactose, lactitol, ribitol, myoinisitol, galactitol, glycerol, cyclitols (e.g., inositol), polyethylene glycol; and polyhydric sugar alcohols;
- suspending agents;
- surfactants or wetting agents such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate, triton, tromethamine, lecithin, cholesterol, tyloxapal; surfactants may be detergents, preferably with a molecular weight of >1.2 KD and/or a polyether, preferably with a molecular weight of >3 KD; non-limiting examples for preferred detergents are Tween 20, Tween 40, Tween 60, Tween 80 and Tween 85; non-limiting examples for preferred polyethers are PEG 3000, PEG 3350, PEG 4000 and PEG 5000;
- stability enhancing agents such as sucrose or sorbitol;
- tonicity enhancing agents such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol;
- parenteral delivery vehicles including sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils;

- intravenous delivery vehicles including fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose).

It is evident to those skilled in the art that the different constituents of the pharmaceutical composition (e.g., those listed above) can have different effects, for example, and amino acid can act as a buffer, a stabilizer and/or an antioxidant; mannitol can act as a bulking agent and/or a tonicity enhancing agent; sodium chloride can act as delivery vehicle and/or tonicity enhancing agent; etc.

It is envisaged that the composition of the invention might comprise, in addition to the polypeptide of the invention defined herein, further biologically active agents, depending on the intended use of the composition. Such agents might be drugs acting on the gastro-intestinal system, drugs acting as cytostatica, drugs preventing hyperurikemia, drugs inhibiting immunoreactions (e.g. corticosteroids), drugs modulating the inflammatory response, drugs acting on the circulatory system and/or agents such as cytokines known in the art. It is also envisaged that the antibody construct of the present invention is applied in a co-therapy, *i.e.*, in combination with another anti-cancer medicament.

In certain embodiments, the optimal pharmaceutical composition will be determined by one skilled in the art depending upon, for example, the intended route of administration, delivery format and desired dosage. See, for example, REMINGTON'S PHARMACEUTICAL SCIENCES, *supra*. In certain embodiments, such compositions may influence the physical state, stability, rate of *in vivo* release and rate of *in vivo* clearance of the antibody construct of the invention. In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection, physiological saline solution or artificial cerebrospinal fluid, possibly supplemented with other materials common in compositions for parenteral administration. Neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. In certain embodiments, the antibody construct of the invention compositions may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (REMINGTON'S PHARMACEUTICAL SCIENCES, *supra*) in the form of a lyophilized cake or an aqueous solution. Further, in certain embodiments, the antibody construct of the invention may be formulated as a lyophilizate using appropriate excipients such as sucrose.

When parenteral administration is contemplated, the therapeutic compositions for use in this invention may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired antibody construct of the invention in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the antibody construct of the invention is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (such as polylactic acid or polyglycolic acid), beads or liposomes, that may provide controlled or sustained release of the product which can be delivered via depot injection. In certain embodiments, hyaluronic acid may also be used, having the effect of promoting sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the desired antibody construct.

Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving the antibody construct of the invention in sustained- or controlled-delivery / release formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. See, for example, International Patent Application No. PCT/US93/00829, which describes controlled release of porous polymeric microparticles for delivery of pharmaceutical compositions. Sustained-release preparations may include semipermeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. Pat. No. 3,773,919 and European Patent Application Publication No. EP 058481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman et al., 1983, Biopolymers 2:547-556), poly (2-hydroxyethyl-methacrylate) (Langer *et al.*, 1981, J. Biomed. Mater. Res. 15:167-277 and Langer, 1982, Chem. Tech. 12:98-105), ethylene vinyl acetate (Langer et al., 1981, *supra*) or poly-D(-)-3-hydroxybutyric acid (European Patent Application Publication No. EP 133,988). Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art. See, e.g., Eppstein et al., 1985, Proc. Natl. Acad. Sci. U.S.A. 82:3688-3692; European Patent Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949.

The antibody construct may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization (for example, hydroxymethylcellulose or gelatine-microcapsules and poly (methylmethacrylate) microcapsules, respectively), in colloidal

drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nanoparticles and nanocapsules), or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Oslo, A., Ed., (1980).

Pharmaceutical compositions used for *in vivo* administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Another aspect of the invention includes self-buffering antibody construct of the invention formulations, which can be used as pharmaceutical compositions, as described in international patent application WO 06138181A2 (PCT/US2006/022599). A variety of expositions are available on protein stabilization and formulation materials and methods useful in this regard, such as Arakawa et al., "Solvent interactions in pharmaceutical formulations," Pharm Res. 8(3): 285-91 (1991); Kendrick et al., "Physical stabilization of proteins in aqueous solution" in: RATIONAL DESIGN OF STABLE PROTEIN FORMULATIONS: THEORY AND PRACTICE, Carpenter and Manning, eds. Pharmaceutical Biotechnology. 13: 61-84 (2002), and Randolph et al., "Surfactant-protein interactions", Pharm Biotechnol. 13: 159-75 (2002), see particularly the parts pertinent to excipients and processes of the same for self-buffering protein formulations in accordance with the current invention, especially as to protein pharmaceutical products and processes for veterinary and/or human medical uses.

Salts may be used in accordance with certain embodiments of the invention to, for example, adjust the ionic strength and/or the isotonicity of a formulation and/or to improve the solubility and/or physical stability of a protein or other ingredient of a composition in accordance with the invention. As is well known, ions can stabilize the native state of proteins by binding to charged residues on the protein's surface and by shielding charged and polar groups in the protein and reducing the strength of their electrostatic interactions, attractive, and repulsive interactions. Ions also can stabilize the denatured state of a protein by binding to, in particular, the denatured peptide linkages ($-CONH$) of the protein. Furthermore, ionic interaction with charged and polar groups in a protein also can reduce intermolecular electrostatic interactions and, thereby, prevent or reduce protein aggregation and insolubility.

Ionic species differ significantly in their effects on proteins. A number of categorical rankings of ions and their effects on proteins have been developed that can be used in formulating pharmaceutical compositions in accordance with the invention. One example is the Hofmeister series, which ranks ionic and polar non-ionic solutes by their effect on the conformational stability of proteins in solution. Stabilizing solutes are referred to as “kosmotropic”. Destabilizing solutes are referred to as “chaotropic”. Kosmotropes commonly are used at high concentrations (e.g., >1 molar ammonium sulfate) to precipitate proteins from solution (“salting-out”). Chaotropes commonly are used to denature and/or to solubilize proteins (“salting-in”). The relative effectiveness of ions to “salt-in” and “salt-out” defines their position in the Hofmeister series.

Free amino acids can be used in the antibody construct of the invention formulations in accordance with various embodiments of the invention as bulking agents, stabilizers, and antioxidants, as well as other standard uses. Lysine, proline, serine, and alanine can be used for stabilizing proteins in a formulation. Glycine is useful in lyophilization to ensure correct cake structure and properties. Arginine may be useful to inhibit protein aggregation, in both liquid and lyophilized formulations. Methionine is useful as an antioxidant.

Polyols include sugars, e.g., mannitol, sucrose, and sorbitol and polyhydric alcohols such as, for instance, glycerol and propylene glycol, and, for purposes of discussion herein, polyethylene glycol (PEG) and related substances. Polyols are kosmotropic. They are useful stabilizing agents in both liquid and lyophilized formulations to protect proteins from physical and chemical degradation processes. Polyols also are useful for adjusting the tonicity of formulations. Among polyols useful in select embodiments of the invention is mannitol, commonly used to ensure structural stability of the cake in lyophilized formulations. It ensures structural stability to the cake. It is generally used with a lyoprotectant, e.g., sucrose. Sorbitol and sucrose are among preferred agents for adjusting tonicity and as stabilizers to protect against freeze-thaw stresses during transport or the preparation of bulks during the manufacturing process. Reducing sugars (which contain free aldehyde or ketone groups), such as glucose and lactose, can glycate surface lysine and arginine residues. Therefore, they generally are not among preferred polyols for use in accordance with the invention. In addition, sugars that form such reactive species, such as sucrose, which is hydrolyzed to fructose and glucose under acidic conditions, and consequently engenders glycation, also is not among preferred polyols of the invention in this

regard. PEG is useful to stabilize proteins and as a cryoprotectant and can be used in the invention in this regard.

Embodiments of the antibody construct of the invention formulations further comprise surfactants. Protein molecules may be susceptible to adsorption on surfaces and to denaturation and consequent aggregation at air-liquid, solid-liquid, and liquid-liquid interfaces. These effects generally scale inversely with protein concentration. These deleterious interactions generally scale inversely with protein concentration and typically are exacerbated by physical agitation, such as that generated during the shipping and handling of a product. Surfactants routinely are used to prevent, minimize, or reduce surface adsorption. Useful surfactants in the invention in this regard include polysorbate 20, polysorbate 80, other fatty acid esters of sorbitan polyethoxylates, and poloxamer 188. Surfactants also are commonly used to control protein conformational stability. The use of surfactants in this regard is protein-specific since, any given surfactant typically will stabilize some proteins and destabilize others.

Polysorbates are susceptible to oxidative degradation and often, as supplied, contain sufficient quantities of peroxides to cause oxidation of protein residue side-chains, especially methionine. Consequently, polysorbates should be used carefully, and when used, should be employed at their lowest effective concentration. In this regard, polysorbates exemplify the general rule that excipients should be used in their lowest effective concentrations.

Embodiments of the antibody construct of the invention formulations further comprise one or more antioxidants. To some extent deleterious oxidation of proteins can be prevented in pharmaceutical formulations by maintaining proper levels of ambient oxygen and temperature and by avoiding exposure to light. Antioxidant excipients can be used as well to prevent oxidative degradation of proteins. Among useful antioxidants in this regard are reducing agents, oxygen/free-radical scavengers, and chelating agents. Antioxidants for use in therapeutic protein formulations in accordance with the invention preferably are water-soluble and maintain their activity throughout the shelf life of a product. EDTA is a preferred antioxidant in accordance with the invention in this regard. Antioxidants can damage proteins. For instance, reducing agents, such as glutathione in particular, can disrupt intramolecular disulfide linkages. Thus, antioxidants for use in the invention are selected to, among other things, eliminate or sufficiently reduce the possibility of themselves damaging proteins in the formulation.

Formulations in accordance with the invention may include metal ions that are protein co-factors and that are necessary to form protein coordination complexes, such as zinc necessary to form certain insulin suspensions. Metal ions also can inhibit some processes that degrade proteins. However, metal ions also catalyze physical and chemical processes that degrade proteins. Magnesium ions (10-120 mM) can be used to inhibit isomerization of aspartic acid to isoaspartic acid. Ca^{+2} ions (up to 100 mM) can increase the stability of human deoxyribonuclease. Mg^{+2} , Mn^{+2} , and Zn^{+2} , however, can destabilize rhDNase. Similarly, Ca^{+2} and Sr^{+2} can stabilize Factor VIII, it can be destabilized by Mg^{+2} , Mn^{+2} and Zn^{+2} , Cu^{+2} and Fe^{+2} , and its aggregation can be increased by Al^{+3} ions.

Embodiments of the antibody construct of the invention formulations further comprise one or more preservatives. Preservatives are necessary when developing multi-dose parenteral formulations that involve more than one extraction from the same container. Their primary function is to inhibit microbial growth and ensure product sterility throughout the shelf-life or term of use of the drug product. Commonly used preservatives include benzyl alcohol, phenol and m-cresol. Although preservatives have a long history of use with small-molecule parenterals, the development of protein formulations that includes preservatives can be challenging. Preservatives almost always have a destabilizing effect (aggregation) on proteins, and this has become a major factor in limiting their use in multi-dose protein formulations. To date, most protein drugs have been formulated for single-use only. However, when multi-dose formulations are possible, they have the added advantage of enabling patient convenience, and increased marketability. A good example is that of human growth hormone (hGH) where the development of preserved formulations has led to commercialization of more convenient, multi-use injection pen presentations. At least four such pen devices containing preserved formulations of hGH are currently available on the market. Norditropin (liquid, Novo Nordisk), Nutropin AQ (liquid, Genentech) & Genotropin (lyophilized--dual chamber cartridge, Pharmacia & Upjohn) contain phenol while Somatropo (Eli Lilly) is formulated with m-cresol. Several aspects need to be considered during the formulation and development of preserved dosage forms. The effective preservative concentration in the drug product must be optimized. This requires testing a given preservative in the dosage form with concentration ranges that confer anti-microbial effectiveness without compromising protein stability.

As might be expected, development of liquid formulations containing preservatives are more challenging than lyophilized formulations. Freeze-dried products can be lyophilized without the preservative and reconstituted with a preservative containing diluent at the time of use. This

shortens the time for which a preservative is in contact with the protein, significantly minimizing the associated stability risks. With liquid formulations, preservative effectiveness and stability should be maintained over the entire product shelf-life (about 18 to 24 months). An important point to note is that preservative effectiveness should be demonstrated in the final formulation containing the active drug and all excipient components.

The antibody constructs disclosed herein may also be formulated as immuno-liposomes. A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes. Liposomes containing the antibody construct are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); US Pat. Nos. 4,485,045 and 4,544,545; and WO 97/38731. Liposomes with enhanced circulation time are disclosed in US Patent No. 5,013, 556. Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody construct of the present invention can be conjugated to the liposomes as described in Martin *et al.* J. Biol. Chem. 257: 286-288 (1982) via a disulfide interchange reaction. A chemotherapeutic agent is optionally contained within the liposome. See Gabizon *et al.* J. National Cancer Inst. 81 (19) 1484 (1989).

Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration.

The biological activity of the pharmaceutical composition defined herein can be determined for instance by cytotoxicity assays, as described in the following examples, in WO 99/54440 or by Schlereth *et al.* (Cancer Immunol. Immunother. 20 (2005), 1-12). "Efficacy" or "*in vivo* efficacy" as used herein refers to the response to therapy by the pharmaceutical composition of the invention, using e.g. standardized NCI response criteria. The success or *in vivo* efficacy of the therapy using a pharmaceutical composition of the invention refers to the effectiveness of the composition for its intended purpose, *i.e.* the ability of the composition to cause its desired

effect, i.e. depletion of pathologic cells, e.g. tumor cells. The *in vivo* efficacy may be monitored by established standard methods for the respective disease entities including, but not limited to white blood cell counts, differentials, Fluorescence Activated Cell Sorting, bone marrow aspiration. In addition, various disease specific clinical chemistry parameters and other established standard methods may be used. Furthermore, computer-aided tomography, X-ray, nuclear magnetic resonance tomography (e.g. for National Cancer Institute-criteria based response assessment [Cheson BD, Horning SJ, Coiffier B, Shipp MA, Fisher RI, Connors JM, Lister TA, Vose J, Grillo-Lopez A, Hagenbeek A, Cabanillas F, Klippensten D, Hiddemann W, Castellino R, Harris NL, Armitage JO, Carter W, Hoppe R, Canellos GP. Report of an international workshop to standardize response criteria for non-Hodgkin's lymphomas. NCI Sponsored International Working Group. J Clin Oncol. 1999 Apr;17(4):1244]), positron-emission tomography scanning, white blood cell counts, differentials, Fluorescence Activated Cell Sorting, bone marrow aspiration, lymph node biopsies/histologies, and various lymphoma specific clinical chemistry parameters (e.g. lactate dehydrogenase) and other established standard methods may be used.

Another major challenge in the development of drugs such as the pharmaceutical composition of the invention is the predictable modulation of pharmacokinetic properties. To this end, a pharmacokinetic profile of the drug candidate, i.e. a profile of the pharmacokinetic parameters that affect the ability of a particular drug to treat a given condition, can be established. Pharmacokinetic parameters of the drug influencing the ability of a drug for treating a certain disease entity include, but are not limited to: half-life, volume of distribution, hepatic first-pass metabolism and the degree of blood serum binding. The efficacy of a given drug agent can be influenced by each of the parameters mentioned above.

"Half-life" means the time where 50% of an administered drug are eliminated through biological processes, e.g. metabolism, excretion, etc. By "hepatic first-pass metabolism" is meant the propensity of a drug to be metabolized upon first contact with the liver, i.e. during its first pass through the liver. "Volume of distribution" means the degree of retention of a drug throughout the various compartments of the body, like e.g. intracellular and extracellular spaces, tissues and organs, etc. and the distribution of the drug within these compartments. "Degree of blood serum binding" means the propensity of a drug to interact with and bind to blood serum proteins, such as albumin, leading to a reduction or loss of biological activity of the drug.

Pharmacokinetic parameters also include bioavailability, lag time (Tlag), Tmax, absorption rates, more onset and/or Cmax for a given amount of drug administered. "Bioavailability" means the amount of a drug in the blood compartment. "Lag time" means the time delay between the administration of the drug and its detection and measurability in blood or plasma. "Tmax" is the time after which maximal blood concentration of the drug is reached, and "Cmax" is the blood concentration maximally obtained with a given drug. The time to reach a blood or tissue concentration of the drug which is required for its biological effect is influenced by all parameters. Pharmacokinetic parameters of bispecific antibody constructs exhibiting cross-species specificity, which may be determined in preclinical animal testing in non-chimpanzee primates as outlined above, are also set forth e.g. in the publication by Schlereth *et al.* (Cancer Immunol. Immunother. 20 (2005), 1-12).

One embodiment provides the antibody construct of the invention or the antibody construct produced according to the process of the invention for use in the prevention, treatment or amelioration of a tumor or cancer disease or of a metastatic cancer disease. It is envisaged that this tumor or cancer or metastatic cancer is CD70 expressing.

The formulations described herein are useful as pharmaceutical compositions in the treatment, amelioration and/or prevention of the pathological medical condition as described herein in a patient in need thereof. The term "treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Treatment includes the application or administration of the formulation to the body, an isolated tissue, or cell from a patient who has a disease/disorder, a symptom of a disease/disorder, or a predisposition toward a disease/disorder, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve, or affect the disease, the symptom of the disease, or the predisposition toward the disease.

The term "amelioration" as used herein refers to any improvement of the disease state of a patient having a tumor or cancer or a metastatic cancer as specified herein below, by the administration of an antibody construct according to the invention to a subject in need thereof. Such an improvement may also be seen as a slowing or stopping of the progression of the tumor or cancer or metastatic cancer of the patient. The term "prevention" as used herein means the avoidance of the occurrence or re-occurrence of a patient having a tumor or cancer or a metastatic cancer as specified herein below, by the administration of an antibody construct according to the invention to a subject in need thereof.

The term “disease” refers to any condition that would benefit from treatment with the antibody construct or the pharmaceutical composition described herein. This includes chronic and acute disorders or diseases including those pathological conditions that predispose the mammal to the disease in question.

A “neoplasm” is an abnormal growth of tissue, usually but not always forming a mass. When also forming a mass, it is commonly referred to as a “tumor”. Neoplasms or tumors can be benign, potentially malignant (pre-cancerous), or malignant. Malignant neoplasms are commonly called cancer. They usually invade and destroy the surrounding tissue and may form metastases, i.e., they spread to other parts, tissues or organs of the body. Hence, the term “metastatic cancer” encompasses metastases to other tissues or organs than the one of the original tumor. Lymphomas and leukemias are lymphoid neoplasms. For the purposes of the present invention, they are also encompassed by the terms “tumor” or “cancer”.

In a preferred embodiment of the invention, the tumor or cancer disease is selected from the group consisting of renal, lung, pancreatic, ovarian, breast, colon, head and neck, stomach, rectal, thymic, and brain tumor or cancer, leukemia, lymphoma, melanoma, Kaposi's Sarcoma, embryonal carcinoma, and a metastatic cancer disease derived from any of the foregoing.

More specifically, the tumor or cancer disease can be selected from the group consisting of renal cell carcinoma (RCC), clear cell RCC (ccRCC), papillary RCC, chromophobe RCC, sarcomatoid RCC, non-small cell lung cancer (NSCLC), lung squamous carcinoma, pancreatic adenocarcinoma such as pancreatic ductal adenocarcinoma, non-small cell lung cancer (NSCLC), lung squamous carcinoma, laryngeal carcinoma, pharyngeal carcinoma, nasopharyngeal carcinoma, undifferentiated carcinoma of the rhino-pharynx, lymphoepithelioma, glioblastoma, glioma, meningioma, acute lymphocytic leukemia (ALL), chronic lymphocytic leukemia (CLL), T-cell leukemia, adult T-cell leukemia, B-cell lineage cancer, B-cell lymphoma, diffuse large B cell lymphoma (DLBCL), non-Hodgkin's lymphoma (NHL), Burkitt's lymphoma, anaplastic large-cell lymphomas (ALCL), multiple myeloma, cutaneous T-cell lymphomas, nodular small cleaved-cell lymphomas, lymphocytic lymphomas, peripheral T-cell lymphomas, Lennert's lymphomas, immunoblastic lymphoma, T-cell lymphoma, enteroblastic/centrocytic (cb/cc) follicular lymphoma, angioimmunoblastic lymphadenopathy (AILD)-like T cell lymphoma, HIV associated body cavity based lymphoma, Castleman's disease, or Waldenstrom's macroglobulinemia. The metastatic cancer disease can be derived from any of the foregoing.

The invention also provides a method for the treatment or amelioration of tumor or cancer disease or a metastatic cancer disease, comprising the step of administering to a subject in need thereof the antibody construct of the invention or the antibody construct produced according to the process of the invention. It is envisaged that this tumor or cancer or metastatic cancer is CD70 expressing.

The terms "subject in need" or those "in need of treatment" includes those already with the disorder, as well as those in which the disorder is to be prevented. The subject in need or "patient" includes human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

The antibody construct of the invention will generally be designed for specific routes and methods of administration, for specific dosages and frequencies of administration, for specific treatments of specific diseases, with ranges of bio-availability and persistence, among other things. The materials of the composition are preferably formulated in concentrations that are acceptable for the site of administration.

Formulations and compositions thus may be designed in accordance with the invention for delivery by any suitable route of administration. In the context of the present invention, the routes of administration include, but are not limited to

- topical routes (such as epicutaneous, inhalational, nasal, ophthalmic, auricular / aural, vaginal, mucosal);
- enteral routes (such as oral, gastrointestinal, sublingual, sublabial, buccal, rectal); and
- parenteral routes (such as intravenous, intraarterial, intraosseous, intramuscular, intracerebral, intracerebroventricular, epidural, intrathecal, subcutaneous, intraperitoneal, extra-amniotic, intraarticular, intracardiac, intradermal, intralesional, intrauterine, intravesical, intravitreal, transdermal, intranasal, transmucosal, intrasynovial, intraluminal).

The pharmaceutical compositions and the antibody construct of this invention are particularly useful for parenteral administration, e.g., subcutaneous or intravenous delivery, for example by injection such as bolus injection, or by infusion such as continuous infusion. Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are described in U.S. Patent Nos. 4,475,196;

4,439,196; 4,447,224; 4,447, 233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163.

In particular, the present invention provides for an uninterrupted administration of the suitable composition. As a non-limiting example, uninterrupted or substantially uninterrupted, *i.e.* continuous administration may be realized by a small pump system worn by the patient for metering the influx of therapeutic agent into the body of the patient. The pharmaceutical composition comprising the antibody construct of the invention can be administered by using said pump systems. Such pump systems are generally known in the art, and commonly rely on periodic exchange of cartridges containing the therapeutic agent to be infused. When exchanging the cartridge in such a pump system, a temporary interruption of the otherwise uninterrupted flow of therapeutic agent into the body of the patient may ensue. In such a case, the phase of administration prior to cartridge replacement and the phase of administration following cartridge replacement would still be considered within the meaning of the pharmaceutical means and methods of the invention together make up one “uninterrupted administration” of such therapeutic agent.

The continuous or uninterrupted administration of the antibody constructs of the invention may be intravenous or subcutaneous by way of a fluid delivery device or small pump system including a fluid driving mechanism for driving fluid out of a reservoir and an actuating mechanism for actuating the driving mechanism. Pump systems for subcutaneous administration may include a needle or a cannula for penetrating the skin of a patient and delivering the suitable composition into the patient's body. Said pump systems may be directly fixed or attached to the skin of the patient independently of a vein, artery or blood vessel, thereby allowing a direct contact between the pump system and the skin of the patient. The pump system can be attached to the skin of the patient for 24 hours up to several days. The pump system may be of small size with a reservoir for small volumes. As a non-limiting example, the volume of the reservoir for the suitable pharmaceutical composition to be administered can be between 0.1 and 50 ml.

The continuous administration may also be transdermal by way of a patch worn on the skin and replaced at intervals. One of skill in the art is aware of patch systems for drug delivery suitable for this purpose. It is of note that transdermal administration is especially amenable to uninterrupted administration, as exchange of a first exhausted patch can advantageously be accomplished simultaneously with the placement of a new, second patch, for example on the

surface of the skin immediately adjacent to the first exhausted patch and immediately prior to removal of the first exhausted patch. Issues of flow interruption or power cell failure do not arise.

If the pharmaceutical composition has been lyophilized, the lyophilized material is first reconstituted in an appropriate liquid prior to administration. The lyophilized material may be reconstituted in, e.g., bacteriostatic water for injection (BWFI), physiological saline, phosphate buffered saline (PBS), or the same formulation the protein had been in prior to lyophilization.

The compositions of the present invention can be administered to the subject at a suitable dose which can be determined e.g. by dose escalating studies by administration of increasing doses of the antibody construct of the invention exhibiting cross-species specificity described herein to non-chimpanzee primates, for instance macaques. As set forth above, the antibody construct of the invention exhibiting cross-species specificity described herein can be advantageously used in identical form in preclinical testing in non-chimpanzee primates and as drug in humans. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical arts, dosages for any one patient depend upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently.

The term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve the desired effect. The term "therapeutically effective dose" is defined as an amount sufficient to cure or at least partially arrest the disease and its complications in a patient already suffering from the disease. Amounts or doses effective for this use will depend on the condition to be treated (the indication), the delivered antibody construct, the therapeutic context and objectives, the severity of the disease, prior therapy, the patient's clinical history and response to the therapeutic agent, the route of administration, the size (body weight, body surface or organ size) and/or condition (the age and general health) of the patient, and the general state of the patient's own immune system. The proper dose can be adjusted according to the judgment of the attending physician such that it can be administered to the patient once or over a series of administrations, and in order to obtain the optimal therapeutic effect.

A typical dosage may range from about 0.1 µg/kg to up to about 30 mg/kg or more, depending on the factors mentioned above. In specific embodiments, the dosage may range from 1.0 µg/kg up to about 20 mg/kg, optionally from 10 µg/kg up to about 10 mg/kg or from 100 µg/kg up to about 5 mg/kg.

A therapeutic effective amount of an antibody construct of the invention preferably results in a decrease in severity of disease symptoms, an increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease affliction. For treating CD70-expressing tumors, a therapeutically effective amount of the antibody construct of the invention, e.g. an anti-CD70 /anti-CD3 antibody construct, preferably inhibits cell growth or tumor growth by at least about 20%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% relative to untreated patients. The ability of a compound to inhibit tumor growth may be evaluated in an animal model predictive of efficacy in human tumors.

The pharmaceutical composition can be administered as a sole therapeutic or in combination with additional therapies such as anti-cancer therapies as needed, e.g. other proteinaceous and non-proteinaceous drugs. These drugs may be administered simultaneously with the composition comprising the antibody construct of the invention as defined herein or separately before or after administration of said antibody construct in timely defined intervals and doses.

The term “effective and non-toxic dose” as used herein refers to a tolerable dose of an inventive antibody construct which is high enough to cause depletion of pathologic cells, tumor elimination, tumor shrinkage or stabilization of disease without or essentially without major toxic effects. Such effective and non-toxic doses may be determined e.g. by dose escalation studies described in the art and should be below the dose inducing severe adverse side events (dose limiting toxicity, DLT).

The term “toxicity” as used herein refers to the toxic effects of a drug manifested in adverse events or severe adverse events. These side events might refer to a lack of tolerability of the drug in general and/or a lack of local tolerance after administration. Toxicity could also include teratogenic or carcinogenic effects caused by the drug.

The term “safety”, “*in vivo* safety” or “tolerability” as used herein defines the administration of a drug without inducing severe adverse events directly after administration (local tolerance) and during a longer period of application of the drug. “Safety”, “*in vivo* safety” or “tolerability” can be evaluated e.g. at regular intervals during the treatment and follow-up period. Measurements include clinical evaluation, e.g. organ manifestations, and screening of laboratory abnormalities. Clinical evaluation may be carried out and deviations to normal findings recorded/coded

according to NCI-CTC and/or MedDRA standards. Organ manifestations may include criteria such as allergy/immunology, blood/bone marrow, cardiac arrhythmia, coagulation and the like, as set forth *e.g.* in the Common Terminology Criteria for adverse events v3.0 (CTCAE). Laboratory parameters which may be tested include for instance hematology, clinical chemistry, coagulation profile and urine analysis and examination of other body fluids such as serum, plasma, lymphoid or spinal fluid, liquor and the like. Safety can thus be assessed *e.g.* by physical examination, imaging techniques (*i.e.* ultrasound, x-ray, CT scans, Magnetic Resonance Imaging (MRI)), other measures with technical devices (*i.e.* electrocardiogram), vital signs, by measuring laboratory parameters and recording adverse events. For example, adverse events in non-chimpanzee primates in the uses and methods according to the invention may be examined by histopathological and/or histochemical methods.

The above terms are also referred to *e.g.* in the Preclinical safety evaluation of biotechnology-derived pharmaceuticals S6; ICH Harmonised Tripartite Guideline; ICH Steering Committee meeting on July 16, 1997.

In a further embodiment, the invention provides a kit comprising an antibody construct of the invention, an antibody construct produced according to the process of the invention, a polynucleotide / nucleic acid molecule of the invention, a vector of the invention, and/or a host cell of the invention.

In the context of the present invention, the term “kit” means two or more components – one of which corresponding to the antibody construct, the pharmaceutical composition, the vector or the host cell of the invention – packaged together in a container, recipient or otherwise. A kit can hence be described as a set of products and/or utensils that are sufficient to achieve a certain goal, which can be marketed as a single unit.

The kit may comprise one or more recipients (such as vials, ampoules, containers, syringes, bottles, bags) of any appropriate shape, size and material (preferably waterproof, *e.g.* plastic or glass) containing the antibody construct or the pharmaceutical composition of the present invention in an appropriate dosage for administration (see above). The kit may additionally contain directions for use (*e.g.* in the form of a leaflet or instruction manual), means for administering the antibody construct of the present invention such as a syringe, pump, infuser or the like, means for reconstituting the antibody construct of the invention and/or means for diluting the antibody construct of the invention.

The invention also provides kits for a single-dose administration unit. The kit of the invention may also contain a first recipient comprising a dried / lyophilized antibody construct and a second recipient comprising an aqueous formulation. In certain embodiments of this invention, kits containing single-chambered and multi-chambered pre-filled syringes (e.g., liquid syringes and lyosyringes) are provided.

The Figures show:**Figure 1:**

Expression control of the constructs used for epitope mapping on CHO cells, using an anti-V5 antibody. See Example 1.

Figure 2:

Schematic representation of a multiplex epitope binning or competition assay and FACS read-out. 14 beads are pre-coated, each with a different antibody. The second antibody "X" is added, and additional binding is determined. If no additional binding can be determined, the antibodies compete for binding with one another.

Figure 3:

Experimental set-up of the epitope mapping analysis, see Example 2. A V5 tag was fused via a glycine/serine linker to the C-terminus of the chimeric molecules, as indicated.

Figure 4:

Epitope mapping result of several exemplary CD70xCD3 bispecific binders in an scFc format, carried out as described in Example 2. Although not specifically indicated in Figure 4A and 4B, all constructs were CD70xCD3 (I2C) bispecific and in scFc format. The x-axis depicts Comp. PE-A (PE = phycoerythrin; A = signal area), and the y-axis depicts counts (events) normalized to mode.

Figure 5:

Bispecific binding, interspecies cross-reactivity and absence of binding to human CD70 paralogue CD40L, shown for a representative number of antibody constructs in an scFc format, as analyzed in Examples 5 and 6. The x-axis depicts Comp. PE-A (PE = phycoerythrin; A = signal area), and the y-axis depicts counts (events).

Figure 6:

Cytotoxic activity of CD70-21D_CCxI2C-scFc as analyzed in a FACS-based cytotoxicity assay using CHO cells transfected with human CD70 as target cells, and unstimulated human PBMC as effector cells. The assay was carried out as described in Example 8.5. In a parallel approach, soluble CD27 was added in a concentration of 1 ng/ml. The presence of the soluble form of CD27 did not impair the cytotoxic activity of the tested antibody construct.

Examples:

The following examples illustrate the invention. These examples should not be construed as to limit the scope of this invention. The present invention is limited only by the claims.

Example 1**Generation of CHO cells expressing wild type and truncated CD70**

The extracellular domain of the CD70 antigen can be subdivided into different sub-domains or regions E1 to E7 that are defined, for the purposes of Examples 1 and 2, by the following amino acid positions:

E1	aa 43-62	SEQ ID NO: 743
E2	aa 63-84	SEQ ID NO: 744
E3	aa 85-109	SEQ ID NO: 745
E4	aa 110-134	SEQ ID NO: 746
E5	aa 135-151	SEQ ID NO: 747
E6	aa 152-175	SEQ ID NO: 748
E7	aa 176-193	SEQ ID NO: 749
E1+2	aa 43-84	SEQ ID NO: 750
E3+4	aa 85-134	SEQ ID NO: 751
E4+5	aa 110-151	SEQ ID NO: 752
E5+6	aa 135-175	SEQ ID NO: 753
E6+7	aa 152-193	SEQ ID NO: 754

For the construction of the human/mouse chimeric CD70 molecules used for epitope mapping (Example 2), the sequences of the respective seven human regions as well as the five combinations of two neighboring human regions (see above) were replaced with the corresponding regions from murine CD70. Furthermore, a V5 tag (GKPIPNNPLLGLDST) was fused via a "GGGGS" linker to the C-terminus of the chimeric molecules. The final chimeric molecule sequences are depicted in SEQ ID NOs: 759-768. In addition, full length human CD70 (SEQ ID NO: 741) and full-length mouse CD70 (SEQ ID NO: 757) were constructed, both having a V5 tag (GKPIPNNPLLGLDST) fused via a "GGGGS" linker to their C-terminus.

For the generation of CHO dhfr- cells expressing the above constructs, the respective coding sequences were cloned into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum

et al. Cancer Immunol Immunother 50 (2001) 141-150). CHO cells transfected with human CD70, but without the V5 tag, were also generated. All cloning procedures were carried out according to standard protocols (Sambrook, Molecular Cloning; A Laboratory Manual, 3rd edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, New York (2001)). For each construct, a corresponding plasmid was transfected into DHFR deficient CHO cells for eukaryotic expression, as described by Kaufman R.J. (1990) Methods Enzymol. 185, 537-566.

The expression of the constructs on the CHO cells was verified using a monoclonal mouse IgG2a anti-v5 tag antibody (1 µg/ml; AbD Serotec, # MCA 1360). Bound monoclonal antibody was detected with an anti-mouse IgG Fc-gamma-PE. As negative control, cells were incubated with isotype control antibody instead of the first antibody. The samples were measured by flow cytometry. CHO transfectants did not express E5 alone or E5+6. See Figure 1.

Example 2

Epitope mapping of anti-CD70 antibody constructs

The CHO cells generated as described in Example 1 were stained with crude, undiluted periplasmic extract containing individual anti-CD70 scFv molecules. Bound scFv were detected with mouse monoclonal anti-FLAG M2 antibody (1 µg/ml; Sigma F1804) followed by an anti-mouse IgG Fc-gamma-PE (1:100; Jackson ImmunoResearch # 115-116-071). All antibodies were diluted in PBS / 1.5% FCS. As negative control, cells were incubated with PBS / 2% FCS instead of the periplasmic extract. The samples were measured by flow cytometry. While all tested anti-CD70 scFv molecules were able to bind to human CD70 w/o the V5 tag (strong FACS signal), none of them was able to bind to murine CD70 (no FACS signal).

The binders were classified into different groups (I, II, III, IIIv, V, VI, VII and VIII), depending on the chimeric CD70 molecule for which a loss of binding was observed. The loss of binding is in most of the cases complete, but can in some cases also be partial. A merely partial loss of binding was observed in particular for the region denominated E6 (see Groups II, IIIv, VI and VIII), but in some cases also for other regions. For some binders tested, the results obtained with the combination of two neighboring regions (E1+2, E3+4, E4+5, E6+7) were not always explicit. Therefore, the classification into the different groups was mainly driven by the results obtained with those chimeric molecules having only one region replaced with the murine counterpart region. Results are shown in Table 4.

Table 4: Several regions of the extracellular CD70 domain (E2, E3, E4, E6 and combinations thereof) were identified as comprising an epitope recognized by the respective anti-CD70 binding molecules, as detected by a complete or partial loss of the FACS signal. *The denomination of the groups and of the binders is also used in the sequence listing.

Group*	Loss of signal in these chimeric molecules:	CD70 binder specific for region:	Denomination of binder: CD70-x*
I	E2, E3, E4, E6 E1+2, E3+4, E4+5, E6+7	E2/E3/E4/E6	x = 4, 7, 9, 13, 35, 44, 45, 47, 48, 49, 50, 52, 57, 61, 62, 65, 67, 68, 73
II	E2, E3, E4, (E6 partial) E1+2, E3+4, E4+5	E2/E3/E4/(E6)	x = 2, 8, 14, 15, 16, 17, 18, 20, 26, 28, 29, 30, 31, 32, 33, 34, 36, 37, 38, 40, 41, 42, 43, 46, 53, 58, 59, 63, 66, 74
III	E2, E3, E6 E1+2, E6+7	E2/E3/E6	x = 1, 11
IIIv	E2, E3, (E6 partial)	E2/E3/(E6)	x = 3
V	E3, E4, E6 E3+4, E4+5, E6+7	E3/E4/E6	x = 12
VI	E3, E4, (E6 partial) E3+4, E4+5	E3/E4/(E6)	x = 19, 21, 22, 23, 24, 25, 27, 39, 51, 54, 64, 69
VII	<i>huCD70-V5 and all chimeric constructs</i>	<i>V5 tag inhibits binding</i>	x = 55, 56, 60, 70, 71, 72
VIII	E3, (E6 partial)	E3/(E6)	x = 5, 6, 10

None of the anti-CD70 scFv molecules showed a loss of binding for the “E1” or for the “E7” chimeric molecule. Hence, the first binding domain of the antibody constructs of the invention seems to not bind to an epitope comprised within the region denominated E1, and it seems to not bind to an epitope comprised within the region denominated E7. In Group VII, it appears that the presence of the V5 tag in the chimeric molecules interferes with the binding of the anti-CD70 scFv molecules. Therefore, the epitope could not be determined. It can be speculated that this group of anti-CD70 scFv molecules binds to an epitope comprised within the region denominated E7, as this region is neighboring to the V5 tag.

Figure 3 shows the experimental set-up, and Figures 4A and B show the epitope mapping result of several exemplary bispecific binders in an scFc format.

Example 3

Biacore- and Octet based determination of antibody affinity to human and cynomolgus CD70 and CD3

Biacore analysis experiments were performed using recombinant human / cyno CD70-ECD fusion proteins with albumin to determine target binding of the antibody constructs of the invention.

In detail, CM5 Sensor Chips (GE Healthcare) were immobilized with approximately 600-800 RU of the respective recombinant antigen using acetate buffer pH 4.5 according to the manufacturer's manual. The CD70xCD3 bispecific antibody construct samples were loaded in a dilution series of the following concentrations: 50 nM, 25 nM, 12.5 nM, 6.25 nM and 3.13 nM diluted in HBS-EP running buffer (GE Healthcare). Flow rate was 30 µl/min for 3 min, then HBS-EP running buffer was applied for 8 min to 20 min again at a flow rate of 30 µl/ml. Regeneration of the chip was performed using 10 mM glycine 10 mM NaCl pH 1.5 solution. Data sets were analyzed using BiaEval Software. In general two independent experiments were performed.

Furthermore, Octet analysis experiments were performed using recombinant human / cyno CD70-NHS-PEG Biotin to determine target binding of the antibody constructs of the invention. In detail, Streptavidin-Tips were immobilized with approximately 0.1-0.2 nm of the respective recombinant antigen according to the manufacturer's manual. The CD70xCD3 bispecific antibody construct samples were prepared in a dilution series of the following concentrations: 300nM, 150nm, 75 nM, 37.5 nM, 18.8 nM, an 9.4 nM diluted in HBS-EP running buffer (GE Healthcare). For every dilution, one Streptavidin-Tip was immobilized with the antigen. The association was measured in a black 96 well MTP, Flow rate was 1000rpm for 8 min association. For dissociation the tips were incubated in HBS-EP running buffer for 15 min to 30 min again at a flow rate of 1000rpm. Data sets were analyzed using ForteBio Data Analysis Software. In general two independent experiments were performed.

The analyzed CD70xCD3 bispecific antibody constructs in an scFc format showed very high affinities to human CD70 in the 1-digit nanomolar range (except for one construct in the very low 2-digit nanomolar range), as determined by Octet analysis. Binding to macaque CD70 was balanced, also showing affinities in the 1-digit nanomolar range. The affinity values as well as the calculated affinity gap are shown in Table 5.

Table 5: Affinities of CD70xCD3 (I2C) bispecific antibody constructs to human and macaque CD70 as determined by Octet analysis, as well as the calculated interspecies affinity gaps. All constructs were measured in two independent experiments each using a dilution series, except for those marked with an (*) which were measured in one experiment only.

CD70xCD3 bispecific antibody construct	Octet based affinity hu CD70 [nM]	Octet based affinity mac CD70 [nM]	Affinity gap KD mac/KD hu
CD70-13D_CCxI2C-scFc	5.84 ± 1.07	5.41 ± 2.33	0.93
CD70-16D_CCxI2C-scFc	2.80 ± 1.30	0.60*	0.21
CD70-21D_CCxI2C-scFc	0.81 ± 0.42	0.34*	0.42
CD70-24D_CCxI2C-scFc	12.75 ± 0.35	8.75 ± 4.74	0.69
CD70-25D_CCxI2C-scFc	1.51 ± 0.43	1.57 ± 0.82	1.04
CD70_1-G2D_CCxI2C-scFc	2.35 ± 0.42	1.44 ± 0.32	0.61
CD70-27D_CCxI2C-scFc	5.84 ± 1.18	5.31 ± 0.22	0.91
CD70-28D_CCxI2C-scFc	5.50 ± 0.59	7.87 ± 0.78	1.43
CD70-31D_CCxI2C-scFc	5.44 ± 2.52	7.45 ± 1.03	1.37
CD70-32D_CCxI2C-scFc	4.07 ± 0.28	4.96 ± 0.57	1.22
CD70-42D_CCxI2C-scFc	2.56 ± 0.13	4.46 ± 0.35	1.74
CD70-43D_CCxI2C-scFc	6.92 ± 1.27	5.82 ± 2.26	0.84
CD70-48D_CCxI2C-scFc	2.12 ± 0.02	3.38 ± 0.10	1.59
CD70-62D_CCxI2C-scFc	3.05 ± 0.04	3.35 ± 0.43	1.10
CD70-23D_CCxI2C-scFc	2.58 ± 0.23	2.57 ± 0.12	1.00

Furthermore, the binding of the bispecific antibody constructs to human CD3 and macaque CD3 as well as to human and cyno FcRn was confirmed in a Biacore assay and was shown to be strong and well balanced. The analyzed CD70xCD3 bispecific antibody constructs in an scFc format showed high affinities to human CD3 in the very low 2-digit or in the 1-digit nanomolar range. Binding to macaque CD3 was balanced, also showing affinities in similar ranges. The affinity values as well as the calculated affinity gap are shown in Table 6.

Table 6: Affinities of CD70xCD3 (I2C) bispecific antibody constructs to human and macaque CD3 as determined by Biacore analysis, as well as the calculated interspecies affinity gaps.

CD70xCD3 bispecific antibody construct	Biacore based affinity hu CD3 [nM]	Biacore based affinity cyno CD3 [nM]	Affinity gap KD mac/KD hu
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CD70-13D_CCxI2C-scFc	13.35 ± 0.78	11.05 ± 0.64	0.83
CD70-16D_CCxI2C-scFc	14.05 ± 0.64	12.50 ± 1.84	0.89
CD70-21D_CCxI2C-scFc	12.60 ± 0.28	10.65 ± 0.35	0.85
CD70-24D_CCxI2C-scFc	13.15 ± 1.48	10.70 ± 1.41	0.81
CD70-25D_CCxI2C-scFc	12.75 ± 2.05	10.39 ± 2.14	0.81
CD70_1-G2D_CCxI2C-scFc	12.95 ± 0.35	10.75 ± 0.21	0.83
CD70-27D_CCxI2C-scFc	12.20 ± 2.26	10.05 ± 2.19	0.82
CD70-28D_CCxI2C-scFc	10.13 ± 1.66	8.56 ± 1.48	0.85
CD70-31D_CCxI2C-scFc	14.60 ± 1.13	12.22 ± 0.99	0.84
CD70-32D_CCxI2C-scFc	13.55 ± 1.91	11.40 ± 1.70	0.84
CD70-42D_CCxI2C-scFc	8.13 ± 0.21	7.96 ± 1.50	0.98
CD70-43D_CCxI2C-scFc	8.21 ± 0.76	6.81 ± 0.74	0.83
CD70-48D_CCxI2C-scFc	10.64 ± 1.22	9.09 ± 0.83	0.85
CD70-62D_CCxI2C-scFc	9.02 ± 1.20	7.67 ± 1.17	0.85
CD70-23D_CCxI2C-scFc	11.70 ± 1.13	9.65 ± 1.06	0.82

Example 4

Scatchard-based analysis of CD70xCD3 bispecific antibody construct affinity to human and macaque CD70 on target antigen positive cells and determination of the interspecies affinity gap

The affinities of CD70xCD3 bispecific antibody constructs to CHO cells transfected with human or macaque CD70 were also determined by Scatchard analysis as the most reliable method for measuring potential affinity gaps between human and macaque CD70. For the Scatchard analysis, saturation binding experiments are performed using a monovalent detection system to precisely determine monovalent binding of the CD70xCD3 bispecific antibody constructs to the respective cell line.

2×10^4 cells of the respective cell line (recombinantly human CD70-expressing CHO cell line, recombinantly macaque CD70-expressing CHO cell line) were incubated each with 50 μ l of a triplet dilution series (twelve dilutions at 1:2) of the respective CD70xCD3 bispecific antibody construct (until saturation is reached) starting at 10-20 nM followed by 16 h incubation at 4°C under agitation and one residual washing step. Then, the cells were incubated for another hour with 30 μ l of a CD3xALEXA488 conjugate solution. After one washing step, the cells were resuspended in 150 μ l FACS buffer containing 3.5 % formaldehyde, incubated for further

15 min, centrifuged, resuspended in FACS buffer and analyzed using a FACS Cantoll machine and FACS Diva software. Data were generated from two independent sets of experiments, each using triplicates. Respective Scatchard analysis was calculated to extrapolate maximal binding (Bmax). The concentrations of CD70xCD3 bispecific antibody constructs at half-maximal binding were determined reflecting the respective KDs. Values of triplicate measurements were plotted as hyperbolic curves and as S-shaped curves to demonstrate proper concentration ranges from minimal to optimal binding.

The results are shown in Table 7 for a representative number of antibody constructs in an scFc format. Cell based Scatchard analysis confirmed that the CD70xCD3 bispecific antibody constructs of the invention are in the low nanomolar range in affinity to human CD70 and to mac CD70 and present with a small and very favorable cyno/human interspecies affinity gap of around 1.

Table 7: Affinities (KD) of CD70xCD3 bispecific antibody constructs as determined in cell based Scatchard analysis with the calculated affinity gap KD macaque CD70 / KD human CD70. Antibody constructs were measured in two independent experiments, each using triplicates.

CD70xCD3 bispecific antibody construct	Cell based affinity hu CD70 [nM]	Cell based affinity mac CD70 [nM]	Affinity gap KD mac/KD hu
CD70-13D_CCxl2C-scFc	7.64 ± 1.20	7.22 ± 1.60	0.95
CD70-16D_CCxl2C-scFc	6.93 ± 1.61	7.71 ± 1.74	1.11
CD70-21D_CCxl2C-scFc	10.77 ± 0.98	11.63 ± 1.22	1.08
CD70-24D_CCxl2C-scFc	8.30 ± 2.75	11.76 ± 2.55	1.42
CD70-25D_CCxl2C-scFc	11.08 ± 4.74	12.57 ± 2.02	1.13
CD70_1-G2D_CCxl2C-scFc	10.56 ± 1.25	9.80 ± 0.73	0.93
CD70-27D_CCxl2C-scFc	9.19 ± 0.54	10.53 ± 0.98	1.15
CD70-28D_CCxl2C-scFc	8.04 ± 1.73	7.18 ± 0.45	0.89
CD70-31D_CCxl2C-scFc	9.40 ± 0.78	10.54 ± 1.51	1.12
CD70-32D_CCxl2C-scFc	9.26 ± 4.36	7.56 ± 0.78	0.82
CD70-42D_CCxl2C-scFc	9.08 ± 2.21	9.15 ± 0.16	1.01
CD70-43D_CCxl2C-scFc	8.73 ± 3.56	9.14 ± 5.73	1.05
CD70-48D_CCxl2C-scFc	6.64 ± 0.13	6.56 ± 0.50	0.99
CD70-62D_CCxl2C-scFc	4.02 ± 0.12	5.17 ± 1.61	1.29
CD70-23D_CCxl2C-scFc	4.72 ± 0.11	6.58 ± 0.85	1.39

Example 5**Bispecific binding and interspecies cross-reactivity**

For confirmation of binding to human CD70 and CD3 and to cyno CD70 and CD3, bispecific antibody constructs of the invention were tested by flow cytometry using

- CHO cells transfected with human CD70 and with macaque CD70, respectively,
- the CD70 positive human ovarian carcinoma cell line OVCAR 8 (but other CD70 positive human cell lines such as the renal clear cell adenocarcinoma cell line O-786 are also conceivable)
- CD3-expressing human T cell leukemia cell line HPB-all (DSMZ, Braunschweig, ACC483), and
- the cynomolgus CD3-expressing T cell line LnPx 4119

For flow cytometry 200,000 cells of the respective cell lines were incubated for 60 min at 4°C with 50 µl of purified bispecific antibody construct at a concentration of 5 µg/ml. The cells were washed twice in PBS/2% FCS and then incubated with an in-house mouse antibody (2 µg/ml) specific for the CD3 binding part of the bispecific antibody constructs for 30 min at 4°C. After washing, bound mouse antibodies were detected with a goat anti-mouse Fcy-PE (1:100) for 30 min at 4°C. Samples were measured by flow cytometry. Non-transfected CHO cells were used as negative control.

The results are shown in Figure 5A-5C for a representative number of antibody constructs in an scFc format. All tested CD70xCD3 constructs stained CHO cells transfected with human CD70 and with cyno CD70, and they also stained the CD70 positive renal clear cell adenocarcinoma cell line O-786 (natural expresser). Human and cyno T cell lines expressing CD3 were also recognized by the bispecific antibody constructs. Moreover, there was no staining of the negative control cells (CHO cells transfected with human CD40L and non-transfected CHO cells).

Example 6**Confirmation of the absence of binding to human paralogues**

Human CD70 paralogue CD40L was stably transfected into CHO cells. The sequence of the paralogue as used in the present example is identified in the sequence listing (SEQ ID NO: 769). Protein expression was confirmed in FACS analyses with specific antibodies. The flow cytometry assay was carried out as described in Example 5. The results are shown in Figure 5A-C and also referred to in Example 5. The analysis confirmed that none of the CD70xCD3 bispecific antibody constructs of the invention cross-reacts with the human CD70 paralogue CD40L.

Example 7:

Identity to human germline

In order to analyze the identity / similarity of the sequence of the antibody constructs to the human antibody germline genes, the CD70 binding domains of the invention were aligned as follows: Full VL including all CDRs was aligned; full VH including CDRs 1 and 2 but except CDR3 was aligned against human antibody germline genes (Vbase). More details can be found in the specification of this application. The results are shown in Table 8 below. All variants show high germline similarity.

Table 8: Percentage of identity of VH and VL to human germline

CD70xCD3 bispecific antibody construct	% identity to human germline [VH]	% identity to human germline [VL]
CD70-13D_CCxI2C-scFc	92,86	95,51
CD70-16D_CCxI2C-scFc	93,88	97,75
CD70-21D_CCxI2C-scFc	92,86	96,63
CD70-24D_CCxI2C-scFc	94,90	98,88
CD70-25D_CCxI2C-scFc	93,88	97,75
CD70_1-G2D_CCxI2C-scFc	93,88	96,63
CD70-27D_CCxI2C-scFc	94,90	96,63
CD70-28D_CCxI2C-scFc	94,90	95,51
CD70-31D_CCxI2C-scFc	91,84	94,38
CD70-32D_CCxI2C-scFc	92,86	95,51
CD70-42D_CCxI2C-scFc	94,90	96,63

CD70-43D_CCxI2C-scFc	92,86	96,63
CD70-48D_CCxI2C-scFc	90,82	95,45
CD70-62D_CCxI2C-scFc	92,86	97,73

Example 8

Cytotoxic activity

The potency of CD70xCD3 bispecific antibody constructs of the invention in redirecting effector T cells against CD70-expressing target cells was analyzed in five *in vitro* cytotoxicity assays:

- The potency of CD70xCD3 bispecific antibody constructs in redirecting stimulated human CD8⁺ effector T cells against human CD70-transfected CHO cells was measured in an 18 hour 51-chromium release assay.
- The potency of CD70xCD3 bispecific antibody constructs in redirecting stimulated human CD8⁺ effector T cells against the the CD70 positive human ovarian carcinoma cell line OVCAR 8 (but other CD70 positive human cell lines are also conceivable) was measured in an 18 hour 51-chromium release assay.
- The potency of CD70xCD3 bispecific antibody constructs in redirecting the T cells in unstimulated human PBMC against human CD70-transfected CHO cells was measured in a 48 hour FACS-based cytotoxicity assay.
- The potency of CD70xCD3 bispecific antibody constructs in redirecting the T cells in unstimulated human PBMC against the the CD70 positive human ovarian carcinoma cell line OVCAR 8 (but other CD70 positive human cell lines are also conceivable) was measured in a 48 hour FACS-based cytotoxicity assay.
- For confirmation that the cross-reactive CD70xCD3 bispecific antibody constructs are capable of redirecting macaque T cells against macaque CD70-transfected CHO cells, a 48 hour FACS-based cytotoxicity assay was performed with a macaque T cell line as effector T cells.

Example 8.1

Chromium release assay with stimulated human T cells

Stimulated T cells enriched for CD8⁺ T cells were obtained as described in the following. A petri dish (145 mm diameter, Greiner bio-one GmbH, Kremsmünster) was coated with a commercially available anti-CD3 specific antibody (OKT3, Orthoclone) in a final concentration of

1 µg/ml for 1 hour at 37°C. Unbound protein was removed by one washing step with PBS. 3 – 5 x 10⁷ human PBMC were added to the precoated petri dish in 120 ml of RPMI 1640 with stabilized glutamine / 10% FCS / IL-2 20 U/ml (Proleukin®, Chiron) and stimulated for 2 days. On the third day, the cells were collected and washed once with RPMI 1640. IL-2 was added to a final concentration of 20 U/ml and the cells were cultured again for one day in the same cell culture medium as above. CD8⁺ cytotoxic T lymphocytes (CTLs) were enriched by depletion of CD4⁺ T cells and CD56⁺ NK cells using Dynal-Beads according to the manufacturer's protocol.

Cyno CD70- or human CD70-transfected CHO target cells were washed twice with PBS and labeled with 11.1 MBq ⁵¹Cr in a final volume of 100 µl RPMI with 50% FCS for 60 minutes at 37°C. Subsequently, the labeled target cells were washed 3 times with 5 ml RPMI and then used in the cytotoxicity assay. The assay was performed in a 96-well plate in a total volume of 200 µl supplemented RPMI with an E:T ratio of 10:1. A starting concentration of 0.01 – 1 µg/ml of purified bispecific antibody construct and threefold dilutions thereof were used. Incubation time for the assay was 18 hours. Cytotoxicity was determined as relative values of released chromium in the supernatant relative to the difference of maximum lysis (addition of Triton-X) and spontaneous lysis (without effector cells). All measurements were carried out in quadruplicates. Measurement of chromium activity in the supernatants was performed in a Wizard 3" gamma counter (Perkin Elmer Life Sciences GmbH, Köln, Germany). Analysis of the results was carried out with Prism 5 for Windows (version 5.0, GraphPad Software Inc., San Diego, California, USA). EC50 values calculated by the analysis program from the sigmoidal dose response curves were used for comparison of cytotoxic activity.

Example 8.2

Potency of redirecting stimulated human effector T cells against human CD70-transfected CHO cells

The cytotoxic activity of CD70xCD3 bispecific antibody constructs according to the invention was analyzed in a 51-chromium (⁵¹Cr) release cytotoxicity assay using CHO cells transfected with human CD70 as target cells, and stimulated human CD8⁺ T cells as effector cells. The experiment was carried out as described in Example 8.1.

The results are shown in Table 9 for a representative number of antibody constructs in an scFc format. The CD70xCD3 (I2C) bispecific antibody constructs showed very potent cytotoxic activity against human CD70 transfected CHO cells in the sub-picomolar range.

Table 9: EC50 values [pM] of CD70xCD3 bispecific antibody constructs analyzed in a 51-chromium (^{51}Cr) release cytotoxicity assay using CHO cells transfected with human CD70 as target cells, and stimulated human CD8 T cells as effector cells.

CD70xCD3 bispecific antibody construct	EC50 [pM]
CD70-13D_CCxI2C-scFc	0.07
CD70-16D_CCxI2C-scFc	0.005
CD70-21D_CCxI2C-scFc	0.06
CD70-24D_CCxI2C-scFc	0.15
CD70-25D_CCxI2C-scFc	0.01
CD70_1-G2D_CCxI2C-scFc	0.01
CD70-27D_CCxI2C-scFc	0.08
CD70-28D_CCxI2C-scFc	0.03
CD70-31D_CCxI2C-scFc	0.11
CD70-32D_CCxI2C-scFc	0.08
CD70-42D_CCxI2C-scFc	0.05
CD70-43D_CCxI2C-scFc	0.08
CD70-48D_CCxI2C-scFc	0.01
CD70-62D_CCxI2C-scFc	0.02
CD70-13D_CCxI2C-scFc	0.05

Example 8.3

Potency of redirecting stimulated human effector T cells against a CD70 positive human cell line

The cytotoxic activity of CD70xCD3 bispecific antibody constructs was analyzed in a 51-chromium (^{51}Cr) release cytotoxicity assay using the CD70 positive human ovarian carcinoma cell line OVCAR 8 as source of target cells, and stimulated human CD8+ T cells as effector cells. The assay was carried out as described in Example 8.1.

The results are shown in Table 10 for a representative number of antibody constructs in an scFc format. In accordance with the results of the 51-chromium release assays with stimulated

enriched human CD8⁺ T lymphocytes as effector cells and human CD70-transfected CHO cells as target cells, the CD70xCD3 bispecific antibody constructs of the present invention are also very potent in cytotoxic activity against natural expresser target cells with a cytotoxic activity against natural expresser cells in the sub-picomolar range.

Table 10: EC₅₀ values [pM] of CD70xCD3 (I2C) bispecific antibody constructs analyzed in an 18-hour 51-chromium (⁵¹Cr) release cytotoxicity assay with the CD70-positive human ovarian carcinoma cell line OVCAR 8 as source of target cells, and stimulated enriched human CD8 T cells as effector cells.

CD70xCD3 bispecific antibody construct	EC ₅₀ [pM]
CD70-13D_CCxI2C-scFc	0.14
CD70-16D_CCxI2C-scFc	0.06
CD70-21D_CCxI2C-scFc	0.10
CD70-24D_CCxI2C-scFc	1.39
CD70-25D_CCxI2C-scFc	0.24
CD70_1-G2D_CCxI2C-scFc	0.12
CD70-27D_CCxI2C-scFc	1.35
CD70-28D_CCxI2C-scFc	0.49
CD70-31D_CCxI2C-scFc	0.64
CD70-32D_CCxI2C-scFc	0.46
CD70-42D_CCxI2C-scFc	0.84
CD70-43D_CCxI2C-scFc	0.67
CD70-48D_CCxI2C-scFc	0.47
CD70-62D_CCxI2C-scFc	0.47
CD70-13D_CCxI2C-scFc	0.36

Example 8.4

FACS-based cytotoxicity assay with unstimulated human PBMC

Isolation of effector cells

Human peripheral blood mononuclear cells (PBMC) were prepared by Ficoll density gradient centrifugation from enriched lymphocyte preparations (buffy coats), a side product of blood

banks collecting blood for transfusions. Buffy coats were supplied by a local blood bank and PBMC were prepared on the same day of blood collection. After Ficoll density centrifugation and extensive washes with Dulbecco's PBS (Gibco), remaining erythrocytes were removed from PBMC via incubation with erythrocyte lysis buffer (155 mM NH_4Cl , 10 mM KHCO_3 , 100 μM EDTA). Platelets were removed via the supernatant upon centrifugation of PBMC at 100 x g. Remaining lymphocytes mainly encompass B and T lymphocytes, NK cells and monocytes. PBMC were kept in culture at 37°C/5% CO_2 in RPMI medium (Gibco) with 10% FCS (Gibco).

Depletion of CD14⁺ and CD56⁺ cells

For depletion of CD14⁺ cells, human CD14 MicroBeads (Milteny Biotec, MACS, #130-050-201) were used, for depletion of NK cells human CD56 MicroBeads (MACS, #130-050-401). PBMC were counted and centrifuged for 10 min at room temperature with 300 x g. The supernatant was discarded and the cell pellet resuspended in MACS isolation buffer [80 μL / 10^7 cells; PBS (Invitrogen, #20012-043), 0.5% (v/v) FBS (Gibco, #10270-106), 2 mM EDTA (Sigma-Aldrich, #E-6511)]. CD14 MicroBeads and CD56 MicroBeads (20 μL / 10^7 cells) were added and incubated for 15 min at 4 - 8°C. The cells were washed with MACS isolation buffer (1 - 2 mL/ 10^7 cells). After centrifugation (see above), supernatant was discarded and cells resuspended in MACS isolation buffer (500 μL / 10^8 cells). CD14/CD56 negative cells were then isolated using LS Columns (Miltenyi Biotec, #130-042-401). PBMC w/o CD14⁺/CD56⁺ cells were cultured in RPMI complete medium i.e. RPMI1640 (Biochrom AG, #FG1215) supplemented with 10% FBS (Biochrom AG, #S0115), 1x non-essential amino acids (Biochrom AG, #K0293), 10 mM Hepes buffer (Biochrom AG, #L1613), 1 mM sodium pyruvate (Biochrom AG, #L0473) and 100 U/mL penicillin/streptomycin (Biochrom AG, #A2213) at 37°C in an incubator until needed.

Target cell labeling

For the analysis of cell lysis in flow cytometry assays, the fluorescent membrane dye DiOC₁₈ (DiO) (Molecular Probes, #V22886) was used to label human CD70- or macaque CD70-transfected CHO cells as target cells and distinguish them from effector cells. Briefly, cells were harvested, washed once with PBS and adjusted to 10^6 cell/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 μL / 10^6 cells). After incubation for 3 min at 37°C, cells were washed twice in complete RPMI medium and the cell number adjusted to 1.25×10^5 cells/mL. The vitality of cells was determined using 0.5 % (v/v) isotonic EosinG solution (Roth, #45380).

Flow cytometry based analysis

This assay was designed to quantify the lysis of cyno or human CD70-transfected CHO cells in the presence of serial dilutions of CD70 bispecific antibody constructs. Equal volumes of DiO-labeled target cells and effector cells (i.e., PBMC w/o CD14⁺ cells) were mixed, resulting in an E:T cell ratio of 10:1. 160 µl of this suspension were transferred to each well of a 96-well plate. 40 µL of serial dilutions of the CD70xCD3 bispecific antibody constructs and a negative control bispecific (a CD3-based bispecific antibody construct recognizing an irrelevant target antigen) or RPMI complete medium as an additional negative control were added. The bispecific antibody-mediated cytotoxic reaction proceeded for 48 hours in a 7% CO₂ humidified incubator. Then cells were transferred to a new 96-well plate and loss of target cell membrane integrity was monitored by adding propidium iodide (PI) at a final concentration of 1 µg/mL. PI is a membrane impermeable dye that normally is excluded from viable cells, whereas dead cells take it up and become identifiable by fluorescent emission.

Samples were measured by flow cytometry on a FACSCanto II instrument and analyzed by FACSDiva software (both from Becton Dickinson). Target cells were identified as DiO-positive cells. PI-negative target cells were classified as living target cells. Percentage of cytotoxicity was calculated according to the following formula:

$$\text{Cytotoxicity [\%]} = \frac{n_{\text{dead target cells}}}{n_{\text{target cells}}} \times 100$$

n = number of events

Using GraphPad Prism 5 software (Graph Pad Software, San Diego), the percentage of cytotoxicity was plotted against the corresponding bispecific antibody construct concentrations. Dose response curves were analyzed with the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope and EC50 values were calculated.

Example 8.5

Potency of redirecting unstimulated human PBMC against human CD70-transfected CHO cells

The cytotoxic activity of CD70xCD3 bispecific antibody constructs was analyzed in a FACS-based cytotoxicity assay using CHO cells transfected with human CD70 as target cells, and unstimulated human PBMC as effector cells. The assay was carried out as described in Example 8.4 above. In a further approach, soluble CD27 was added in a concentration of

1 ng/ml, in order to verify whether the presence of the soluble form of CD27 would impair the cytotoxic activity of the tested antibody constructs.

The results of the FACS-based cytotoxicity assays are shown in Table 11 for a representative number of antibody constructs in an scFc format with unstimulated human PBMC as effector cells and human CD70-transfected CHO cells as targets. The EC₅₀ values were not significantly influenced by the presence of CD27. See also Figure 6 which shows the results for the construct CD70-21D_CCxI2C-scFc.

Table 11: EC₅₀ values [pM] of CD70xCD3 (I2C) bispecific antibody constructs as measured in a 48-hour FACS-based cytotoxicity assay with unstimulated human PBMC as effector cells and CHO cells transfected with human CD70 as target cells.

CD70xCD3 bispecific antibody construct	EC₅₀ [pM] w/o sCD27	EC₅₀ [pM] w/ 1 ng/ml sCD27
CD70-13D_CCxI2C-scFc	0.21	0.21
CD70-16D_CCxI2C-scFc	0.27	0.18
CD70-21D_CCxI2C-scFc	0.22	0.17
CD70-24D_CCxI2C-scFc	0.32	0.43
CD70-25D_CCxI2C-scFc	0.29	0.21
CD70_1-G2D_CCxI2C-scFc	0.49	0.25
CD70-27D_CCxI2C-scFc	0.49	0.29
CD70-28D_CCxI2C-scFc	0.19	0.20
CD70-31D_CCxI2C-scFc	0.48	0.60
CD70-32D_CCxI2C-scFc	0.26	0.24
CD70-42D_CCxI2C-scFc	0.29	0.23
CD70-43D_CCxI2C-scFc	0.22	0.15
CD70-48D_CCxI2C-scFc	0.26	0.29
CD70-62D_CCxI2C-scFc	0.35	0.21
CD70-13D_CCxI2C-scFc	0.25	0.18

Expectedly, EC₅₀ values were generally higher in cytotoxicity assays with unstimulated PBMC as effector cells compared with cytotoxicity assays using stimulated human CD8⁺ T cells (see Example 8.2).

Example 8.6**Potency of redirecting unstimulated human PBMC against a CD70 positive human ovarian carcinoma cell line**

The cytotoxic activity of CD70xCD3 bispecific antibody constructs was furthermore analyzed in a FACS-based cytotoxicity assay using the CD70 positive human ovarian carcinoma cell line OVCAR 8 as a source of target cells and unstimulated human PBMC as effector cells. The assay was carried out as described in Example 8.4 above. The results are shown in Table 12 for a representative number of antibody constructs in an scFc format.

Table 12: EC₅₀ values [pM] of CD70xCD3 (I2C) bispecific antibody constructs as measured in a 48-hour FACS-based cytotoxicity assay with unstimulated human PBMC as effector cells and the human cell line SHP-77 as source of target cells.

CD70xCD3 bispecific antibody construct	EC₅₀ [pM]
CD70-13D_CCxI2C-scFc	0.07
CD70-16D_CCxI2C-scFc	0.10
CD70-21D_CCxI2C-scFc	0.06
CD70-24D_CCxI2C-scFc	0.50
CD70-25D_CCxI2C-scFc	0.05
CD70_1-G2D_CCxI2C-scFc	0.08
CD70-27D_CCxI2C-scFc	0.56
CD70-28D_CCxI2C-scFc	0.12
CD70-31D_CCxI2C-scFc	1.03
CD70-32D_CCxI2C-scFc	0.06
CD70-42D_CCxI2C-scFc	0.13
CD70-43D_CCxI2C-scFc	0.14
CD70-48D_CCxI2C-scFc	0.14
CD70-62D_CCxI2C-scFc	0.26
CD70-13D_CCxI2C-scFc	0.09

Example 8.7

Potency of redirecting macaque T cells against macaque CD70-expressing CHO cells

Finally, the cytotoxic activity of CD70xCD3 bispecific antibody constructs was analyzed in a FACS-based cytotoxicity assay using CHO cells transfected with macaque (cyno) CD70 as target cells, and the macaque T cell line 4119LnPx (Knappe et al. Blood 95:3256-61 (2000)) as source of effector cells. Target cell labeling of macaque CD70-transfected CHO cells and flow cytometry based analysis of cytotoxic activity was performed as described above.

Results are shown in Table 13 for a representative number of antibody constructs in an scFc format. Macaque T cells from cell line 4119LnPx were induced to efficiently kill macaque CD70-transfected CHO cells by CD70xCD3 (I2C) bispecific antibody constructs according to the invention. The antibody constructs presented potently with sub-picomolar EC50-values in this assay, confirming that they are very active in the macaque system.

Table 13: EC50 values [pM] of CD70xCD3 bispecific antibody constructs as measured in a 48-hour FACS-based cytotoxicity assay with macaque T cell line 4119LnPx as effector cells and CHO cells transfected with macaque CD70 as target cells.

CD70xCD3 bispecific antibody construct	EC50 [pM]
CD70-13D_CCxI2C-scFc	0.07
CD70-16D_CCxI2C-scFc	0.03
CD70-21D_CCxI2C-scFc	0.03
CD70-24D_CCxI2C-scFc	0.14
CD70-25D_CCxI2C-scFc	0.03
CD70_1-G2D_CCxI2C-scFc	0.03
CD70-27D_CCxI2C-scFc	0.12
CD70-28D_CCxI2C-scFc	0.08
CD70-31D_CCxI2C-scFc	0.23
CD70-32D_CCxI2C-scFc	0.03
CD70-42D_CCxI2C-scFc	0.05
CD70-43D_CCxI2C-scFc	0.07
CD70-48D_CCxI2C-scFc	0.04
CD70-62D_CCxI2C-scFc	0.04

CD70-13D_CCxI2C-scFc	0.06
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Example 9

Monomer to dimer conversion after (i) three freeze/thaw cycles and (ii) 7 days of incubation at 250 µg/ml

Bispecific CD70xCD3 antibody monomeric construct was subjected to different stress conditions followed by high performance SEC to determine the percentage of initially monomeric antibody construct, which had been converted into dimeric antibody construct.

(i) 25 µg of monomeric antibody construct were adjusted to a concentration of 250 µg/ml with generic formulation buffer and then frozen at -80°C for 30 min followed by thawing for 30 min at room temperature. After three freeze/thaw cycles the dimer content was determined by HP-SEC.

(ii) 25 µg of monomeric antibody construct were adjusted to a concentration of 250 µg/ml with generic formulation buffer followed by incubation at 37°C for 7 days. The dimer content was determined by HP-SEC.

A high resolution SEC Column TSK Gel G3000 SWXL (Tosoh, Tokyo-Japan) was connected to an Äkta Purifier 10 FPLC (GE Lifesciences) equipped with an A905 Autosampler. Column equilibration and running buffer consisted of 100 mM KH₂PO₄ – 200 mM Na₂SO₄ adjusted to pH 6.6. The antibody solution (25 µg protein) was applied to the equilibrated column and elution was carried out at a flow rate of 0.75 ml/min at a maximum pressure of 7 MPa. The whole run was monitored at 280, 254 and 210 nm optical absorbance. Analysis was done by peak integration of the 210 nm signal recorded in the Äkta Unicorn software run evaluation sheet. Dimer content was calculated by dividing the area of the dimer peak by the total area of monomer plus dimer peak.

The results are shown in Table 14 for a representative number of antibody constructs in an scFc format. The CD70xCD3 (I2C) bispecific antibody constructs of the invention presented with dimer percentages of ≤ 1.5% (with most of the constructs presenting with a dimer percentage of ≤ 1.0%) after three freeze/thaw cycles, and with dimer percentages of ≤ 0.6% (with most of the constructs presenting with a dimer percentage of 0%) after 7 days of incubation at 37°C.

Table 14: Percentage of monomeric versus dimeric CD70xCD3 bispecific antibody constructs as determined by High Performance Size Exclusion Chromatography (HP-SEC).

CD70xCD3 bispecific antibody construct	Percentage of dimer after 7 days of incubation at 37°C	Percentage of dimer after three freeze/thaw cycles
CD70-13D_CCxI2C-scFc	0.1	0.4
CD70-16D_CCxI2C-scFc	0.0	0.0
CD70-21D_CCxI2C-scFc	0.0	0.2
CD70-24D_CCxI2C-scFc	0.3	1.1
CD70-25D_CCxI2C-scFc	0.3	0.2
CD70_1-G2D_CCxI2C-scFc	0.0	0.4
CD70-27D_CCxI2C-scFc	0.0	1.5
CD70-28D_CCxI2C-scFc	0.3	0.1
CD70-31D_CCxI2C-scFc	0.0	1.5
CD70-32D_CCxI2C-scFc	0.0	0.8
CD70-42D_CCxI2C-scFc	0.0	0.3
CD70-43D_CCxI2C-scFc	0.0	0.4
CD70-48D_CCxI2C-scFc	0.6	0.5
CD70-62D_CCxI2C-scFc	0.0	0.8
CD70-13D_CCxI2C-scFc	0.0	0.7

Example 10

Thermostability

Antibody aggregation temperature was determined as follows: 40 µl of antibody construct solution at 250 µg/ml were transferred into a single use cuvette and placed in a Wyatt Dynamic Light Scattering device DynaPro Nanostar (Wyatt). The sample was heated from 40°C to 70°C at a heating rate of 0.5°C/min with constant acquisition of the measured radius. Increase of radius indicating melting of the protein and aggregation was used by the software package delivered with the DLS device to calculate the aggregation temperature of the antibody construct.

All tested CD70xCD3 (I2C) bispecific antibody constructs of the invention showed thermal stability with aggregation temperatures $\geq 52.0^{\circ}\text{C}$, as shown in Table 15 below for a representative number of antibody constructs in an scFc format.

Table 15: Thermostability of the CD70xCD3 bispecific antibody constructs as determined by DLS (dynamic light scattering)

CD70xCD3 bispecific antibody construct	Thermostability (DLS °C aggregation)
CD70-13D_CCxI2C-scFc	52.4
CD70-16D_CCxI2C-scFc	57.7
CD70-21D_CCxI2C-scFc	57.3
CD70-24D_CCxI2C-scFc	57.4
CD70-25D_CCxI2C-scFc	57.6
CD70_1-G2D_CCxI2C-scFc	57.7
CD70-27D_CCxI2C-scFc	57.5
CD70-28D_CCxI2C-scFc	57.5
CD70-31D_CCxI2C-scFc	56.4
CD70-32D_CCxI2C-scFc	57.7
CD70-42D_CCxI2C-scFc	57.6
CD70-43D_CCxI2C-scFc	57.2
CD70-48D_CCxI2C-scFc	56.7
CD70-62D_CCxI2C-scFc	55.5
CD70-13D_CCxI2C-scFc	57.7

Example 11

Stability after incubation for 24 hours in human plasma

Purified bispecific antibody constructs were incubated at a ratio of 1:5 in a human plasma pool at 37°C for 96 hours at a final concentration of 2-20 $\mu\text{g/ml}$. After plasma incubation the antibody

constructs were compared in a 51-chromium release assay with stimulated enriched human CD8⁺ T cells and human CD70-transfected CHO cells at a starting concentration of 0.01-0.1 µg/ml and with an effector to target cell (E:T) ratio of 10:1 (assay as described in Example 8.1). Non-incubated, freshly thawed bispecific antibody constructs were included as controls.

The results are shown in Table 16 for a representative number of antibody constructs in an scFc format. Most tested antibody constructs had a very favourable plasma stability (EC_{50} plasma / EC_{50} control) of ≤ 3.0 or ≤ 2.5 .

Table 16: EC_{50} values of the CD70xCD3 (I2C) antibody constructs with and without plasma incubation and calculated plasma / control value

CD70xCD3 bispecific antibody construct	EC_{50} [pM]		Plasma to Control ratio (EC_{50} plasma/ EC_{50} control)
	w/ plasma	w/o plasma	
CD70-13D_CCxI2C-scFc	0.06	0.07	0.8
CD70-16D_CCxI2C-scFc	0.01	0.005	1.8
CD70-21D_CCxI2C-scFc	0.05	0.06	0.9
CD70-24D_CCxI2C-scFc	n.a.	0.15	n.a.
CD70-25D_CCxI2C-scFc	0.00	0.01	0.2
CD70_1-G2D_CCxI2C-scFc	0.07	0.01	6.8
CD70-27D_CCxI2C-scFc	0.08	0.08	1.1
CD70-28D_CCxI2C-scFc	0.01	0.03	0.5
CD70-31D_CCxI2C-scFc	0.18	0.11	1.6
CD70-32D_CCxI2C-scFc	0.03	0.08	0.4
CD70-42D_CCxI2C-scFc	0.07	0.05	1.4
CD70-43D_CCxI2C-scFc	0.11	0.08	1.4
CD70-48D_CCxI2C-scFc	0.03	0.01	3.0
CD70-62D_CCxI2C-scFc	0.05	0.02	2.2
CD70-13D_CCxI2C-scFc	0.02	0.05	0.3

Example 12

Turbidity at 2500 µg/ml antibody concentration

1 ml of purified antibody construct solution of a concentration of 250 µg/ml was concentrated by spin concentration units to 2500 µg/ml. After 16h storage at 5°C the turbidity of the antibody solution was determined by OD340 nm optical absorption measurement against the generic formulation buffer.

The results are shown in Table 17 for a representative number of CD70xCD3 (I2C) antibody constructs in an scFc format. All tested antibody constructs have a very favourable turbidity of ≤ 0.05 .

Table 17: Turbidity of the antibody constructs after concentration to 2.5 mg/ml over night

CD70xCD3 bispecific antibody construct	Turbidity at 2500 µg/ml [OD340]
CD70-13D_CCxI2C-scFc	0.023
CD70-16D_CCxI2C-scFc	0.017
CD70-21D_CCxI2C-scFc	0.015
CD70-24D_CCxI2C-scFc	0.019
CD70-25D_CCxI2C-scFc	0.027
CD70_1-G2D_CCxI2C-scFc	0.022
CD70-27D_CCxI2C-scFc	0.034
CD70-28D_CCxI2C-scFc	0.011
CD70-31D_CCxI2C-scFc	0.015
CD70-32D_CCxI2C-scFc	0.024
CD70-42D_CCxI2C-scFc	0.019
CD70-43D_CCxI2C-scFc	0.023
CD70-48D_CCxI2C-scFc	0.023
CD70-62D_CCxI2C-scFc	0.031
CD70-13D_CCxI2C-scFc	0.017

Example 13**Protein Homogeneity by high resolution cation exchange chromatography**

The protein homogeneity the antibody constructs of the invention was analyzed by high resolution cation exchange chromatography CIEX.

50 µg of antibody construct monomer were diluted with 50 ml binding buffer A (20 mM sodium dihydrogen phosphate, 30 mM NaCl, 0.01% sodium octanate, pH 5.5), and 40 ml of this solution were applied to a 1 ml BioPro SP-F column (YMC, Germany) connected to an Äkta Micro FPLC device (GE Healthcare, Germany). After sample binding, a wash step with further binding buffer was carried out. For protein elution, a linear increasing salt gradient using buffer B (20 mM sodium dihydrogen phosphate, 1000 mM NaCl, 0.01% sodium octanate, pH 5.5) up to 50% percent buffer B was applied over 10 column volumes. The whole run was monitored at 280, 254 and 210 nm optical absorbance. Analysis was done by peak integration of the 280 nm signal recorded in the Äkta Unicorn software run evaluation sheet.

The results are shown in Table 18 for a representative number of CD70xCD3 (I2C) antibody constructs in an scFc format. All tested antibody constructs have a favourable homogeneity of $\geq 60\%$ (area under the curve (= AUC) of the main peak), nine out of 15 constructs have a homogeneity of $\geq 70\%$.

Table 18: Protein homogeneity of the antibody constructs (% AUC of main peak)

CD70xCD3 bispecific antibody construct	Protein homogeneity % AUC of main peak
CD70-13D_CCxI2C-scFc	81
CD70-16D_CCxI2C-scFc	79
CD70-21D_CCxI2C-scFc	74
CD70-24D_CCxI2C-scFc	73
CD70-25D_CCxI2C-scFc	71
CD70_1-G2D_CCxI2C-scFc	69
CD70-27D_CCxI2C-scFc	70
CD70-28D_CCxI2C-scFc	67

CD70-31D_CCxI2C-scFc	68
CD70-32D_CCxI2C-scFc	76
CD70-42D_CCxI2C-scFc	67
CD70-43D_CCxI2C-scFc	62
CD70-48D_CCxI2C-scFc	70
CD70-62D_CCxI2C-scFc	66
CD70-13D_CCxI2C-scFc	73

Example 14**Surface hydrophobicity as measured by HIC Butyl**

The surface hydrophobicity of bispecific antibody constructs of the invention was tested in Hydrophobic Interaction Chromatography HIC in flow-through mode.

50 µg of antibody construct monomer were diluted with generic formulation buffer to a final volume of 500 µl (10 mM citric acid, 75 mM lysine HCl, 4% trehalose, pH 7.0) and applied to a 1 ml Butyl Sepharose FF column (GE Healthcare, Germany) connected to a Äkta Purifier FPLC system (GE Healthcare, Germany). The whole run was monitored at 280, 254 and 210 nm optical absorbance. Analysis was done by peak integration of the 280 nm signal recorded in the Äkta Unicorn software run evaluation sheet. Elution behavior was evaluated by comparing area and velocity of rise and decline of protein signal thereby indicating the strength of interaction of the BiTE albumin fusion with the matrix.

A representative number of CD70xCD3 (I2C) antibody constructs in an scFc format was analysed and shown to have a good elution behaviour, which was mostly rapid and complete.

Example 15**Potency gap between the monomeric and the dimeric isoform of bispecific antibody constructs**

In order to determine the difference in cytotoxic activity between the monomeric and the dimeric isoform of individual CD70xCD3 bispecific antibody constructs (referred to as potency gap), an 18 hour ⁵¹-chromium release cytotoxicity assay was carried out as described hereinabove (Example 8.1) with purified bispecific antibody construct monomer and dimer. Effector cells were stimulated enriched human CD8⁺ T cells. Target cells were hu CD70 transfected CHO cells. Effector to target cell (E:T) ratio was 10:1. The potency gap was calculated as ratio between EC₅₀ values.

Results are shown in Table 19 for a representative number of antibody constructs in an scFc format. Potency gaps of the tested CD70xCD3 (I2C) bispecific antibody constructs were between 0.0 and 1.5. There is hence no substantially more active dimer compared to its respective monomer.

Table 19: Potency gap between the monomeric and the dimeric isoform

CD70xCD3 bispecific antibody construct	EC₅₀ [pM] Monomer	EC₅₀ [pM] dimer	Ratio EC₅₀ monomer / EC₅₀ dimer
CD70-13D_CCxI2C-scFc	0.07	0.11	0.6
CD70-16D_CCxI2C-scFc	0.005	0.07	0.1
CD70-21D_CCxI2C-scFc	0.06	0.04	1.5
CD70-24D_CCxI2C-scFc	0.15	0.24	0.6
CD70-25D_CCxI2C-scFc	0.01	0.09	0.1
CD70_1-G2D_CCxI2C-scFc	0.01	0.06	0.2
CD70-27D_CCxI2C-scFc	0.08	0.25	0.3
CD70-28D_CCxI2C-scFc	0.03	0.09	0.3
CD70-31D_CCxI2C-scFc	0.11	0.24	0.5
CD70-32D_CCxI2C-scFc	0.08	0.23	0.3
CD70-42D_CCxI2C-scFc	0.05	70	0.0
CD70-43D_CCxI2C-scFc	0.08	0.20	0.4
CD70-48D_CCxI2C-scFc	0.01	0.09	0.1
CD70-62D_CCxI2C-scFc	0.02	0.17	0.1
CD70-13D_CCxI2C-scFc	0.05	0.12	0.4

Example 16**CD27 does not inhibit binding of anti-CD70 scFv molecules**

This assay was carried out to test whether the soluble form of CD27 (136-458 pg/ml soluble CD27 in human serum; Huang J. et al. (2013) J Immunol 190: 1-9) would impair binding of the anti-CD70 binding domains according to the invention to CD70.

To verify binding of human CD27 to CHO cells transfected with human CD70, cells were incubated with human CD27 for 30 minutes at 4°C (1 µg/ml; R&D #382-CD-100). Bound CD27 was detected with an anti-HIS antibody (5 µg/ml; AbD Serotec) followed by an anti-mouse IgG Fc-gamma-PE (1:100; Jackson Immunoresearch # 115-116-071). As negative control cells were incubated with PBS/2%FCS instead of CD27.

To test replacement of anti-CD70 scFv by CD27, CHO cells transfected with human CD70 were incubated with or without CD27 for 30 minutes at 4°C (1 µg/ml; R&D #382-CD-100). Afterwards cells were washed twice and then stained with crude, undiluted periplasmic extract containing scFv binding to CD70. Bound scFv was detected with mouse monoclonal anti-FLAG M2 antibody (1 µg/ml; Sigma F1804) followed by an anti-mouse IgG Fc-gamma-PE (1:100; Jackson Immunoresearch # 115-116-071). As negative control, cells were incubated with an unspecific scFv instead of anti-CD70 scFv. CD27 and all antibodies were diluted in PBS with 2%FCS.

No competition between soluble CD27 and the anti-CD70 scFv was observed for any of the CD70 binders of the present invention that were analyzed.

Table 20: Sequence listing

SEQ ID NO:	CD70 epitope	Designation	Format / Source	Amino acid sequence
1		CD70-1	VH CDR1	TYGMH
2		CD70-1	VH CDR2	VIWYDGSNKYYGDSVKG
3		CD70-1	VH CDR3	DNSHYYYGMDV
4		CD70-1	VL CDR1	TGSSSNIGAGYDVN
5		CD70-1	VL CDR2	VNNNRPS
6		CD70-1	VL CDR3	QSYDTSLSASV
7		CD70-1	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSTYGMHWVRQAPGKGLEWVAVIWIYDGSNKYYGDS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGT'TVTVSS
8		CD70-1	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNNRPSGVDPDR FSGTSGTSASLAITGLQAEDEADYYCQSYDTSLSASVFGGGTRLTVL
9	III	CD70-1	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSTYGMHWVRQAPGKGLEWVAVIWIYDGSNKYYGDS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGT'TVTVSSGGGSG GGGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVDPDRFSGTSGTSASLAITGLQAEDEADYYCQSYDTSLSASVFGGGTRLTVLS
10		CD70-1	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTTFSTYGMHWVRQAPGKGLEWVAVIWIYDGSNKYYGDS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGT'TVTVSSGGGSG GGGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVDPDRFSGTSGTSASLAITGLQAEDEADYYCQSYDTSLSASVFGGGTRLTVLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDN SKNTAYLQMNLLKTEDTAVYYCVRHGFGNSYISWAYWGQGT'LVTVSSG GGGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN IGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAFYCYVLWYSNRWVFGGGT'KLTVL

11		CD70-2	VH CDR1	SYGMH	
12		CD70-2	VH CDR2	VIWYDGSDKYFADSVKG	
13		CD70-2	VH CDR3	DGIAGARYVYFDY	
14		CD70-2	VL CDR1	RASQGISNYLA	
15		CD70-2	VL CDR2	AASSLQG	
16		CD70-2	VL CDR3	QQYYNYPFT	
17		CD70-2	VH	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAVIWYDGSDKYFADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGIAGARYVYFDYWGQGLTVTVSS	
18		CD70-2	VL	DIQMTQSPSSLSASVGRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAASSLQGGVPSKFS GSGGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGPGTTVDIK	
19	II	CD70-2	scFv	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAVIWYDGSDKYFADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGIAGARYVYFDYWGQGLTVTVSSGGGG SGGGSGGGSDIQMTQSPSSLSASVGRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAAS SLQGGVPSKFSGSGGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGPGTTVDIK	
20		CD70-2	bispecific molecule	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAVIWYDGSDKYFADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDGIAGARYVYFDYWGQGLTVTVSSGGGG SGGGSGGGSDIQMTQSPSSLSASVGRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAAS SLQGGVPSKFSGSGGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGPGTTVDIKSGGGGSEV QLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG GSGGGSGGGGQTVVTVQEPSTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG GTKFLAPGTPARFSGSLLGGKAAALTLSGVQPEDEAEYCYLWYSNRWVFGGGTKLTVL	
21		CD70-3	VH CDR1	SYGMH	
22		CD70-3	VH CDR2	VTWYDGSNKYYGDSVKG	
23		CD70-3	VH	DLLRGVKGYAMDV	

			CDR3	
24		CD70-3	VL CDR1	RASQSLRRIYLA
25		CD70-3	VL CDR2	DVFD RAT
26		CD70-3	VL CDR3	QQYSDSPFT
27		CD70-3	VH	QEQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVTWYDGSNKYYGDS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMDVGQGTTVTVSS
28		CD70-3	VL	EIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLAWYQQKPGQAPRLLIYDVFD RATGIPDRF SGGSGTDFTLTISRLEPEDFAVYYCQQYSDSPFTFGPGTKVDIK
29	III _v	CD70-3	scFv	QEQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVTWYDGSNKYYGDS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMDVGQGTTVTVSSGGGG SGGGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLAWYQQKPGQAPRLLIYDV FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSDSPFTFGPGTKVDIK
30		CD70-3	bispecific molecule	QEQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVTWYDGSNKYYGDS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMDVGQGTTVTVSSGGGG SGGGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLAWYQQKPGQAPRLLIYDV FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSDSPFTFGPGTKVDIKSGGGSE VQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGG GGGGSGGGSGQTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
31		CD70-4	VH CDR1	SYGIS
32		CD70-4	VH CDR2	WISAYNGYTHYAQLQG
33		CD70-4	VH CDR3	DYGGNDYYGMDV
34		CD70-4	VL CDR1	SGSSSNIGINYVY
35		CD70-4	VL CDR2	RSDQRPS

36		CD70-4	VL CDR3	AAWDDSLSGVV	
37		CD70-4	VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGYTHYAQK LQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTITVTVSS	
38		CD70-4	VL	QSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVVYQQLPGTAPKLLIYRSDQRPSPGVDRF SGSKSGTSASIALSGLRSEADYYCAAWDDSLSGVFFGGGKLTIVL	
39	I	CD70-4	scFv	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGYTHYAQK LQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTITVTVSSGGGGS GGGSGGGGSQSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVVYQQLPGTAPKLLIYRSD QRPSPGVDRFSGSKSGTSASIALSGLRSEADYYCAAWDDSLSGVFFGGGKLTIVL	
40		CD70-4	bispecific molecule	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGYTHYAQK LQGRVTMTTDTSTSTAYMELSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTITVTVSSGGGGS GGGSGGGGSQSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVVYQQLPGTAPKLLIYRSD QRPSPGVDRFSGSKSGTSASIALSGLRSEADYYCAAWDDSLSGVFFGGGKLTIVL EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTITVTVSSG GGSGGGGGSGGSQTVVTQEPSTLTVSPGGTITLTCGSSTGAVTSNYPNWVQKPGQAPRGL IGTKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTIVL	
41		CD70-5	VH CDR1	SGGYIYWS	
42		CD70-5	VH CDR2	YIFYSGSTDYNPSLKS	
43		CD70-5	VH CDR3	SGYSYALFDH	
44		CD70-5	VL CDR1	RASQFIGRYFN	
45		CD70-5	VL CDR2	AESSLQS	
46		CD70-5	VL CDR3	QQSYSTPWT	
47		CD70-5	VH	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQHPGKGLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARSGYSYALFDHWGQGTITVTVSS	
48		CD70-5	VL	DIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSLQSGVPSRFS	

49	VIII	CD70-5	scFv	GGSGTFTLTISLQPEDFARYYCQQSYSTPWTFGQGTKVEIK QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQHPGKGLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSSTAAATAVYCARSGYSYALFDHWGQGTTLTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSL QSGVPSRFSGSGTFTLTISLQPEDFARYYCQQSYSTPWTFGQGTKVEIK
50		CD70-5	bispecific molecule	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQHPGKGLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSSTAAATAVYCARSGYSYALFDHWGQGTTLTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSL QSGVPSRFSGSGTFTLTISLQPEDFARYYCQQSYSTPWTFGQGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGNSYISYWAYWGQGTTLTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSL KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
51		CD70-6	VH CDR1	SGGYWS
52		CD70-6	VH CDR2	YIFYSGSTDYNPSLKS
53		CD70-6	VH CDR3	SGYSYALFDH
54		CD70-6	VL CDR1	RASQFIGRYFN
55		CD70-6	VL CDR2	AESSLQS
56		CD70-6	VL CDR3	QQSYSTPFT
57		CD70-6	VH	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSSTAAATAVYCARSGYSYALFDHWGQGTTLTVSS
58		CD70-6	VL	DIQMTQSPSSLSASVGDRTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSLQSGVPSRFS GGSGTFTLTISLQPEDFARYYCQQSYSTPWTFGQGTKVEIK
59	VIII	CD70-6	scFv	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSSTAAATAVYCARSGYSYALFDHWGQGTTLTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSL QSGVPSRFSGSGTFTLTISLQPEDFARYYCQQSYSTPWTFGQGTKVEIK

60		CD70-6	bispecific molecule	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYICARSGYSYALFDHWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTVTSRQSFYGRYFNWYQQQPGKAPKVLIIYAESSL QSGVPSRFSGSGSGTEFTLTISLQPEDFARYCQQSYSTPFTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYICVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSIGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
61		CD70-7	VH CDR1	SYYLH
62		CD70-7	VH CDR2	IVDPGGGSTSYDQKFQG
63		CD70-7	VH CDR3	DYGDYVFDY
64		CD70-7	VL CDR1	SGSSSNIGNTVN
65		CD70-7	VL CDR2	INNQRPS
66		CD70-7	VL CDR3	ATWDDSLNGPV
67		CD70-7	VH	QVHLVQSGAEVKKPGASVRVSCKASGYTFTSYLHWVRQAPGQCLEWMGIVDPGGGSTSYDQK FQGRFTMTTRDTSTSTVYMELSLRSEDTAVYICARDYGDYVFDYWGGQGLTVTVSS
68		CD70-7	VL	QSVLTQPPSASGTPGQRTVTSKSSSSNIGNTVNWYQQLPGTAPQLLIYINNQRPSGVPDRF SGSKSGTSASLAISGLQSEDEADYICATWDDSLNGPVVGGCGTKLTVL
69	I	CD70-7	scFv	QVHLVQSGAEVKKPGASVRVSCKASGYTFTSYLHWVRQAPGQCLEWMGIVDPGGGSTSYDQK FQGRFTMTTRDTSTSTVYMELSLRSEDTAVYICARDYGDYVFDYWGGQGLTVTVSSGGGSGGG GSGGGGQSVLTQPPSASGTPGQRTVTSKSSSSNIGNTVNWYQQLPGTAPQLLIYINNQRPS SGVPDRFSGSKSGTSASLAISGLQSEDEADYICATWDDSLNGPVVGGCGTKLTVL
70		CD70-7	bispecific molecule	QVHLVQSGAEVKKPGASVRVSCKASGYTFTSYLHWVRQAPGQCLEWMGIVDPGGGSTSYDQK FQGRFTMTTRDTSTSTVYMELSLRSEDTAVYICARDYGDYVFDYWGGQGLTVTVSSGGGSGGG GSGGGGQSVLTQPPSASGTPGQRTVTSKSSSSNIGNTVNWYQQLPGTAPQLLIYINNQRPS SGVPDRFSGSKSGTSASLAISGLQSEDEADYICATWDDSLNGPVVGGCGTKLTVL LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV

				KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
71	CD70-8	VH CDR1		SYGMH
72	CD70-8	VH CDR2		VIWYDGSDKYFADSVKG
73	CD70-8	VH CDR3		DGIAGARYVYFDY
74	CD70-8	VL CDR1		RASQGISNYLA
75	CD70-8	VL CDR2		AASSLQG
76	CD70-8	VL CDR3		QQYYNYPFT
77	CD70-8	VH		QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVIWDGSDKYFADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDGIAGARYVYFDYWGQGLTVTVSS
78	CD70-8	VL		DIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWFQQKPGKAPKSLIYAASSLQGGVPSKFS GSGGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGCGTTVDIK
79	CD70-8	scFv	II	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVIWDGSDKYFADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDGIAGARYVYFDYWGQGLTVTVSSGGGG SGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWFQQKPGKAPKSLIYAAS SLQGGVPSKFSGSGGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGCGTTVDIK
80	CD70-8	bispecific molecule		QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVIWDGSDKYFADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDGIAGARYVYFDYWGQGLTVTVSSGGGG SGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWFQQKPGKAPKSLIYAAS SLQGGVPSKFSGSGGTDFTLTISSLQPEDFATYYCQQYYNYPFTFGCGTTVDIKSGGGSEV QLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGG GSGGGSGGGSQTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIG GTKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
81	CD70-9	VH CDR1		SYGIS

82	CD70-9	VH CDR2	WISAYNGYTHYAQKLQG
83	CD70-9	VH CDR3	DYGGNDYYGMDV
84	CD70-9	VL CDR1	SGSSSNIGINYVY
85	CD70-9	VL CDR2	RSDQRPS
86	CD70-9	VL CDR3	AAWDDSLSGVV
87	CD70-9	VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYNGYTHYAQK LQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTVTIVSS
88	CD70-9	VL	QSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVVYVYQQLPGTAPKLLIYRSDQRPSPGVPDRF SGSKSGTSASLALSGLRSEDEADYYCAAWDDSLSGVVFSGGCKLTIVL
89	I CD70-9	scFv	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYNGYTHYAQK LQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTVTIVSSGGGGS GGGGGGGGSQSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVVYVYQQLPGTAPKLLIYRSD QRPSPGVPDRFSGSKSGTSASLALSGLRSEDEADYYCAAWDDSLSGVVFSGGCKLTIVL
90	CD70-9	bispecific molecule	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQCLEWMGWISAYNGYTHYAQK LQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDYGGNDYYGMDVWGQGTVTIVSSGGGGS GGGGGGGGSQSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVVYVYQQLPGTAPKLLIYRSD QRPSPGVPDRFSGSKSGTSASLALSGLRSEDEADYYCAAWDDSLSGVVFSGGCKLTIVL EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTIVTVSSG GGGGGGGGSQSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVVYVYQQLPGTAPKLLIYRSD IGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGCKLTIVL
91	CD70-10	VH CDR1	SGGYIYWS
92	CD70-10	VH CDR2	YIFYSGSTDYNPSLKS
93	CD70-10	VH CDR3	SGYSYALFDH
94	CD70-10	VL	RASQFIGRYFN

			CDR1	
95		CD70-10	VL CDR2	AESSLQS
96		CD70-10	VL CDR3	QQSYSTPWT
97		CD70-10	VH	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDHWGQGTLLVTVSS
98		CD70-10	VL	DIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSLQSGVPSRFS GSGGTEFTLTISLQPEDFARYYCQQSYSTPWTFGCGTKVEIK
99	VIII	CD70-10	scFv	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDHWGQGTLLVTVSSGGGSG GGSGGGSDIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSL QSGVPSRFSGSGGTEFTLTISLQPEDFARYYCQQSYSTPWTFGCGTKVEIK
100		CD70-10	bispecific molecule	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQHPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDHWGQGTLLVTVSSGGGSG GGSGGGSDIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSL QSGVPSRFSGSGGTEFTLTISLQPEDFARYYCQQSYSTPWTFGCGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTLLVTVSSGGGGS GGSGGGGSDIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQQPGKAPKVLIIYAESSL KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
101		CD70-11	VH CDR1	TYGMH
102		CD70-11	VH CDR2	VIWYDGSNKYYGDSVKG
103		CD70-11	VH CDR3	DNSHYYYGMDV
104		CD70-11	VL CDR1	TGSSSNIGAGYDVN
105		CD70-11	VL CDR2	VNNNRPS
106		CD70-11	VL CDR3	QSYETLSASV

107		CD70-11	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFTSYGMHWVRQAPGKCLEWVAVIWDGSKNKYYGDS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGT'TVTVSS
108		CD70-11	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNNRPSGVPDR FSGTSGTSASLAITGLQAEDEADYYCQSYETSLASVFGCGTRLTVL
109	III	CD70-11	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFTSYGMHWVRQAPGKCLEWVAVIWDGSKNKYYGDS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGT'TVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSGTSASLAITGLQAEDEADYYCQSYETSLASVFGCGTRLTVL
110		CD70-11	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFTSYGMHWVRQAPGKCLEWVAVIWDGSKNKYYGDS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGT'TVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSGTSASLAITGLQAEDEADYYCQSYETSLASVFGCGTRLTVLSSGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSIYWAYWGQGT'LVTVSSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSGTSASLAITGLQAEDEADYYCQSYETSLASVFGCGTRLTVLSSGGGS IGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVL
111		CD70-12	VH CDR1	YYGMH
112		CD70-12	VH CDR2	VIWYDGSNKYYADSVKG
113		CD70-12	VH CDR3	DREMGSRGDFDY
114		CD70-12	VL CDR1	RASQGINNYLA
115		CD70-12	VL CDR2	AVSILQS
116		CD70-12	VL CDR3	QQYNFYFYS
117		CD70-12	VH	QAQLVESGGGVVQPGRSLRLSCAASGFTFTSYGMHWVRQAPGKCLEWVAVIWDGSKNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDREMGSRGDFDYWGQGT'LVTVSS
118		CD70-12	VL	DIQMTQSPSSLSASVGDRVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSILQSGVPSKFS GSGGTDFTLTIGNLQPEDFATYYCQQYNFYFYSFGCGTKVDIK
119	V	CD70-12	scFv	QAQLVESGGGVVQPGRSLRLSCAASGFTFTSYGMHWVRQAPGKCLEWVAVIWDGSKNKYYADS

120	I	CD70-13	bispecific molecule	VKGRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARDREMGSRGDFDYWGQGLVTVSSGGGGS GGGGGGGSDIQMTQSPSSLSASVGRVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSI LQSGVPSKFSGSGTDFTLTIGNLQPEDFATYCCQYNFYPSFGCGTKVDIK QAQLVESGGGVVQPGRLRLSCAASGFTFSYYGMHWVRQAPGKCLEWVAWIYDGSNKYYADS VKGRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARDREMGSRGDFDYWGQGLVTVSSGGGGS GGGGGGGSDIQMTQSPSSLSASVGRVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSI LQSGVPSKFSGSGTDFTLTIGNLQPEDFATYCCQYNFYPSFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
121		CD70-13	VH CDR1	SYAMS
122		CD70-13	VH CDR2	VISGSGGRPNYADSVKG
123		CD70-13	VH CDR3	VDYSNYLFFDY
124		CD70-13	VL CDR1	RAGQSVRSSYLG
125		CD70-13	VL CDR2	GASSRAT
126		CD70-13	VL CDR3	QQYGYSPPT
127		CD70-13	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSVISGSGGRPNYADS VKGRFTISRDNKNTLYLQMNLSRDEDTAVYYCAKVDYSNYLFFDYWGQGLVTVSS
128		CD70-13	VL	EIVLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGYSPPTFGGGTKLEIK
129	I	CD70-13	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSVISGSGGRPNYADS VKGRFTISRDNKNTLYLQMNLSRDEDTAVYYCAKVDYSNYLFFDYWGQGLVTVSSGGGSG GGGGGGGSEI VLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGYSPPTFGGGTKLEIK
130		CD70-13	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSVISGSGGRPNYADS VKGRFTISRDNKNTLYLQMNLSRDEDTAVYYCAKVDYSNYLFFDYWGQGLVTVSSGGGSG

			molecule	GGSGGGGSEIVLTQSPGTLSPGEGATLSCRAGQSVRRSSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYQCQYGYSPPTFGGGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLTSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
131		CD70-14	VH CDR1	IYAMS
132		CD70-14	VH CDR2	AISGSGGSTFYADSVKG
133		CD70-14	VH CDR3	HDYSNYPYFDY
134		CD70-14	VL CDR1	RASQSVRRSSYLA
135		CD70-14	VL CDR2	GASSRAT
136		CD70-14	VL CDR3	QQYGDLPFT
137		CD70-14	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLVTVSSGGGGSG
138		CD70-14	VL	EIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTI SRLEPEDFAVYQCQYGDLPFTFGPGTKLEIK
139	II	CD70-14	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYQCQYGDLPFTFGPGTKLEIKSGGGGSEVQ
140		CD70-14	bispecific molecule	EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG

				TKFLAPGTPARFSGSLLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
141		CD70-15	VH CDR1	SYAMS
142		CD70-15	VH CDR2	AISGSGGRTFYADSVEG
143		CD70-15	VH CDR3	HDYSNYPYFDY
144		CD70-15	VL CDR1	RASQSVRRSSYLA
145		CD70-15	VL CDR2	GASSRAT
146		CD70-15	VL CDR3	QQYGSSPFT
147		CD70-15	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
148		CD70-15	VL	EIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKLEIK
149	II	CD70-15	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKLEIK
150		CD70-15	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGTFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
151		CD70-16	VH CDR1	SYAMS
152		CD70-16	VH CDR2	AISGSGGRTFYADSVEG

153		CD70-16	VH CDR3	HDYSNYPYFDY	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
154		CD70-16	VL CDR1	RASQIRSSYLA	EIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTTFGPGTKLEIK
155		CD70-16	VL CDR2	GASSRAT	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG
156		CD70-16	VL CDR3	QQYGDLPFT	GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGDLPTTFGPGTKLEIK
159	II	CD70-16	scFv		EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGDLPTTFGPGTKLEIK
160		CD70-16	bispecific molecule		EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGDLPTTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
161		CD70-17	VH CDR1	SYAMS	
162		CD70-17	VH CDR2	AISGSGGRTHYADSVKG	
163		CD70-17	VH CDR3	HDYSNYPYFDY	
164		CD70-17	VL CDR1	RASQSVRSSYLA	
165		CD70-17	VL	GASSRAT	

166			CDR2 VL CDR3	QQYGSSPFT	
167		CD70-17	VH	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS	
168		CD70-17	VL	EIVLTQSPGTLISLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKLEIK	
169	II	CD70-17	scFv	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKLEIK	
170		CD70-17	bispecific molecule	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKLEIKSGGGGSEVQ LIVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVL	
171		CD70-18	VH CDR1	SYAMS	
172		CD70-18	VH CDR2	LISGSGGRTHYADSVKG	
173		CD70-18	VH CDR3	HDYSNYPYFDY	
174		CD70-18	VL CDR1	RASQSVRSTYLA	
175		CD70-18	VL CDR2	DASSRAT	
176		CD70-18	VL CDR3	QQYGSSPPT	
177		CD70-18	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSLISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS	

178		CD70-18	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTKLEIK
179	II	CD70-18	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSLISGSGGRTHYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTKLEIK
180		CD70-18	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSLISGSGGRTHYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
181		CD70-19	VH CDR1	TYAMS
182		CD70-19	VH CDR2	AISGGSGSTFYADSVKG
183		CD70-19	VH CDR3	HDYSNYPYFDY
184		CD70-19	VL CDR1	RASQSVRSSYLA
185		CD70-19	VL CDR2	GASSRAT
186		CD70-19	VL CDR3	QQYGDLPFT
187		CD70-19	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGSTFYADS VKGRFTISRDNKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
188		CD70-19	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYFCQQYGDLPTFTFGPGTKLEIK
189	VI	CD70-19	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGSTFYADS VKGRFTISRDNKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASS

190		CD70-19	bispecific molecule	RATGIPDRFSGSGGTDFTLTIISRLEPEDFAVYCCQQYGDLPFTFGPGTKLEIK EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VKGRFTISRDN SKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQVRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLEPEDFAVYCCQQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTGAVTSGNYPNWWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGTKLTVL
191		CD70-20	VH CDR1	TYAMS
192		CD70-20	VH CDR2	LISGSGGRTYYADSVKG
193		CD70-20	VH CDR3	HDYSNYPYFDY
194		CD70-20	VL CDR1	RASQGVRS DYLA
195		CD70-20	VL CDR2	GASSRAT
196		CD70-20	VL CDR3	QQYGSTPPT
197		CD70-20	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
198		CD70-20	VL	EIVLTQSPGTLSPGERATLSCRASQGVRS DYLA WYQQKPGQALRLLIYGASSRATGIPDRF SGSGGTDFTLTIISRLEPEDFAVYHCQQYGSTPPTFGGGTKLEIK
199	II	CD70-20	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRS DYLA WYQQKPGQALRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLEPEDFAVYHCQQYGSTPPTFGGGTKLEIK
200		CD70-20	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRS DYLA WYQQKPGQALRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLEPEDFAVYHCQQYGSTPPTFGGGTKLEIKSGGGGSEVQ

				LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTFTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
201		CD70-21	VH CDR1	TYAMS
202		CD70-21	VH CDR2	AISGGGRTFYADSV
203		CD70-21	VH CDR3	HDYSNYPYFDY
204		CD70-21	VL CDR1	RASQSVRSTYLA
205		CD70-21	VL CDR2	GASSRAT
206		CD70-21	VL CDR3	QQYGDLPFT
207		CD70-21	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFTYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFYDWGQGLTVTVSS
208		CD70-21	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKLEIK
209	VI	CD70-21	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFTYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFYDWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKLEIK
210		CD70-21	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFTYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFYDWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTFTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
211		CD70-22	VH	SYAMS

			CDR1	
212		CD70-22	VH CDR2	AISGSGGYTYADSVKG
213		CD70-22	VH CDR3	HDYSNYPYFDY
214		CD70-22	VL CDR1	RASQSVRSNYLA
215		CD70-22	VL CDR2	GASSRAT
216		CD70-22	VL CDR3	QQYGDLPFT
217		CD70-22	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGYTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
218		CD70-22	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGPGTKVEIK
219	VI	CD70-22	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGYTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGSGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGPGTKVEIK
220		CD70-22	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGYTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGSGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLLTVSSGGGSGGGSGGSGTQVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
221		CD70-23	VH CDR1	VYAMS
222		CD70-23	VH CDR2	TISDSGGSTFYADSVKG
223		CD70-23	VH CDR3	HDYSNYPYFDY

224		CD70-23	VL CDR1	RASQSVRSSYLA	
225		CD70-23	VL CDR2	GASSRAT	
226		CD70-23	VL CDR3	QQYGDLPFT	
227		CD70-23	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSS	
228		CD70-23	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIK	
229	VI	CD70-23	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSSLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIK	
230		CD70-23	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSSLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNRLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTFTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL	
231		CD70-24	VH CDR1	SYAMS	
232		CD70-24	VH CDR2	AISGGSGSTFYADSVKG	
233		CD70-24	VH CDR3	HDYSNYPYFDY	
234		CD70-24	VL CDR1	RASQSVRSSYLA	
235		CD70-24	VL CDR2	GASSRAT	
236		CD70-24	VL	QQYGDLPFT	

			CDR3	EVQLLESGGGLAQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSS
237		CD70-24	VH	
238		CD70-24	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYCYCQYQYGDLPFTFGPGTKVEIK
239	VI	CD70-24	scFv	EVQLLESGGGLAQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCYCQYQYGDLPFTFGPGTKVEIK
240		CD70-24	bispecific molecule	EVQLLESGGGLAQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCYCQYQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYCYVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTVQEPSTVSPGGTFTLTTCGSGTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
241		CD70-25	VH CDR1	SYAMS
242		CD70-25	VH CDR2	AISGSGGRTFYADSVEG
243		CD70-25	VH CDR3	HDYSNYPYFDY
244		CD70-25	VL CDR1	RASQSVRSNYLA
245		CD70-25	VL CDR2	GASSRAT
246		CD70-25	VL CDR3	QQYGDLPFT
247		CD70-25	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYCYCAKHDYSNYPFDYWGQGLTVTVSS
248		CD70-25	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYCYCQYQYGDLPFTFGPGTKVEIK

249	VI	CD70-25	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIK
250		CD70-25	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
251		CD70-26	VH CDR1	SYAMS
252		CD70-26	VH CDR2	AISGSGGRTFYADSV
253		CD70-26	VH CDR3	HDYSNYPYFDY
254		CD70-26	VL CDR1	RASQSVRSYYLA
255		CD70-26	VL CDR2	GASSRAT
256		CD70-26	VL CDR3	QQYGSSPFT
257		CD70-26	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
258		CD70-26	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTFTLTISRLEPEDFAVYYCQQYGSPPFTFGPGTKVEIK
259	II	CD70-26	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGSPPFTFGPGTKVEIK
260		CD70-26	bispecific	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS

			c molecule	VEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPG TSLSPGERATLSCRASQSVRS SYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGG SGGGSGGGGQT VVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKKAAL T LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
261		CD70-27	VH CDR1	TYAMS
262		CD70-27	VH CDR2	AISGSGGGTFYADSVKG
263		CD70-27	VH CDR3	HDYSNYPYFDY
264		CD70-27	VL CDR1	RASQIRSNYLA
265		CD70-27	VL CDR2	GASSRAT
266		CD70-27	VL CDR3	QQYGSSPFT
267		CD70-27	VH	EVQLLESGGGLVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGGTFYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSS EIVLTQSPG TSLSPGERATLSCRASQSI RSNYLA WYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKVEIK
268		CD70-27	VL	EVQLLESGGGLVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGGTFYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPG TSLSPGERATLSCRASQSI RSNYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKVEIK
269	VI	CD70-27	scFv	EVQLLESGGGLVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGGTFYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPG TSLSPGERATLSCRASQSI RSNYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGG
270		CD70-27	bispecific c molecule	

				SGGGSGGGGQTVVTQEPSTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
271		CD70-28	VH CDR1	TYAMS
272		CD70-28	VH CDR2	LISGSGGRTYYADSVKG
273		CD70-28	VH CDR3	HDYSNYPYFDY
274		CD70-28	VL CDR1	RASQSVRSNYLA
275		CD70-28	VL CDR2	GASNRAT
276		CD70-28	VL CDR3	QQYGISPPT
277		CD70-28	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
278		CD70-28	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASNRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYGISPTFFGGGKVEIK
279	II	CD70-28	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGISPTFFGGGKVEIK
280		CD70-28	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGISPTFFGGGKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
281		CD70-29	VH CDR1	SYAMS
282		CD70-29	VH	VISGSGGRTHYADSGKG

			CDR2	
283		CD70-29	VH CDR3	HDYSNYPYFDY
284		CD70-29	VL CDR1	RASQSVRRSSYLA
285		CD70-29	VL CDR2	GASSRAT
286		CD70-29	VL CDR3	EQYGNSPPT
287		CD70-29	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTNFASYAMSWMVRQAPGKGLEWVSVISGSGGRTHYADS GKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
288		CD70-29	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRF SGESGTDFTLTINRLEPEDFAVYYCEQYGNSPPTFGGKVEIK
289	II	CD70-29	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTNFASYAMSWMVRQAPGKGLEWVSVISGSGGRTHYADS GKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIFGASS RATGIPDRFSGSESGTDFTLTINRLEPEDFAVYYCEQYGNSPPTFGGKVEIK
290		CD70-29	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTNFASYAMSWMVRQAPGKGLEWVSVISGSGGRTHYADS GKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIFGASS RATGIPDRFSGSESGTDFTLTINRLEPEDFAVYYCEQYGNSPPTFGGKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWMVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTFTLTCSGSTGAVTSIGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGKTLTVL
291		CD70-30	VH CDR1	TYAMS
292		CD70-30	VH CDR2	LISGSGGRYYADSVKG
293		CD70-30	VH CDR3	HDYSNYPYFDY
294		CD70-30	VL CDR1	RASQSVRRSSYLA

295		CD70-30	VL CDR2	GASSRAT	
296		CD70-30	VL CDR3	QQYGSSPPP	
297		CD70-30	VH	EVQLLESGGKVQPGRSRLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSS	
298		CD70-30	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGKVEIK	
299	II	CD70-30	scFv	EVQLLESGGKVQPGRSRLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSSGGGSG GGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGKVEIK	
300		CD70-30	bispecific molecule	EVQLLESGGKVQPGRSRLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSSGGGSG GGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTFTLTCGSSTGAVTSNYPNWRVQKPGQAPRGLIGG TKFLAPGTPTARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL	
301		CD70-31	VH CDR1	SYAMS	
302		CD70-31	VH CDR2	AISGSGGRAQYADSVQ	
303		CD70-31	VH CDR3	HDYSNYPYFDY	
304		CD70-31	VL CDR1	RASQSVSSNLA	
305		CD70-31	VL CDR2	GSSSRAT	
306		CD70-31	VL CDR3	QQYGSSPPP	
307		CD70-31	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQSPGKGLEWVSAISGSGGRAQYADS	

				VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSS
308		CD70-31	VL	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSRATGIPDRFS GSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGGTKVEIK
309	II	CD70-31	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKGLEWVSAISGSGGRAQYADS VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGGTKVEIK
310		CD70-31	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKGLEWVSAISGSGGRAQYADS VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTAVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
311		CD70-32	VH CDR1	SYAMS
312		CD70-32	VH CDR2	AISGSGGRTFYADSVEG
313		CD70-32	VH CDR3	HDYSNYPYFDY
314		CD70-32	VL CDR1	RASQGVRS DYLA
315		CD70-32	VL CDR2	GASSRAT
316		CD70-32	VL CDR3	QQYGSTPPT
317		CD70-32	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGLTVTVSS
318		CD70-32	VL	EIVLTQSPGTLSPGERATLSCRASQGVRS DYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGGGTKVEIK
319	II	CD70-32	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGLTVTVSSGGGSG

320	II	CD70-32	bispecific molecule	GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLPEDEFAVYHCQQYGSTPPTFGGGTKVEIK EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLPEDEFAVYHCQQYGSTPPTFGGGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGSQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL TYAMS
321		CD70-33	VH CDR1	TISSDSGGSTFYADSVMG
322		CD70-33	VH CDR2	HDYSNYAFFDY
323		CD70-33	VH CDR3	RASQSVSSNLA
324		CD70-33	VL CDR1	GASSRAT
325		CD70-33	VL CDR2	QQYYSTPFT
326		CD70-33	VL CDR3	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VMGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLLTVSS EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSRATGIPDRFS GSGGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGGGTKVEIK EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VMGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSR ATGIPDRFSGSGGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGGGTKVEIK
327	II	CD70-33	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VMGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSR ATGIPDRFSGSGGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGGGTKVEIK
328		CD70-33	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VMGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSR ATGIPDRFSGSGGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGGGTKVEIK
329		CD70-33	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VMGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSR ATGIPDRFSGSGGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGGGTKVEIK
330		CD70-33	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VMGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASSR ATGIPDRFSGSGGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGGGTKVEIK

				ATGIPDRFSGSGGTDFTLTISSLAEDVAVYQCQYYSTPFTFGPGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
331		CD70-34	VH CDR1	TYAMS
332		CD70-34	VH CDR2	TISDSGGSTFYADSVMG
333		CD70-34	VH CDR3	HDYSNYAFFDY
334		CD70-34	VL CDR1	RASQSVSSNLA
335		CD70-34	VL CDR2	GASTRAT
336		CD70-34	VL CDR3	QQYYSTPFT
337		CD70-34	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKLEWVSTISDSGGSTFYADS VMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGLTVTVSS
338		CD70-34	VL	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFS GSGSGTEFTLAI SRLEPEDFAVYYCQYYSTPFTFGGGTKVEIK
339	II	CD70-34	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKLEWVSTISDSGGSTFYADS VMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYAFFDYWGQGLTVTVSSGGGSG GGGGGGGSEI VLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTR ATGIPARFSGSGGTEFTLAI SRLEPEDFAVYYCQYYSTPFTFGGGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
340		CD70-34	bispecific molecule	

341		CD70-35	VH CDR1	TYAMS	
342		CD70-35	VH CDR2	AISGSGGYTYADSV	
343		CD70-35	VH CDR3	HDYSNYAWFDP	
344		CD70-35	VL CDR1	RASQSVSSAYLA	
345		CD70-35	VL CDR2	GASSRAT	
346		CD70-35	VL CDR3	QQFGSSPFT	
347		CD70-35	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLDWSAISGSGGYTYADSV VEGRFTISRDNSTLYLQMNLSRAEDTAVYYCASHDYSNYAWFDPWGQGLTVTVSS	
348		CD70-35	VL	EIVLTQSPGTLSPGERATLSCRASQSVSSAYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGPGTKVEIK	
349	I	CD70-35	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLDWSAISGSGGYTYADSV VEGRFTISRDNSTLYLQMNLSRAEDTAVYYCASHDYSNYAWFDPWGQGLTVTVSSGGGSGG GGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSAYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGPGTKVEIK	
350		CD70-35	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLDWSAISGSGGYTYADSV VEGRFTISRDNSTLYLQMNLSRAEDTAVYYCASHDYSNYAWFDPWGQGLTVTVSSGGGSGG GGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSAYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNLSRAEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVTVTQEPSTLTVSPGGTFTLTTCGSSGTAFTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL	
351		CD70-36	VH CDR1	SYAMS	
352		CD70-36	VH CDR2	AISGSGGRTYYADSVKG	
353		CD70-36	VH	HDYSNYPYFDY	

			CDR3	
354		CD70-36	VL CDR1	RASQSVRGSYLA
355		CD70-36	VL CDR2	SASSRAT
356		CD70-36	VL CDR3	QQYGDSPFT
357		CD70-36	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGQGLEWVSAISGSGGRTYYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
358		CD70-36	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRGSYLAWYQQKPGQAPRLLIYSASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGPGTKVEIK
359	II	CD70-36	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGQGLEWVSAISGSGGRTYYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRGSYLAWYQQKPGQAPRLLIYSASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGPGTKVEIK
360		CD70-36	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGQGLEWVSAISGSGGRTYYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRGSYLAWYQQKPGQAPRLLIYSASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
361		CD70-37	VH CDR1	SYAMS
362		CD70-37	VH CDR2	AIGDGGGYTYADSVKG
363		CD70-37	VH CDR3	HDYSNYPYFDY
364		CD70-37	VL CDR1	RASQGVRRSSYFA
365		CD70-37	VL CDR2	GASTRAT

366		CD70-37	VL CDR3	QQYGSSPPT	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAIGDGGYTYADSVKGRFTISRDNKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSS
367		CD70-37	VH		EIVLTQSPGTLSPGERATLSCRASQGVRSYFAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGQTKVEIK
368		CD70-37	VL		EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAIGDGGYTYADSVKGRFTISRDNKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSG
369	II	CD70-37	scFv		GGGSGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYFAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGQTKVEIK
370		CD70-37	bispecific molecule		EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAIGDGGYTYADSVKGRFTISRDNKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSGRFTISRDNKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSGRATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGQTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGSGGGSGGSGTQVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTTLVLSYAMS
371		CD70-38	VH CDR1		SYAMS
372		CD70-38	VH CDR2		AISGSGGRTFYADSVEG
373		CD70-38	VH CDR3		HDYSNYPYFDY
374		CD70-38	VL CDR1		RASQIRSNNYLA
375		CD70-38	VL CDR2		GASSRAT
376		CD70-38	VL CDR3		QQYGSSPPS
377		CD70-38	VH		EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
378		CD70-38	VL		EIVLTQSPGTLSPGERATLSCRASQIRSNNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF

379	II	CD70-38	scFv	SGSGGTDFTLTISRLEPEDFAVYQCQYGSSPPSFGQGTKVEIK EVQLLESGGGVVQPGRSLRLSCLAAAGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYQCQYGSSPPSFGQGTKVEIK
380		CD70-38	bispecific molecule	EVQLLESGGGVVQPGRSLRLSCLAAAGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYQCQYGSSPPSFGQGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCLAAAGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVL
381		CD70-39	VH CDR1	SYAMS
382		CD70-39	VH CDR2	AISGSGGGTFYADSVEG
383		CD70-39	VH CDR3	HDYSNYPYFDY
384		CD70-39	VL CDR1	RASQSVRRSSYLA
385		CD70-39	VL CDR2	GASSRAT
386		CD70-39	VL CDR3	QQYGDLPFT
387		CD70-39	VH	EVQLLESGGGVVQPGRSLRLSCLAAAGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGGLTVTVSS
388		CD70-39	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFLTISRLEPEDFAVYSCQYQYGDLPFTFGPGTKVEIK
389	VI	CD70-39	scFv	EVQLLESGGGVVQPGRSLRLSCLAAAGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYSCQYQYGDLPFTFGPGTKVEIK

390		CD70-39	bispecific molecule	EVQLLESGGGVVPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGGTFFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGGLTGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYSCQQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTFTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
391		CD70-40	VH CDR1	SYAMS
392		CD70-40	VH CDR2	AISGSGGRTFYADSVEG
393		CD70-40	VH CDR3	HDYSNYPYFDY
394		CD70-40	VL CDR1	RASQSIRSSYLA
395		CD70-40	VL CDR2	GASSRAT
396		CD70-40	VL CDR3	QQYGDLPFT
397		CD70-40	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
398		CD70-40	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTI SRLEPEDFAVYCCQQYGDLPFTFGPGTKVDIK
399	II	CD70-40	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYCCQQYGDLPFTFGPGTKVDIK
400		CD70-40	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYCCQQYGDLPFTFGPGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNIATYYADSV

				KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
401		CD70-41	VH CDR1	SYAMS
402		CD70-41	VH CDR2	AISGSGGRTFYADSVEG
403		CD70-41	VH CDR3	HDYSNYPYFDY
404		CD70-41	VL CDR1	RASQSVRRSSYLA
405		CD70-41	VL CDR2	GASSRAT
406		CD70-41	VL CDR3	QQYGDLPFT
407		CD70-41	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGLTVTVSS
408		CD70-41	VL	EIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVDIK
409	II	CD70-41	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVDIK
410		CD70-41	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
411		CD70-42	VH CDR1	TYAMS

412		CD70-42	VH CDR2	LISGGGRTYYADSVKG
413		CD70-42	VH CDR3	HDYSNYPYFDY
414		CD70-42	VL CDR1	RASQGVRSYLA
415		CD70-42	VL CDR2	GASSRAT
416		CD70-42	VL CDR3	QQYGSSPPT
417		CD70-42	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
418		CD70-42	VL	EIVLTQSPGTLSPGERATLSCRASQGVRSYLAWEYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGKVDIK
419	II	CD70-42	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYLAWEYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGKVDIK
420		CD70-42	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYLAWEYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKLTVL
421		CD70-43	VH CDR1	SYAMS
422		CD70-43	VH CDR2	AISGGGRTFYADSVEG
423		CD70-43	VH CDR3	HDYSNYPYFDY
424		CD70-43	VL	RASQSVRSNYLA

			CDR1	
425		CD70-43	VL CDR2	GASSRAT
426		CD70-43	VL CDR3	QQYGSSPPT
427		CD70-43	VH	EVQLLESGGGVVPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
428		CD70-43	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKVDIK
429	II	CD70-43	scFv	EVQLLESGGGVVPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKVDIK
430		CD70-43	bispecific molecule	EVQLLESGGGVVPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWSVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTFTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
431		CD70-44	VH CDR1	SYAMS
432		CD70-44	VH CDR2	VISDSGGITDFADSVKG
433		CD70-44	VH CDR3	HDYSNYFFFDY
434		CD70-44	VL CDR1	RASQDISNYLN
435		CD70-44	VL CDR2	AASSLQS
436		CD70-44	VL CDR3	QQSYISPPT

437		CD70-44	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSISDSGGITDFADS VKGRFII SRDNSRNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSS
438		CD70-44	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKSGKAPPELLIYAASSLQSGVPSRFS GSGGTDFTLTISSLQPEDFATYYCQQSYISPPTFGQGTKVEIK
439	I	CD70-44	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSISDSGGITDFADS VKGRFII SRDNSRNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSG GGSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKSGKAPPELLIYAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYISPPTFGQGTKVEIK
440		CD70-44	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSISDSGGITDFADS VKGRFII SRDNSRNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSG GGSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKSGKAPPELLIYAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYISPPTFGQGTKVEIKSGGGSEVQL VESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYICVRHGFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGQTQVTEPSTLTVSPGGTTLTCGSSTGAVTSNYPNWWQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
441		CD70-45	VH CDR1	SYAMS
442		CD70-45	VH CDR2	VISDSGGITDFADSVKG
443		CD70-45	VH CDR3	HDYSNYFFFDY
444		CD70-45	VL CDR1	RASQSISSYLN
445		CD70-45	VL CDR2	AASSLQS
446		CD70-45	VL CDR3	QQSYISPPT
447		CD70-45	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSISDSGGITDFADS VKGRFII SRDNSRNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSS
448		CD70-45	VL	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKSGKAPKLLIYAASSLQSGVPSRFS GSGGTDFTLTISSLQPEDFATYYCQQSYISPPTFGQGTKVEIK
449	I	CD70-45	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSISDSGGITDFADS

450		CD70-45	bispecific molecule	VKGRFTISRDNSTLTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLLTVSSGGGGSG GGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQQKPKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISLQPEDFATYQCQSYISPPTFGGTKVEIK EVQLLESGGGVVPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSIVSDSGGITDFADS VKGRFTISRDNSTLTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLLTVSSGGGGSG GGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQQKPKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISLQPEDFATYQCQSYISPPTFGGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYICVRHGNFNSYISYWAYWGQGTLLTVSSGGGG GGSGGGGSDTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
451		CD70-46	VH CDR1	SYAMS
452		CD70-46	VH CDR2	VISGGGRTDYADSVKG
453		CD70-46	VH CDR3	HDYSNRFYFDY
454		CD70-46	VL CDR1	RASQSISSYLN
455		CD70-46	VL CDR2	AASSLQS
456		CD70-46	VL CDR3	QQSYSAPPT
457		CD70-46	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQVPGKGLEWVSIVSGSGGRTDYADS VKGRFTISRDNSTLTLYLQMNSLRAEDTAVYFCARHDYSNRFYFDYWGQGTLLTVSS
458		CD70-46	VL	DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFS GSGGTDFTLTISLQPEDFATYQCQSYISPPTFGGTKVEIK
459	II	CD70-46	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQVPGKGLEWVSIVSGSGGRTDYADS VKGRFTISRDNSTLTLYLQMNSLRAEDTAVYFCARHDYSNRFYFDYWGQGTLLTVSSGGGGSG GGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQQKPKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISLQPEDFATYQCQSYISPPTFGGTKVEIK
460		CD70-46	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQVPGKGLEWVSIVSGSGGRTDYADS VKGRFTISRDNSTLTLYLQMNSLRAEDTAVYFCARHDYSNRFYFDYWGQGTLLTVSSGGGGSG

			molecule	GGSGGGGSDIQMTQSPSSLSASVGDVRVITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISSLPEDFATYQCQSYSAPTFFGGGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL SYAMS
461	CD70-47		VH CDR1	
462	CD70-47		VH CDR2	VISDSGGITDYADSVKG
463	CD70-47		VH CDR3	HDYSNRYYFDY
464	CD70-47		VL CDR1	RASQSISSYLN
465	CD70-47		VL CDR2	AASSLQS
466	CD70-47		VL CDR3	QQSYSTPLT
467	CD70-47		VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDYADS VKGRFTISRDN SKNTLYLQMNSLRAEDRAVYVCARHDYSNRYYFDYWGQGLTVTVSS
468	CD70-47		VL	DIQMTQSPSSLSASVGDVRVITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFS GSGGTDFTLTISSLPEDFATYQCQSYSTPLTFGGGTKVEIK
469	I CD70-47		scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDYADS VKGRFTISRDN SKNTLYLQMNSLRAEDRAVYVCARHDYSNRYYFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDVRVITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISSLPEDFATYQCQSYSTPLTFGGGTKVEIK
470	CD70-47		bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDYADS VKGRFTISRDN SKNTLYLQMNSLRAEDRAVYVCARHDYSNRYYFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDVRVITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISSLPEDFATYQCQSYSTPLTFGGGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT

471		CD70-48	VH CDR1	KFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL SYAMS
472		CD70-48	VH CDR2	VISDSGGITDFADSVKG
473		CD70-48	VH CDR3	HDYSNYFFFDY
474		CD70-48	VL CDR1	RASQGISNYLA
475		CD70-48	VL CDR2	AASILQS
476		CD70-48	VL CDR3	QQYFAYPIT
477		CD70-48	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADS VKGRFTISRDNSTNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSS
478		CD70-48	VL	DIQMTQSPSSLSASVGDRTVITCRASQGISNYLAHYQQKPGKVPKLLIYAASILQSGVPSKFS GSGSGTFTLTITSSLPEDFAIYYCQQYFAYPITFTGQGRLEIK
479	I	CD70-48	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADS VKGRFTISRDNSTNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTVITCRASQGISNYLAHYQQKPGKVPKLLIYAASIL QSGVPSKFSGSGTFTLTITSSLPEDFAIYYCQQYFAYPITFTGQGRLEIK
480		CD70-48	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADS VKGRFTISRDNSTNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTVITCRASQGISNYLAHYQQKPGKVPKLLIYAASIL QSGVPSKFSGSGTFTLTITSSLPEDFAIYYCQQYFAYPITFTGQGRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYCYVHRHGFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTFTVTVQEPSTVSPGGTFTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
481		CD70-49	VH CDR1	SYAMS
482		CD70-49	VH CDR2	VISDSGGITDFADSVKG

483		CD70-49	VH CDR3	HDYSNYFFFDY
484		CD70-49	VL CDR1	RASQSISSYLN
485		CD70-49	VL CDR2	AASSLQS
486		CD70-49	VL CDR3	QQSYSTPIT
487		CD70-49	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADS VKGRSTISRDNSTLTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLLTVSS
488		CD70-49	VL	DIQMTQSPSSVSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFS GSGGTDFTLTISSLQPEDFATYYCQQSYSTPITFGQGTREIK
489	I	CD70-49	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADS VKGRSTISRDNSTLTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLLTVSSGGGSG GGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYSTPITFGQGTREIK
490		CD70-49	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAMSWVRQAPGKGLEWVSVISDSGGITDFADS VKGRSTISRDNSTLTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTLLTVSSGGGSG GGSGGGGSDIQMTQSPSSVSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYSTPITFGQGTREIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCYVRHGNFNSYISYWAYWGQGTLLTVSSGGGGS GGSGGGGSGQTAVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
491		CD70-50	VH CDR1	TYAMS
492		CD70-50	VH CDR2	AISGSGGYTYADSVEG
493		CD70-50	VH CDR3	HDYSNYAWFDP
494		CD70-50	VL CDR1	RASQSISSYLN
495		CD70-50	VL	AASSLQS

			CDR2	
496		CD70-50	VL CDR3	QQSYSTPFT
497		CD70-50	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLDWVSAISGSGGYTYIYADS VEGRFTISRDNSTNTLYLQMNSLRAEDTAVYYCASHDYSNYAFDPWGQGLTVTVSS
498		CD70-50	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFS GSGGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTRLEIK
499	I	CD70-50	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLDWVSAISGSGGYTYIYADS VEGRFTISRDNSTNTLYLQMNSLRAEDTAVYYCASHDYSNYAFDPWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTRLEIK
500		CD70-50	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLDWVSAISGSGGYTYIYADS VEGRFTISRDNSTNTLYLQMNSLRAEDTAVYYCASHDYSNYAFDPWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPSTLTVSPGGTTLTCSGSTGAVTSNYPNWWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTTLTVL
501		CD70-51	VH CDR1	TDGYIYWS
502		CD70-51	VH CDR2	YIYSGSTNYNPSLKS
503		CD70-51	VH CDR3	GIGLGFY
504		CD70-51	VL CDR1	GGNNIGSKSVH
505		CD70-51	VL CDR2	DDSDRPS
506		CD70-51	VL CDR3	QVWDRSSDQDVV
507		CD70-51	VH	QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYIYWSWIRQPPGKGLEWIGIYIYSGSTNYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGIGLGFYWGQGLTVTVSS

508		CD70-51	VL	SYVLTQLTSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDSDRPSGIPERFSG SNSGNTATLTISRVEAGDEADFYCQVWDRSSDQDVVFGGTKLTVL
509	VI	CD70-51	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGGSVTDGYYSWIRQPPGKGLEWIGIYIYSGSTNYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGIGLGFEYWGQGTLLTVSSGGGGGGG GSGGGSSYVLTQLTSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDSDRPSG IPERFSGNSGNTATLTISRVEAGDEADFYCQVWDRSSDQDVVFGGTKLTVL
510		CD70-51	bispecific molecule	QVQLQESGPGLVKPSSETLSLTCTVSGGSVTDGYYSWIRQPPGKGLEWIGIYIYSGSTNYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGIGLGFEYWGQGTLLTVSSGGGGGGG GSGGGSSYVLTQLTSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDSDRPSG IPERFSGNSGNTATLTISRVEAGDEADFYCQVWDRSSDQDVVFGGTKLTVL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYICVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGG GGGGGGGSGTQVVTQEPSTVSPGGTTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCYLVWSNRWVFGGTKLTVL
511		CD70-52	VH CDR1	TDGYYS
512		CD70-52	VH CDR2	YIYSGSTNYNPSLKS
513		CD70-52	VH CDR3	GIGLGFEY
514		CD70-52	VL CDR1	GGNNIGSKSVH
515		CD70-52	VL CDR2	DDSDRPS
516		CD70-52	VL CDR3	QVWDRSSDQDVV
517		CD70-52	VH	QVQLQESGPGLVKPSSETLSLTCTVSGGSVTDGYYSWIRQPPGKGLEWIGIYIYSGSTNYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGIGLGFEYWGQGTLLTVSS
518		CD70-52	VL	SYVLTQLSSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDSDRPSGIPERFSG SNSGNTATLTISRVEAGDEADFYCQVWDRSSDQDVVFGGTKLTVL
519	I	CD70-52	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGGSVTDGYYSWIRQPPGKGLEWIGIYIYSGSTNYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYVCARGIGLGFEYWGQGTLLTVSSGGGGGGG GSGGGSSYVLTQLSSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDSDRPSG

520			CD70-52	bispecific molecule	IPERFSGNSGNTATLTISRVEAGDEADYYCQVWDRSSDQDVVFGGGTKLTVL QVQLQESGPGLVKPSETLSLTCTVSGGSVSTDGYYSWIRQPPGKGLEWIGYIYSGSTNYNP SLKSRVTISVDTSKNQFSLKLSSTAAADTAVYCAARGIGLGFYWGQGLTVTVSSGGGGSGG GGGGSSSYVLTQLSSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDSDRPSG IPERFSGNSGNTATLTISRVEAGDEADYYCQVWDRSSDQDVVFGGGTKLTVLSSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTAVTQEPSTVSPGGTTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
521			CD70-53	VH CDR1	SYAMS
522			CD70-53	VH CDR2	AISGGGRTFYADSVEG
523			CD70-53	VH CDR3	HDYSNYPYFDY
524			CD70-53	VL CDR1	RASQSVRRSSYLA
525			CD70-53	VL CDR2	GASSRAT
526			CD70-53	VL CDR3	QQYGSSPPT
527			CD70-53	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
528			CD70-53	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTRLEIK
529	II		CD70-53	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGGGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTRLEIK
530			CD70-53	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGGGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTRLEIKSGGGGSEVQ

				LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
531		CD70-54	VH CDR1	IYAMS
532		CD70-54	VH CDR2	AIGDSGGSTFYADSVKG
533		CD70-54	VH CDR3	HDYSNYPYFDY
534		CD70-54	VL CDR1	RASQSVRSSYVA
535		CD70-54	VL CDR2	GASSRAT
536		CD70-54	VL CDR3	QQYGDLPFT
537		CD70-54	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAIGDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
538		CD70-54	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTRLEIK
539	VI	CD70-54	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAIGDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTRLEIK
540		CD70-54	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAIGDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
541		CD70-55	VH	SYGMH

			CDR1	
542		CD70-55	VH CDR2	VISYDGSNKYYADSVKG
543		CD70-55	VH CDR3	GRYYGSGNYNHGMDV
544		CD70-55	VL CDR1	RASQISSYLN
545		CD70-55	VL CDR2	AASSLQS
546		CD70-55	VL CDR3	QQSYSTPFT
547		CD70-55	VH	QVQLVESGGGVVQPGRSRLRLSCAASGFMFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGNYNHGMDVWGQGT'TVTVSS
548		CD70-55	VL	DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFS GRSGTDFTLTISLQPEDFATYYCQQSYSTPFTFGPGTKVEIK
549	VII	CD70-55	scFv	QVQLVESGGGVVQPGRSRLRLSCAASGFMFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGNYNHGMDVWGQGT'TVTVSSGG GGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQSYSTPFTFGPGTKVEIK
550		CD70-55	bispecific molecule	QVQLVESGGGVVQPGRSRLRLSCAASGFMFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGNYNHGMDVWGQGT'TVTVSSGG GGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQSYSTPFTFGPGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFGNSYISYWAYWGQGT'LTVTVSSG GGSGGGSGGGSGTQVTVTQEPSTLTVSPGGT'TLTCGSSTGAVTSIGNYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYCYLWYSNRWVFGGGTKLTVL
551		CD70-56	VH CDR1	SYGMH
552		CD70-56	VH CDR2	VISYDGSNKYYADSVKG
553		CD70-56	VH CDR3	GRYYGSGSYNYGMDV

554		CD70-56	VL CDR1	RASQSI FDYLN
555		CD70-56	VL CDR2	AASSLQS
556		CD70-56	VL CDR3	QQSYSTPLT
557		CD70-56	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGSYNYGMDVWGQGT TTVTVSS
558		CD70-56	VL	DIQMTQSPSSLSASVGDRVTITCRASQSI FDYLNWYQQKPKAPKLLIYAASSLQSGVPSRFS GSGFGDTFTLTISLQPEDFATYYCQQSYSTPLTFGGGTKLEIK
559	VII	CD70-56	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGSYNYGMDVWGQGT TTVTVSSGG GGGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSI FDYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGSGFGDTFTLTISLQPEDFATYYCQQSYSTPLTFGGGTKLEIK
560		CD70-56	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGSYNYGMDVWGQGT TTVTVSSGG GGGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSI FDYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGSGFGDTFTLTISLQPEDFATYYCQQSYSTPLTFGGGTKLEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARISKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVTVSSG GGGGGGGGGGSQT VVTQEPSTLVSPGGT VTLTCSGSTGAVTSGNYPNWWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYCYLWYSNRWVFGGGTKLTVL
561		CD70-57	VH CDR1	SYGMH
562		CD70-57	VH CDR2	VIWYDGSSEYYADSVKG
563		CD70-57	VH CDR3	DNSYNYYGMDV
564		CD70-57	VL CDR1	TGSSSNIGAAAYDVH
565		CD70-57	VL CDR2	VNSHRPP
566		CD70-57	VL	LSYDNLSGSV

567			CDR3	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWAVAIWYDGSSEYYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDNSYNYGMDVWGQGTITVTVSS
568			VH	QSVLTQPPSVSGAPGQRTISCTGSSSNIGAAVDHWYQQFPGTAPKLLIYVNSHRPPPGVPDR FSGSKSGTSASLAITGLQAEDEADYYCLSYDNSLSGSVFGGGTKLTVL
569	I	CD70-57	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWAVAIWYDGSSEYYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDNSYNYGMDVWGQGTITVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAAVDHWYQQFPGTAPKLLIYVNS HRPPGVPDRFSGSKSGTSASLAITGLQAEDEADYYCLSYDNSLSGSVFGGGTKLTVL
570		CD70-57	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWAVAIWYDGSSEYYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDNSYNYGMDVWGQGTITVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAAVDHWYQQFPGTAPKLLIYVNS HRPPGVPDRFSGSKSGTSASLAITGLQAEDEADYYCLSYDNSLSGSVFGGGTKLTVL EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNHWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSG GGSGGGGGSGGGSQSVLTQEPSTLTVSPGGTTLTCGSTGAVTSGNYPNWVQQKPGQAPRGL IGGKFLAPGTPARFSGSLLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
571		CD70-58	VH CDR1	SSSYWYG
572		CD70-58	VH CDR2	SIYHSGGTYNPPLSKS
573		CD70-58	VH CDR3	HYEILTGYYPDVFDI
574		CD70-58	VL CDR1	RASQSISSYLN
575		CD70-58	VL CDR2	AASNLS
576		CD70-58	VL CDR3	QQSFSSPRT
577		CD70-58	VH	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSYWGWIRQPPGKGLEWIGSIYHSGGTYNP SLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARHYEILTGYYPDVFDIWGQGTMTVSS
578		CD70-58	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKGAPKLLIYAASNLSQSGVSSRFS GSGSGTDFTLTISSLQPEDFATYYCQQSFSPRTFGQGTKVEIK

579	II	CD70-58	scFv	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPPGKGLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHYEILTGYYPDVDFDIWGQGTMTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIY AASNLSQGVSSRFSGSGGTDTLTITSSLPEDFATYYCQSFSSPRTFGQGTKEIK
580		CD70-58	bispecific molecule	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPPGKGLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHYEILTGYYPDVDFDIWGQGTMTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIY AASNLSQGVSSRFSGSGGTDTLTITSSLPEDFATYYCQSFSSPRTFGQGTKEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSS GGSGGGGGGGGSDIVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRG LIGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
581		CD70-59	VH CDR1	GFYWS
582		CD70-59	VH CDR2	EIDHSGSTNYPNPSLKS
583		CD70-59	VH CDR3	NGYSGYLEFDY
584		CD70-59	VL CDR1	RASQIISYYLN
585		CD70-59	VL CDR2	GASSMQS
586		CD70-59	VL CDR3	QQSYSIPT
587		CD70-59	VH	QVQLQQWAGALLKPSETLSLTCAVYDGSVSGFYWSWIRQPPGKGLEWIGEIDHSGSTNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADSAVYYCARNGYSGYLFQWQGTGLTVTVSS
588		CD70-59	VL	DIQMTQSPSSLSASVGDRTITCRASQIISYLNWYQQKPKAPKVLIIYGASSMQSGVPSRFS GSGYGTDTLTITSSLPEDFATYYCQSYSIPTFGQGTKEIK
589	II	CD70-59	scFv	QVQLQQWAGALLKPSETLSLTCAVYDGSVSGFYWSWIRQPPGKGLEWIGEIDHSGSTNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADSAVYYCARNGYSGYLFQWQGTGLTVTVSSGGGGGGG GGGGSDIQMTQSPSSLSASVGDRTITCRASQIISYLNWYQQKPKAPKVLIIYGASSMQS GVPSRFSGSGGTDTLTITSSLPEDFATYYCQSYSIPTFGQGTKEIK
590		CD70-59	bispecific	QVQLQQWAGALLKPSETLSLTCAVYDGSVSGFYWSWIRQPPGKGLEWIGEIDHSGSTNYPNPSL

				c molecule	KSRVTISVDTSKNQFSLKLSVTAADSAVYYCARNGYSGYLFDYWGGQTLVTVSSGGGGGGGG GGGGGSDIQMTQSPSSLSASVGDRTITCRASQIISSYLNWYQQKPKAPKVLIIYGASSMQS GVPSRFSGGYGTDFTLTISSLPEDFATYYCQSYISIPRTFGQGTKLEIKSGGGGSEVQLVE SGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLVTVSSGGGGGG GGGGGGSQTAVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFK LAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
591		CD70-60		VH CDR1	TYYWS
592		CD70-60		VH CDR2	RIYPTGITNYPNPSLKS
593		CD70-60		VH CDR3	DRRFLEPSYYYYGMDV
594		CD70-60		VL CDR1	RSSQSLHSHNGYNYLD
595		CD70-60		VL CDR2	LGSNRAS
596		CD70-60		VL CDR3	MQGLRTPFT
597		CD70-60		VH	QVQLQESGPGLVKPSSETLSLTCTVSGDSISTYYWSWIRQPAKGLEWIGRIYPTGITNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDRRFLEPSYYYYGMDVWGQGTITVTVSS
598		CD70-60		VL	DIVLTQSPPLSLPVTGPGEPAISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRASGV PDRFSGSVSGTDFTLKISRVEAEDVGYYCMQGLRTPFTFGPGTKLEIK
599	VII	CD70-60		scFv	QVQLQESGPGLVKPSSETLSLTCTVSGDSISTYYWSWIRQPAKGLEWIGRIYPTGITNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDRRFLEPSYYYYGMDVWGQGTITVTVSSG GGGGGGGGGSDIVLTQSPPLSLPVTGPGEPAISCRSSQSLHSHNGYNYLDWYLQKPGQSP QLLIYLGSNRASGVDPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQGLRTPFTFGPGTKLEIK
600		CD70-60		bispecific molecule	QVQLQESGPGLVKPSSETLSLTCTVSGDSISTYYWSWIRQPAKGLEWIGRIYPTGITNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDRRFLEPSYYYYGMDVWGQGTITVTVSSG GGGGGGGGGSDIVLTQSPPLSLPVTGPGEPAISCRSSQSLHSHNGYNYLDWYLQKPGQSP QLLIYLGSNRASGVDPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQGLRTPFTFGPGTKLEIK SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT

				VTVSSGGGGGGGGGGGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWVQQKPG QAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKL TVL
601		CD70-61	VH CDR1	SYAMS
602		CD70-61	VH CDR2	VISDSGGITDFADSVKG
603		CD70-61	VH CDR3	HDYSNYFFFDY
604		CD70-61	VL CDR1	RASQISNYLN
605		CD70-61	VL CDR2	AASSLQS
606		CD70-61	VL CDR3	QQSYIIPPT
607		CD70-61	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSVISDSGGITDFADS VKGRFTISRDNSTLYLQMNLSRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSS
608		CD70-61	VL	DIQMTQSPSSLSASVGDRITITCRASQISNYLNWYQQKPKAPKLLISAASSLQSGVPSRFS GSGGTDFTLTISSLQPEDFATYYCQQSYIIPPTFGQGTKVDIK
609	I	CD70-61	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSVISDSGGITDFADS VKGRFTISRDNSTLYLQMNLSRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSG GGSGGGSDIQMTQSPSSLSASVGDRITITCRASQISNYLNWYQQKPKAPKLLISAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYIIPPTFGQGTKVDIK
610		CD70-61	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSVISDSGGITDFADS VKGRFTISRDNSTLYLQMNLSRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSG GGSGGGSDIQMTQSPSSLSASVGDRITITCRASQISNYLNWYQQKPKAPKLLISAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYIIPPTFGQGTKVDIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCYVRHGNFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
611		CD70-62	VH CDR1	SYSMN

612		CD70-62	VH CDR2	YISSSGGYIYYADSVKG
613		CD70-62	VH CDR3	GDYSNYAYFDY
614		CD70-62	VL CDR1	RASQGISNYLA
615		CD70-62	VL CDR2	AASTLQS
616		CD70-62	VL CDR3	QQYYSTPLT
617		CD70-62	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSGGYIYYADS VKGRFTISRDNKNSLYLQMNLSRAEDAAVYYCSRGDYSNYAYFDYWGQGLTVTVSS
618		CD70-62	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGKVPKLLIYAASLTQSGVPSRFS GSGGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGKVEIK
619	I	CD70-62	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSGGYIYYADS VKGRFTISRDNKNSLYLQMNLSRAEDAAVYYCSRGDYSNYAYFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGKVPKLLIYAASLT QSGVPSRFSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGKVEIK
620		CD70-62	bispecific molecule	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSGGYIYYADS VKGRFTISRDNKNSLYLQMNLSRAEDAAVYYCSRGDYSNYAYFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGKVPKLLIYAASLT QSGVPSRFSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFGGGKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGQTVVTEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTAPRFSGLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
621		CD70-63	VH CDR1	TYTMN
622		CD70-63	VH CDR2	SISSSSGYIYYADSVKG
623		CD70-63	VH CDR3	GDYSNYLYFDL
624		CD70-63	VL	RASQSFRRSSYLA

			CDR1	
625		CD70-63	VL CDR2	GASSRAT
626		CD70-63	VL CDR3	QLYGSLPIT
627		CD70-63	VH	EVQLVESGGGLVKPGGSLRLSCAASGITFTSTYTMNWVRQAPGKGLEWVSSISSSSGYIYYADS VKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGDYSNYLYFDLWGRGTLTVTVSS
628		CD70-63	VL	EIVLTQSPGTLSPGERATLSCRASQSFRRSSYLAWYQQKPGQAPRLLIHGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQLYGSLPITTFGQGRLEIK
629	II	CD70-63	scFv	EVQLVESGGGLVKPGGSLRLSCAASGITFTSTYTMNWVRQAPGKGLEWVSSISSSSGYIYYADS VKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGDYSNYLYFDLWGRGTLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSFRRSSYLAWYQQKPGQAPRLLIHGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQLYGSLPITTFGQGRLEIK
630		CD70-63	bispecific molecule	EVQLVESGGGLVKPGGSLRLSCAASGITFTSTYTMNWVRQAPGKGLEWVSSISSSSGYIYYADS VKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGDYSNYLYFDLWGRGTLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSFRRSSYLAWYQQKPGQAPRLLIHGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQLYGSLPITTFGQGRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTFTLTCSGSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
631		CD70-64	VH CDR1	VYAMS
632		CD70-64	VH CDR2	TISDSGGSTFYADSVKG
633		CD70-64	VH CDR3	HDYSNYAYFDY
634		CD70-64	VL CDR1	RASQSVRRSSYLA
635		CD70-64	VL CDR2	GASSRAT
636		CD70-64	VL CDR3	QQYGDLPFT

637		CD70-64	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSS
638		CD70-64	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGCGTKVEIK
639	VI	CD70-64	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGCGTKVEIK
640		CD70-64	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVL
641		CD70-65	VH CDR1	TYAMS
642		CD70-65	VH CDR2	AISGSGGYTYADSV
643		CD70-65	VH CDR3	HDYSNYAWFDP
644		CD70-65	VL CDR1	RASQSVSSAYLA
645		CD70-65	VL CDR2	GASSRAT
646		CD70-65	VL CDR3	QQFGSSPFT
647		CD70-65	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLDWVSAISGSGGYTYADS VEGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCASHDYSNYAWFDPWGQGLTVTVSS
648		CD70-65	VL	EIVLTQSPGTLSPGERATLSCRASQSVSSAYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGCGTKVEIK
649	I	CD70-65	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLDWVSAISGSGGYTYADS

650	II	CD70-66	bispecific molecule	VEGRFTISRDNSENRTLYLQMNLSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLLTVSSGGGGSGGGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSAYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGCGTKVEIK
651		CD70-66	VH CDR1	EVQLLESGGGLVQPGGSLRLSCAASGFTTFTSYAMSWVRQAPGKCLDWVSATSGSGGYTYADSV
652		CD70-66	VH CDR2	VEGRFTISRDNSENRTLYLQMNLSLRAEDTAVYYCASHDYSNYAWFDPWGQGTLLTVSSGGGGSGGGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSAYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQFGSSPFTFGCGTKVEIKSGGGGSEVQ
653		CD70-66	VH CDR3	LIVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNIATYYADSV
654		CD70-66	VL CDR1	KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGSGGGGGGGSQTVVTQEPSLTVSPGGTTLTTCGSSGTGAVTSGNYPNWWVQKPGQAPRGLIGG
655		CD70-66	VL CDR2	TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
656		CD70-66	VL CDR3	SYAMS
657		CD70-66	VH	AISGSGGRTYYADSVKG
658		CD70-66	VL	HDYSNYPYFDY
659	II	CD70-66	scFv	RASQSVRGSYLA
660		CD70-66	bispecific	SASSRAT
				QQYGDSPFT
		CD70-66	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTTFTSYAMSWVRQAPGQCLEWVSATSGSGGRTYYADSV
		CD70-66	VL	VKGRFTISRDNSENRTLYLQMNLSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSS
		CD70-66	VL	EIVLTQSPGTLSPGERATLSCRASQSVRGSYLAWYQKPGQAPRLLIYSASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGCGTKVEIK
		CD70-66	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTTFTSYAMSWVRQAPGQCLEWVSATSGSGGRTYYADSV
		CD70-66	scFv	VKGRFTISRDNSENRTLYLQMNLSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSSGGGGSGGGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRGSYLAWYQKPGQAPRLLIYSASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGCGTKVEIK
		CD70-66	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTTFTSYAMSWVRQAPGQCLEWVSATSGSGGRTYYADSV
		CD70-66	bispecific	VKGRFTISRDNSENRTLYLQMNLSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSSGGGGSGGGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRGSYLAWYQKPGQAPRLLIYSASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDSPFTFGCGTKVEIK

			molecule	GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRGSYLAWYQQKPGQAPRLLIYSASS RATGIPDRFSGSGGTDFTLTIISRLPEDEFAVYCCQYGDSPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGLLTVTSSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLISGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL SYAMS
661		CD70-67	VH CDR1	
662		CD70-67	VH CDR2	VISDSGGITDFADSVKG
663		CD70-67	VH CDR3	HDYSNYFFFDY
664		CD70-67	VL CDR1	RASQDISNYLN
665		CD70-67	VL CDR2	AASSLQS
666		CD70-67	VL CDR3	QQSYISPPT
667		CD70-67	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISDSGGITDFADS VKGRFII SRDNSRNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLLTVTVSS DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKSGKAPPELLIYAASSLQSGVPSRFS GSGGTDFTLTISSLQPEDFATYYCQQSYISPPTFGCGTKVEIK
668		CD70-67	VL	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISDSGGITDFADS VKGRFII SRDNSRNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKSGKAPPELLIYAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYISPPTFGCGTKVEIK
669	I	CD70-67	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISDSGGITDFADS VKGRFII SRDNSRNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKSGKAPPELLIYAASSL QSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYISPPTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGLLTVTVSSGGGGS GGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG
670		CD70-67	bispecific molecule	

671		CD70-68	VH CDR1	KFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL SYAMS
672		CD70-68	VH CDR2	VISDSGGITDFADSVKG
673		CD70-68	VH CDR3	HDYSNYFFFDY
674		CD70-68	VL CDR1	RASQGISNYLA
675		CD70-68	VL CDR2	AASILQS
676		CD70-68	VL CDR3	QQYFAYPIT
677		CD70-68	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSVISDSGGITDFADS VKGRFTISRDNSTNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSS
678		CD70-68	VL	DIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKVPKLLIYAASILQSGVPSKFS GSGGTDFTLTITSSLPEDFAIYYCQQYFAYPITTFGCGTRLEIK
679	I	CD70-68	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSVISDSGGITDFADS VKGRFTISRDNSTNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKVPKLLIYAASIL QSGVPSKFSGSGGTDFTLTITSSLPEDFAIYYCQQYFAYPITTFGCGTRLEIK
680		CD70-68	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSVISDSGGITDFADS VKGRFTISRDNSTNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKVPKLLIYAASIL QSGVPSKFSGSGGTDFTLTITSSLPEDFAIYYCQQYFAYPITTFGCGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYCYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
681		CD70-69	VH CDR1	TDGYIYWS
682		CD70-69	VH CDR2	YIYSGSTNYPNPSLKS

683		CD70-69	VH CDR3	GIGLGFEY
684		CD70-69	VL CDR1	GGNNIGSKSVH
685		CD70-69	VL CDR2	DDSDRPS
686		CD70-69	VL CDR3	QVWDRSSDQDVV
687		CD70-69	VH	QVQLQESGPGLVKPSSETLSLTCTVSGGSVTDGYIYWSWIRQPPGKCLEWIGIYIYSGSTNYP SLKSRVTISVDTSKNQFSLKLI SVTAADTAVYICARGIGLGFEEYWGQGLTVTVSS
688		CD70-69	VL	SYVLTQLSSVSAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVDSDDRPSGIPERFSG SNSGNTATLTISRVEAGDEADYICQVWDRSSDQDVVFGCGTKLTVL
689	VI	CD70-69	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGGSVTDGYIYWSWIRQPPGKCLEWIGIYIYSGSTNYP SLKSRVTISVDTSKNQFSLKLI SVTAADTAVYICARGIGLGFEEYWGQGLTVTVSSGGGSGGG GSGGGSSYVLTQLSSVSAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVDSDDRPSG IPERFSGNSGNTATLTISRVEAGDEADYICQVWDRSSDQDVVFGCGTKLTVL
690		CD70-69	bispecific molecule	QVQLQESGPGLVKPSSETLSLTCTVSGGSVTDGYIYWSWIRQPPGKCLEWIGIYIYSGSTNYP SLKSRVTISVDTSKNQFSLKLI SVTAADTAVYICARGIGLGFEEYWGQGLTVTVSSGGGSGGG GSGGGSSYVLTQLSSVSAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVDSDDRPSG IPERFSGNSGNTATLTISRVEAGDEADYICQVWDRSSDQDVVFGCGTKLTVL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYICVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGQTAVTQEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYICVLWYSNRWVFGGGTKLTVL
691		CD70-70	VH CDR1	SYGMH
692		CD70-70	VH CDR2	VISYDGSNKYYADSVKG
693		CD70-70	VH CDR3	GRYYGSGNYNHGMDV
694		CD70-70	VL CDR1	RASQSISSYLN
695		CD70-70	VL	AASSLIQS

			CDR2		QQSYSTPFT	
696		CD70-70	VL CDR3			
697		CD70-70	VH		QVQLVESGGGVVQPGRSRLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYYGSGNHNHGMVDVWGQGTITVTVSS	
698		CD70-70	VL		DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFS GRSGTDTLTITSSLPEDFATYYCQQSYSTPFTFGCGTKVEIK	
699	VII	CD70-70	scFv		QVQLVESGGGVVQPGRSRLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYYGSGNHNHGMVDVWGQGTITVTVSSGG GSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDTLTITSSLPEDFATYYCQQSYSTPFTFGCGTKVEIK	
700		CD70-70	bispecific molecule		QVQLVESGGGVVQPGRSRLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYYGSGNHNHGMVDVWGQGTITVTVSSGG GSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDTLTITSSLPEDFATYYCQQSYSTPFTFGCGTKVEIKSGGGGS EVQLVESGGGLVQPGSLKLSAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSIYWAYWGQGTITVTVSSG GGSGGGSGGGGQTAVTQEPSTLTVSPGGTTLTCGSSTGAVTSIGNYPNWWVQQKPKGQAPRGL IGGTFKFLAPGTPARFSGSLGKKAALTLGVSQPEDEAFYYCVLWYSNRWVFGGGTKLTVL	
701		CD70-71	VH CDR1		SYGMH	
702		CD70-71	VH CDR2		VISYDGSNKYYADSVKG	
703		CD70-71	VH CDR3		GRYYGSGSYNYGMDV	
704		CD70-71	VL CDR1		RASQSI FDYLN	
705		CD70-71	VL CDR2		AASSLQS	
706		CD70-71	VL CDR3		QQSYSTPLT	
707		CD70-71	VH		QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYYGSGSYNYGMVDVWGQGTITVTVSS	

708		CD70-71	VL	DIQMTQSPSSLSASVGDRVTITCRASQSI FDYLNWYQQKPGKAPKLLIYAASSLSQSGVPSRFS GSGFGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGCGTKLEIK
709	VII	CD70-71	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGRYYGSGSYNYGMDVWGQGT'TVTVSSGG GGGGGGGGSDIQMTQSPSSLSASVGDRTITCRASQSI FDYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGFGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGCGTKLEIK
710		CD70-71	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGRYYGSGSYNYGMDVWGQGT'TVTVSSGG GGGGGGGGSDIQMTQSPSSLSASVGDRTITCRASQSI FDYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGSGFGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGCGTKLEIKSGGGGS EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFNSYISYWAYWGQGT'TVTVSSG GGGGGGGGGGSTVVTQEPSTLTVSPGGT'TLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGTKKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
711		CD70-72	VH CDR1	TYYWS
712		CD70-72	VH CDR2	RIYPTGITNYPNPSLKS
713		CD70-72	VH CDR3	DRRFLEPSYYYYYGM DV
714		CD70-72	VL CDR1	RSSQSLHLSNGYNYLD
715		CD70-72	VL CDR2	LGSNRAS
716		CD70-72	VL CDR3	MQGLRTPFT
717		CD70-72	VH	QVQLQESGPGLVKPSSETLSLTCTVSGDSISTYYWSWIRQAPGKCLEWIGRIYPTGITNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDRRFLEPSYYYYYGM DVWGQGT'TVTVSS
718		CD70-72	VL	DIVLTQSPPLSLPVTGPGEPAISCRSSQSLHLSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGV PDRFSGSVSGTDFTLKISRVEAEDVGVYCMQGLRTPFTTFGCGTKLEIK
719	VII	CD70-72	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGDSISTYYWSWIRQAPGKCLEWIGRIYPTGITNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDRRFLEPSYYYYYGM DVWGQGT'TVTVSSG GGGGGGGGGGSDIVLTQSPPLSLPVTGPGEPAISCRSSQSLHLSNGYNYLDWYLQKPGQSP

720			CD70-72	bispecific molecule	QLLIYLGSNRASGVPDFRFGSVSGTDFTLKISRVEAEDVGYVCMQGLRTPFTFGCGTKLEIK QVQLQESGPGLVKPSETLSLTCTVSGDSISTYYWSWIRQPAKGKLEWIGRIYPTGITNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDRRFLEPSYYYYGMDVWGQGTITVTVSSG GGSGGGGGGSDIVLTQSPFLSLPTPGEPAISCRSSQSLLSNGYNLYLDWYLQKPGQSP QLLIYLGSNRASGVPDFRFGSVSGTDFTLKISRVEAEDVGYVCMQGLRTPFTFGCGTKLEIK SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNN YATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGT LTVTVSSGGGGGGGGGGGQTVVTEPSLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPG QAPRGLIGGTFKFLAPGTPARFSGSLLGKAAALTLGVPQPEDEAEYYCVLWYSNRWVFGGGTKL TVL
721			CD70-73	VH CDR1	YSYMN
722			CD70-73	VH CDR2	YISSSGGYIYYADSVKG
723			CD70-73	VH CDR3	GDYSNYAYFDY
724			CD70-73	VL CDR1	RASQGISNYLA
725			CD70-73	VL CDR2	AASTLQS
726			CD70-73	VL CDR3	QQYYSTPLT
727			CD70-73	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYSISSSGGYIYYADS VKGRFTISRDNAKNSLYLQMNSLRAEDAAYVYCSRGDYSNYAYFDYWGQGTITVTVSS
728			CD70-73	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASLTQSGVPSRFS GSGGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFTFGCGTKVEIK
729	I		CD70-73	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYSISSSGGYIYYADS VKGRFTISRDNAKNSLYLQMNSLRAEDAAYVYCSRGDYSNYAYFDYWGQGTITVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASLT QSGVPSRFGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLTFTFGCGTKVEIK
730			CD70-73	bispecific molecule	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYSISSSGGYIYYADS VKGRFTISRDNAKNSLYLQMNSLRAEDAAYVYCSRGDYSNYAYFDYWGQGTITVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASLT

				QSGVPSRFSGSGTDFTLTISSLQAEADVAYYCQQYYSTPLTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSQT VVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
731		CD70-74	VH CDR1	SYAMS
732		CD70-74	VH CDR2	AISGSGGSTFYADSVQG
733		CD70-74	VH CDR3	HDYSNYPYFDY
734		CD70-74	VL CDR1	RASQSVRGNLYA
735		CD70-74	VL CDR2	GASSRAT
736		CD70-74	VL CDR3	QQYGYSPFT
737		CD70-74	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPYFDYWGQGLTVTVSS
738		CD70-74	VL	EIVLTQSPGTLSPGERATLSCRASQSVRGNLYAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGYSPFTFGPGTKVDIK
739	II	CD70-74	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPYFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRGNLYAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGYSPFTFGPGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGSQT VVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
740		CD70-74	bispecific molecule	

741	-	Human CD70	human	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFAQAQQQLPLESLGWDVAELQLN HTGPQQDPRLYWQGGPALGRSFLHGPPELDKGQLRIHRDGIYMVHIQVTLAICSSTTASRHHPT TLAVGICSPASRSISLLRLSFHQGTIASQRLTPLARGDTLCTNLTGTLLPSRNTDETFFGVQ WVRP
742	-	Human CD70 ECD (aa 43-193)	human	QAQQQLPLESLGWDVAELQLNHTGPQQDPRLYWQGGPALGRSFLHGPPELDKGQLRIHRDGIY VHIQVTLAICSSTTASRHHPTTLAVGICSPASRSISLLRLSFHQGTIASQRLTPLARGDTLCT TNLTGTLLPSRNTDETFFGVQWVRP
743	-	Hu CD70- E1 (aa 43-62)	human	QAQQQLPLESLGWDVAELQL
744	-	Hu CD70- E2 (aa 63-84)	human	NHTGPQQDPRLYWQGGPALGRS
745	-	Hu CD70- E3 (aa 85-109)	human	FLHGPPELDKGQLRIHRDGIYMVHIQ
746	-	Hu CD70- E4 (aa 110-134)	human	VTLAICSSTTASRHHPTTLAVGICS
747	-	Hu CD70- E5 (aa 135-151)	human	PASRSISLLRLSFHQGC
748	-	Hu CD70- E6 (aa 152-175)	human	TIASQRLTPLARGDTLCTNLTGTLL
749	-	Hu	human	LPSRNTDETFFGVQWVRP

		CD70-E7 (aa 176-193)		
750	-	Hu CD70-E1+2 (aa 43-84)	human	QAQQQLPLESLGWDVAELQLNHTGPPQDPRLYWQGGPALGRS
751	-	Hu CD70-E3+4 (aa 85-134)	human	FLHGPELDKGQLRIHRDGIYMVHIQVTLAICSSTTASRHHPTTLAVGICS
752	-	Hu CD70-E4+5 (aa 110-151)	human	VTLAICSSTTASRHHPTTLAVGICSPASRSISLLRLSFHQGC
753	-	Hu CD70-E5+6 (aa 135-175)	human	PASRSISLLRLSFHQGCTIASQRLTPLARGDTLCTNLGTGL
754	-	Hu CD70-E6+7 (aa 152-193)	human	TIASQRLTPLARGDTLCTNLGTGLPSRNTDETFFGVQWVRP
755	-	Macaque CD70	macaque	MPEEGSGCAVRRRPYACVLRAAVPLVAGLAICLVVCVQRLSRAQQQLPLESLGWDIAELQLN HTGPPQDPRLYWQGGPALGRSFLRGPELDKGQLRIHRDGIYMVHIQVTLAICSSSTSRHHHP TTLAVGICSPASRSISLLRLSFHQGCTIASQRLTPLARGDTLCTNLGTGLPSRNTDETFFGV QWVRP
756	-	Macaque CD70 ECD	macaque	RAQQQLPLESLGWDIAELQLNHTGPPQDPRLYWQGGPALGRSFLRGPELDKGQLRIHRDGIY VHIQVTLAICSSSTSRHHPTTLAVGICSPASRSISLLRLSFHQGCTIASQRLTPLARGDTL CTNLGTGLPSRNTDETFFGVQWVRP
757	-	Murine CD70	murine	MPEEGRPCFVWRWSGTAFQRQWPWLLLVVFTVFCCWFHCSSLKQQQRLLEHPEPHTAELQ LNLTVPKDPPTLRWAGAPALGRSFTHGPELEEGLRIHQDGLYRLHIQVTLANCSSPGSTLQH RATLAVGICSPA AHGISLLRGRFGQDCTVALQRLTYLVHGDVLCNLTLPLPSRNADETFFG

				VQWICP
758	-	Murine CD70 ECD	murine	SKQQQRLLLEHPEPHTAELQLNLTVPRKDPTRLRWGAGPALGRSFTHGPELEEGHLRIHQDGLYR LHIQVTLANCSSPGSTLQHRATLAVGICSPAAGHISLLRGRFGQDCTVALQRLTYLVHGDVLC TNLTPLLLPSRNADETFFGVQWICP
759	-	Hu CD70 mu E1	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFASQKQQQLLEHPEPHTAELQLN HTGPQQDPRLYWQGGPALGRSFLHGPDLKGQLRIHRDGIYMVHIQVTLAICSSTTASRHHPT TLAVGICSPASRSISLLRSLFHQGTIASQRLTPLARGDTLCTNLTGTLLPSRNTDETFFGVQ WVRPGGGSGGKPIPNPLGLDST
760	-	Hu CD70 mu E2	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFASQKQQQLPLESLGWDVAELQLN LTVPRKDPTRLRWGAGPALGRSFLHGPDLKGQLRIHRDGIYMVHIQVTLAICSSTTASRHHPT TLAVGICSPASRSISLLRSLFHQGTIASQRLTPLARGDTLCTNLTGTLLPSRNTDETFFGVQ WVRPGGGSGGKPIPNPLGLDST
761	-	Hu CD70 mu E3	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFASQKQQQLPLESLGWDVAELQLN HTGPQQDPRLYWQGGPALGRSFLHGPDLKGQLRIHQDGLYRLHIQVTLAICSSTTASRHHPT TLAVGICSPASRSISLLRSLFHQGTIASQRLTPLARGDTLCTNLTGTLLPSRNTDETFFGVQ WVRPGGGSGGKPIPNPLGLDST
762	-	Hu CD70 mu E4	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFASQKQQQLPLESLGWDVAELQLN HTGPQQDPRLYWQGGPALGRSFLHGPDLKGQLRIHRDGIYMVHIQVTLANCSSPGSTLQHRA TLAVGICSPASRSISLLRSLFHQGTIASQRLTPLARGDTLCTNLTGTLLPSRNTDETFFGVQ WVRPGGGSGGKPIPNPLGLDST
763	-	Hu CD70 mu E6	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFASQKQQQLPLESLGWDVAELQLN HTGPQQDPRLYWQGGPALGRSFLHGPDLKGQLRIHRDGIYMVHIQVTLAICSSTTASRHHPT TLAVGICSPASRSISLLRSLFHQGTVALQRLTYLVHGDVLCNTLTPLLPSRNTDETFFGVQ WVRPGGGSGGKPIPNPLGLDST
764	-	Hu CD70 mu E7	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFASQKQQQLPLESLGWDVAELQLN HTGPQQDPRLYWQGGPALGRSFLHGPDLKGQLRIHRDGIYMVHIQVTLAICSSTTASRHHPT TLAVGICSPASRSISLLRSLFHQGTIASQRLTPLARGDTLCTNLTGTLLPSRNADETFFGVQ WICPGGGSGGKPIPNPLGLDST
765	-	Hu CD70 mu E1+2	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFASQKQQQLLEHPEPHTAELQLN LTVPRKDPTRLRWGAGPALGRSFLHGPDLKGQLRIHRDGIYMVHIQVTLAICSSTTASRHHPT TLAVGICSPASRSISLLRSLFHQGTIASQRLTPLARGDTLCTNLTGTLLPSRNTDETFFGVQ WVRPGGGSGGKPIPNPLGLDST
766	-	Hu	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFASQKQQQLPLESLGWDVAELQLN

		CD70 mu E3+4		HTGPQQDPRLYWQGGPALGRSFTHGPELEEGHLRIHQDGLYRLHIQVTLANCSPPGSTLQHRA TLAVGICSPASRSISLLRSLSFHQGCTIASQRLTPLARGDTLCTNLTGTLLPSRNTDETFFGVQ WVRPGGGSGKPIPNPLGLDST
767	-	Hu CD70 mu E4+5	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFQAQQQLPLESLGWDVAELQLN HTGPQQDPRLYWQGGPALGRSFLHGPELDKGQLRIHRDGIYMVHIQVTLANCSPPGSTLQHRA TLAVGICSPAAGHISLLRGRFGQDCTIASQRLTPLARGDTLCTNLTGTLLPSRNTDETFFGVQ WVRPGGGSGKPIPNPLGLDST
768	-	Hu CD70 mu E6+7	artificial	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFQAQQQLPLESLGWDVAELQLN HTGPQQDPRLYWQGGPALGRSFLHGPELDKGQLRIHRDGIYMVHIQVTLAICSSTTASRHHPT TLAVGICSPASRSISLLRSLSFHQGCTVALQRLTYLVHGDVICTNLTPLLLPSRNADETFFGVQ WICPGGGGSGKPIPNPLGLDST
769	-	CD40L	human	MIETYNQTSRPSAATGLPISMKIFMYLLTVFLITQMIGSALFAVYLHRRLDKIEDERNLHEDF VFMKTIQRCNTGERSLSLLNCEEIKSQFEGFVKDIMLNKEETKENSEFEMQKGDQNPQIAAHV ISEASSKTTSVLQWAEKGYTMSNNLVTTLENGKQLTVKRQGLYIYAQVTFCSNREASSQAPF IASLCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFELQPGASVFVNVTDPSPVSHGTG FTSFGLLKL
770	-	linker 1	artificial	GGGG
771	-	linker 2	artificial	GGGGG
772	-	linker 3	artificial	GGGGQ
773	-	linker 4	artificial	SGGGG
774	-	linker 5	artificial	PGGGG
775	-	linker 6	artificial	PGDGS
776	-	linker 7	artificial	GGGGSGGG
777	-	linker 8	artificial	GGGGSGGGG
778	-	linker 9	artificial	GGGGSGGGSGGGG
779	-	Hexa- histidine	artificial	HHHHHH
780	-	Ab156	artificial	RDWDFDVFEGGGTPVGG

781	-	linear FcRn BP	artificial	QRFVTGHFGGLXPANG
782	-	linear FcRn BP-Y	artificial	QRFVTGHFGGLYPANG
783	-	linear FcRn BP-H	artificial	QRFVTGHFGGLHPANG
784	-	core FcRn BP-H	artificial	TGHFGGLHP
785	-	cyclic FcRn BP-H	artificial	QRFCTGHFGGLHPCNG
786	-	HALB	human	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQC PFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYEIAARRHPYFYAPELFFAKRYKA AFTECCQAADKAACLLPKLDELDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLT KVHTECCCHGDILLE CADDRADLAKY ICENQDSI SSKLKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVF LGMFLYEYARRHPDYSVLLLR LAKTYETTL EKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNC ELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALEVDETYVPKEFNA ETTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDDKETC FAEEGKKLVAASQAALGL
787	-	HALB variant 1	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQC PFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYEIAARRHPYFYAPELFFAKRYKA AFTECCQAADKAACLLPKLDELDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLT KVHTECCCHGDILLE CADDRADLAKY ICENQDSI SSKLKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVF LGMFLYEYARRHPDYSVLLLR LAKTYETTL EKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNC ELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALEVDETYVPKEFNA GTTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDDKETC

788	-	HALB variant 2	artificial	FAEEGKLVAAASQAALGL DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQC PFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPELLFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVF LGMFLYEYARRHPDYSVVL LRLAKTYET TLEKCCAAADPHECYAKVFFDEFK PLVEEPQNL IKQNC ELFQ LGEYKFQNAL LVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALGDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAAASQAALGL
789	-	HALB variant 3	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQC PFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPELLFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVF LGMFLYEYARRHPDYSVVL LRLAKTYET TLEKCCAAADPHECYAKVFFDEFK PLVEEPQNL IKQNC ELFQ LGEYKFQNAL LVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALGDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAAASQAALGL
790	-	HALB variant 4	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQC PFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPELLFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVF LGMFLYEYARRHPDYSVVL LRLAKTYET TLEKCCAAADPHECYAKVFFDEFK PLVEEPQNL IKQNC ELFQ LGEYKFQNAL LVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALGDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAAASQAALGL
791	-	HALB variant 5	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQC PFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP NL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPELLFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEG

792	-	HALB variant 6	artificial	<p>KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDKFAAFVEKCCCKADDKETC FAEEGPHLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPELFFAKRYKA AFTTECCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDKFAAFVEKCCCKADDKETC FAEEGPHLVAASQAALGL</p>
793	-	HALB variant 7	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPELFFAKRYKA AFTTECCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDKFAAFVEKCCCKADDKETC FAEEGPHLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPELFFAKRYKA AFTTECCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDKFAAFVEKCCCKADDKETC FAEEGPHLVAASQAALGL</p>
794	-	HALB variant 8	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPELFFAKRYKA AFTTECCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP</p>

795	-	HALB variant 9	artificial	EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEEGPKLVAASKAALGL DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAATECCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFELGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEEGPKLVAASKAALGL
796	-	HALB variant 10	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAATECCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFELGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEEGPKLVAASKAALGL
797	-	HALB variant 11	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAATECCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFELGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA GTTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAVMDKFAAFVEKCKCKADDDKETC FAEEGPKLVAASKAALGL
798	-	HALB	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQSPFEDHVKL VNEVTEFAKTCVADESAENCD

		variant 12	KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDMCTA FHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAFTTECCQAADKAACLLPKLDELDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVLLLLRLAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAASQAALGL
799	-	HALB variant 13	DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDMCTA FHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAFTTECCQAADKAACLLPKLDELDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVLLLLRLAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAASQAALGL
800	-	HALB variant 14	DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDMCTA FHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAFTTECCQAADKAACLLPKLDELDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVLLLLRLAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAASQAALGL
801	-	HALB variant 15	DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDMCTA FHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAFTTECCQAADKAACLLPKLDELDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV

802	-	HALB variant 16	artificial	<p>CKNYAEAKDVFLGMFLYEYARRHPDYSVVLILLRLAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVEYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCCKADDKETC FAEGPPLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQSQPFEDHVKLNVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDMCTA FHDNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAATECCQAADKAACLLPKLDELREDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLILLRLAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCCKADDKETC FAEGPPLVAASQAALGL</p>
803	-	HALB variant 17	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQSQPFEDHVKLNVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDMCTA FHDNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAATECCQAADKAACLLPKLDELREDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLILLRLAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCCKADDKETC FAEGPPLVAASQAALGL</p>
804	-	HALB variant 18	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQSQPFEDHVKLNVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDMCTA FHDNEETFLKKLYEIAARRHPYFYAPPELLFFAKRYKAATECCQAADKAACLLPKLDELREDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLILLRLAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCCCKADDKETC FAEGPPLVAASQAALGL</p>

805	-	HALB variant 19	artificial	FAEEGPKLVAAASKAALGL DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPRLPRLVRPEVDVMCTA FHDNEETFLKKLYEIAARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDELDRDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKYICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVVLILLRLAKTYETTLEKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVEDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCCKADDKETC FAEEGPKLVAAASKAALGL
806	-	HALB variant 20	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPRLPRLVRPEVDVMCTA FHDNEETFLKKLYEIAARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDELDRDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKYICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVVLILLRLAKTYETTLEKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCCKADDKETC FAEEGPKLVAAASKAALGL
807	-	HALB variant 21	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPRLPRLVRPEVDVMCTA FHDNEETFLKKLYEIAARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDELDRDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKYICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVVLILLRLAKTYETTLEKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCCKADDKETC FAEEGPKLVAAASKAALGL
808	-	HALB variant 22	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPRLPRLVRPEVDVMCTA FHDNEETFLKKLYEIAARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDELDRDEG

809	-	HALB variant 23	artificial	<p>KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDILLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYE IARRHPYFYAPELFFAKRYKAATFECQAAADKAACLLPKLDELREDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDILLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAASQAALGL</p>
810	-	HALB variant 24	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYE IARRHPYFYAPELFFAKRYKAATFECQAAADKAACLLPKLDELREDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDILLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYE IARRHPYFYAPELFFAKRYKAATFECQAAADKAACLLPKLDELREDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDILLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALGVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEEGPKLVAASQAALGL</p>
811	-	HALB variant 25	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYE IARRHPYFYAPELFFAKRYKAATFECQAAADKAACLLPKLDELREDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDILLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCCCKHP</p>

812	-	HALB variant 26	artificial	<p>EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVEDYVVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEEGPKLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAATECCQAADKAACLLPKLDELDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEEGPHLVAASQAALGL</p>
813	-	HALB variant 27	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAATECCQAADKAACLLPKLDELDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEEGPHLVAASQAALGL</p>
814	-	HALB variant 28	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAATECCQAADKAACLLPKLDELDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCSELFELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEEGPKLVAASQAALGL</p>
815	-	HALB	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKL VNEVTEFAKTCVADESAENCD</p>

		variant 29	KSLHTLFGDKLCTVATILRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDMCTA FHDNEETFLKKYLYEIAARRHPYFYAPELLFFAKRYKAFTTECCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSCLVTDLTKVHTECCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFGLGMFLYEYARRHPDYSVLLLRLLRAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNCSELFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVEDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCCKADDKETC FAEEGPKLVAASKAALGL
816	-	Cross body 1 HC	ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYDTTPPVLDSGDSFFLYSLDITVDKSRWQQGNVFCSCVMHEAL HNHYTQKSLSLSPGK
817	-	Cross body 1 LC	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN NKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCECSDKTHTCPPCPAPELLGGPSV FLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLKSDGSEFFLYSKLITVDKSRWQQGNVFCSCVMH EALHNHYTQKSLSLSPGK
818	-	Cross body 2 HC	ASTKGPSVFFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFFPAVLQSSGLY SLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVETPKSSDKTHTCPPCPAPEAAGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYDTTPPVLDSGDSFFLYSLDITVDKSRWQQGNVFCSCVMHEAL HNHYTQKSLSLSPGK
819	-	Cross body 2 LC	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSN NKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTCECSEPKSSDKTHTCPPCPAPEAA GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRKEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLKSDGSEFFLYSKLITVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
820	-	Hetero-	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE

821	-	Hetero- Fc partner Fc	VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDSGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
822	-	Maxibod y 1 target Fc	DKHTTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPVYITLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
823	-	Maxibod y 1 CD3 Fc	EPKSSDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGEVHNNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPVYITLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
824	-	Maxibod y 2 target Fc	EPKSSDKTHTCPAPAEAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPVYITLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
825	-	Maxibod y 2 CD3 Fc	EPKSSDKTHTCPAPAEAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPVYITLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
826	-	Mono Fc	APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVITLPPSRRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLKSDGSFFLYSDLTVDKSRWQQ GNVFCSCVMHEALHNHYTQKSLSLSPGK
827	-	CDR-L1 of F6A	GSSTGAVTSGYYPN
828	-	CDR-L2 of F6A	GTKFLAP
829	-	CDR-L3 of F6A	ALWYSNRWV

830	-	CDR-H1 of F6A	artificial	I YAMN	
831	-	CDR-H2 of F6A	artificial	RIRSKYNNYATYYADSVKS	
832	-	CDR-H3 of F6A	artificial	HGNFGNSYVSFFAY	
833	-	VH of F6A	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN IYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYVCVRHGNFGNSYVSFFAYWGQGTLLTVSS	
834	-	VL of F6A	artificial	QTVVTQEPSTLTVSPGGT VTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL	
835	-	VH-VL of F6A	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN IYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYVCVRHGNFGNSYVSFFAYWGQGTLLTVSSG GGSGGGGGGGGQT VVTQEPSTLTVSPGGT VTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL	
836	-	CDR-L1 of H2C	artificial	GSSTGAVTSGYYPN	
837	-	CDR-L2 of H2C	artificial	GTKFLAP	
838	-	CDR-L3 of H2C	artificial	ALWYSNRWV	
839	-	CDR-H1 of H2C	artificial	KYAMN	
840	-	CDR-H2 of H2C	artificial	RIRSKYNNYATYYADSVKD	
841	-	CDR-H3 of H2C	artificial	HGNFGNSYISYWAY	
842	-	VH of H2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYVCVRHGNFGNSYISYWAYWGQGTLLTVSS	
843	-	VL of H2C	artificial	QTVVTQEPSTLTVSPGGT VTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL	
844	-	VH-VL of H2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYVCVRHGNFGNSYISYWAYWGQGTLLTVSSG GGSGGGGGGGGQT VVTQEPSTLTVSPGGT VTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGL	

845	-	CDR-L1 of H1E	artificial	IGGTKFLAPGTPARFSGSLGGKKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
846	-	CDR-L2 of H1E	artificial	GSSTGAVTSGYYPN
847	-	CDR-L3 of H1E	artificial	GTKFLAP
848	-	CDR-H1 of H1E	artificial	ALWYSNRWV
849	-	CDR-H2 of H1E	artificial	SYAMN
850	-	CDR-H3 of H1E	artificial	RIRSKYNNYATYYADSVKG
851	-	VH of H1E	artificial	HGNFGNSYLSFWAY
852	-	VL of H1E	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGNSYLSFWAYWGQGLTVTVSS
853	-	VH-VL of H1E	artificial	QTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLGGKKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
854	-	CDR-L1 of G4H	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGNSYLSFWAYWGQGLTVTVSSG
855	-	CDR-L2 of G4H	artificial	GGSGGGSGGGGQTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGYYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLGGKKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
856	-	CDR-L3 of G4H	artificial	GSSTGAVTSGYYPN
857	-	CDR-H1 of G4H	artificial	GTKFLAP
858	-	CDR-H2 of G4H	artificial	ALWYSNRWV
859	-	CDR-H3 of G4H	artificial	RYAMN
				RIRSKYNNYATYYADSVKG
				HGNFGNSYLSFYAY

860	-	VH of G4H	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLLTVSS
861	-	VL of G4H	artificial	QTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
862	-	VH-VL of G4H	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGTLLTVSSG GGSGGGGGGGGQTIVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
863	-	CDR-L1 of A2J	artificial	RSSTGAVTSGYYPN
864	-	CDR-L2 of A2J	artificial	ATDMRPS
865	-	CDR-L3 of A2J	artificial	ALWYSNRWV
866	-	CDR-H1 of A2J	artificial	VYAMN
867	-	CDR-H2 of A2J	artificial	RIRSKYNNYATYYADSVKK
868	-	CDR-H3 of A2J	artificial	HGNFGNSYLSWVAY
869	-	VH of A2J	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYLSWVAYWGQGTLLTVSS
870	-	VL of A2J	artificial	QTVVTQEPSTLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
871	-	VH-VL of A2J	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYLSWVAYWGQGTLLTVSSG GGSGGGGGGGGQTIVTQEPSTLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGL IGATDMRPSGTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
872	-	CDR-L1 of E1L	artificial	GSSTGAVTSGYYPN
873	-	CDR-L2 of E1L	artificial	GTKFLAP
874	-	CDR-L3	artificial	ALWYSNRWV

		of E1L		
875	-	CDR-H1 of E1L	artificial	KYAMN
876	-	CDR-H2 of E1L	artificial	RIRSKYNNYATYYADSVKS
877	-	CDR-H3 of E1L	artificial	HGNFGNSYTSYYAY
878	-	VH of E1L	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKSRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGLTVTVSS
879	-	VL of E1L	artificial	QTVVTQEPSTLVSPGGTFTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
880	-	VH-VL of E1L	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKSRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGLTVTVSSG GGSGGGSGGGGSGTQVVTQEPSTLVSPGGTFTLTTCGSSTGAVTSGYYPNWVQKPGQAPRGL IGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
881	-	CDR-L1 of E2M	artificial	RSSTGAVTSGYYPN
882	-	CDR-L2 of E2M	artificial	ATDMRPS
883	-	CDR-L3 of E2M	artificial	ALWYSNRWV
884	-	CDR-H1 of E2M	artificial	GYAMN
885	-	CDR-H2 of E2M	artificial	RIRSKYNNYATYYADSVKE
886	-	CDR-H3 of E2M	artificial	HRNFGNSYLSWFAY
887	-	VH of E2M	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKERFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYLSWFAYWGQGLTVTVSS
888	-	VL of E2M	artificial	QTVVTQEPSTLVSPGGTFTLTTCRSSTGAVTSGYYPNWVQKPGQAPRGLIGATDMRPSGTPAR FSGSLLGKKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
889	-	VH-VL of E2M	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKERFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYLSWFAYWGQGLTVTVSSG

890	-	CDR-L1 of F70	artificial	GGSGGGGGGGGSGQT VVTQEP SLTVSPGGTVTLTCRSSSTGAVTSGYYPNWWVQKPGQAPRGL IGATDMRPSGT PARFSGSLGGKAAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
891	-	CDR-L2 of F70	artificial	GSSTGAVTSGYYPN
892	-	CDR-L3 of F70	artificial	GTKFLAP
893	-	CDR-H1 of F70	artificial	ALWYSNRWV
894	-	CDR-H2 of F70	artificial	VYAMN
895	-	CDR-H3 of F70	artificial	RIRSKYNNYATYYADSVKK
896	-	VH of F70	artificial	HGNFGNSYISWAY
897	-	VL of F70	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWRQAPGKGLEWVARIRSKYNNYATYYA DSVKRRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISWAYWGQGT LTVTVSS
898	-	VH-VL of F70	artificial	QTVVTQEP SLTVSPGGTVTLTCGSSSTGAVTSGYYPNWWVQKPGQAPRGLIGG TKFLAPGTPAR FSGSLGGKAAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
899	-	CDR-L1 of F12Q	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFN VYAMNWRQAPGKGLEWVARIRSKYNNYATYYA DSVKRRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISWAYWGQGT LTVTVSSG
900	-	CDR-L2 of F12Q	artificial	GGSGGGGGGGGSGQT VVTQEP SLTVSPGGTVTLTCGSSSTGAVTSGYYPNWWVQKPGQAPRGL IGG TKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
901	-	CDR-L3 of F12Q	artificial	GSSTGAVTSGNYPN
902	-	CDR-H1 of F12Q	artificial	GTKFLAP
903	-	CDR-H2 of F12Q	artificial	VLWYSNRWV
904	-	CDR-H3	artificial	SYAMN
				RIRSKYNNYATYYADSVKG
				HGNFGNSYVSWWAY

905	-	of F12Q	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWGQGTLLTVSS
906	-	VL of F12Q	artificial	QTVVTQEPSTLTVSPGGTDTLTGSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
907	-	VH-VL of F12Q	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYVSWWAYWGQGTLLTVSSG GGSGGGSGGGGSGTQVVTQEPSTLTVSPGGTDTLTGSGSTGAVTSGNYPNWVQQKPGQAPRGL IGGKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
908	-	CDR-L1 of I2C	artificial	GSSTGAVTSGNYPN
909	-	CDR-L2 of I2C	artificial	GTKFLAP
910	-	CDR-L3 of I2C	artificial	VLWYSNRWV
911	-	CDR-H1 of I2C	artificial	KYAMN
912	-	CDR-H2 of I2C	artificial	RIRSKYNNYATYYADSVKD
913	-	CDR-H3 of I2C	artificial	HGNFGNSYISYWAY
914	-	VH of I2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTLLTVSS
915	-	VL of I2C	artificial	QTVVTQEPSTLTVSPGGTDTLTGSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
916	-	VH-VL of I2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTLLTVSSG GGSGGGSGGGGSGTQVVTQEPSTLTVSPGGTDTLTGSGSTGAVTSGNYPNWVQQKPGQAPRGL IGGKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
917	-	VH of F12q	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGNGFNSYVSWWAYWGQGTLLTVSS
918	-	VL of F12q	artificial	QTVVTQEPSTLTVSPGGTDTLTGSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPAR FSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

919	-	VH-VL of F12q	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNLSLKTEDTAVYYCVRHGNGNSYVSWWAYWGQGLTVTVSSG GGSGGGGGSGGSGTQVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGTKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL
920		CD70- 13_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSISGSGGRPNYADS VKGRFTISRDN SKNTLYLQMNLSLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSS
921		CD70- 13_CC	VL	EIVLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIK
922		CD70- 13_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSISGSGGRPNYADS VKGRFTISRDN SKNTLYLQMNLSLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIK
923		CD70- 13_CCx12 C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSISGSGGRPNYADS VKGRFTISRDN SKNTLYLQMNLSLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIKSKSGGGSEVQ LVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLSLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSGTQVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL
924		CD70- 14_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNLSLRDEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
925		CD70- 14_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIK
926		CD70- 14_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNLSLRDEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIK
927		CD70- 14_CCx1 2C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNLSLRDEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS

				RATGIPDRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
928	CD70- 15_CC	VH		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLFLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGTTLTVTVSS
929	CD70- 15_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPFTFGCGTKLEIK
930	CD70- 15_CC	scFv		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLFLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGTTLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPFTFGCGTKLEIK
931	CD70- 15_CCx12 C	bispecific molecule		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLFLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGTTLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGGSPFTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
932	CD70- 16_CC	VH		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGTTLTVTVSS
933	CD70- 16_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDTFTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIK
934	CD70- 16_CC	scFv		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGTTLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIK
935	CD70- 16_CCx12 C	bispecific molecule		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGTTLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTFTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIKSGGGSEVQ

				LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVL
936	CD70- 17_CC	VH		EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
937	CD70- 17_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYQYGSPPFTFGCGTKLEIK
938	CD70- 17_CC	scFv		EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQYQYGSPPFTFGCGTKLEIK
939	CD70- 17_CCx12 C	bispecific molecule		EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQYQYGSPPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVL
940	CD70- 18_CC	VH		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSLISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
941	CD70- 18_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYDASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYQYGSPPFTFGCGTKLEIK
942	CD70- 18_CC	scFv		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSLISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYDASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQYQYGSPPFTFGCGTKLEIK
943	CD70- 18_CCx12 C	bispecific molecule		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSLISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYDASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQYQYGSPPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV

				KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
944	CD70- 19_CC	VH		EVQLLESGGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVS AISGSGGSTFYADS VKGRFTISRDN SKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG VKGRFTISRDN SKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
945	CD70- 19_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLA WYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGCGTKLEIK
946	CD70- 19_CC	scFv		EVQLLESGGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVS AISGSGGSTFYADS VKGRFTISRDN SKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGCGTKLEIK
947	CD70- 19_CCx12 C	bispecific molecule		EVQLLESGGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVS AISGSGGSTFYADS VKGRFTISRDN SKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
948	CD70- 21_CC	VH		EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVS AISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVS
949	CD70- 21_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLA WYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQYQYGDLPFTFGCGTKLEIK
950	CD70- 21_CC	scFv		EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVS AISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQYQYGDLPFTFGCGTKLEIK
951	CD70- 21_CCx12 C	bispecific molecule		EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVS AISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQYQYGDLPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG

				SGGGSGGGGQTVVTQEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
952	CD70- 22_CC	VH		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATSGSGGYTYIYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
953	CD70- 22_CC	VL		EIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVEIK
954	CD70- 22_CC	scFv		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATSGSGGYTYIYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVEIK
955	CD70- 22_CCx12 C	bispecific molecule		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATSGSGGYTYIYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
956	CD70- 24_CC	VH		EVQLLESGGGLAQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATSGSGGSTFYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYFCAKHDYSNYPFDYWGQGTLLTVSS
957	CD70- 24_CC	VL		EIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVEIK
958	CD70- 24_CC	scFv		EVQLLESGGGLAQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATSGSGGSTFYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYFCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVEIK
959	CD70- 24_CCx12 C	bispecific molecule		EVQLLESGGGLAQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATSGSGGSTFYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYFCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLRLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG

				TKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
960	CD70- 25_CC	VH		EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
961	CD70- 25_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGCGTKVEIK
962	CD70- 25_CC	scFv		EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGCGTKVEIK
963	CD70- 25_CCx12 C	bispecific molecule		EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
964	CD70- 26_CC	VH		EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
965	CD70- 26_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYYCQYGSSPFTFGCGTKVEIK
966	CD70- 26_CC	scFv		EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQYGSSPFTFGCGTKVEIK
967	CD70- 26_CCx12 C	bispecific molecule		EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQYGSSPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

968	CD70_1-G2	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGTLLTVSS
969	CD70_1-G2	VL	EIVLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYGYSPFTFGPGTKVEIK
970	CD70_1-G2	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPFTFGPGTKVEIK
971	CD70_1-G2x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
972	CD70_1-G2_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGSTFYADS VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGTLLTVSS
973	CD70_1-G2_CC	VL	EIVLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYGYSPFTFGCGTKVEIK
974	CD70_1-G2_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGSTFYADS VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPFTFGCGTKVEIK
975	CD70_1-G2_CCx12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGSTFYADS VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

976	CD70- 27_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGGTFTYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
977	CD70- 27_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGCGTKVEIK
978	CD70- 27_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGGTFTYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGCGTKVEIK
979	CD70- 27_CCx12 C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGGTFTYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
980	CD70- 28_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
981	CD70- 28_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGCGTKVEIK
982	CD70- 28_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGCGTKVEIK
983	CD70- 28_CCx12 C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

984	CD70-31_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKCLEWVSATSGSGGRAQYADS VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
985	CD70-31_CC	VL	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSRATGIPDRFS GSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGCGTKVEIK
986	CD70-31_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKCLEWVSATSGSGGRAQYADS VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGCGTKVEIK
987	CD70-31_CCx12_C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKCLEWVSATSGSGGRAQYADS VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGS GGSGGGGSGTQVVTQEPSTVSPGGTTLTTCGSGTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
988	CD70-32_CC	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSS
989	CD70-32_CC	VL	EIVLTQSPGTLSPGERATLSCRASQGVRSYDLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGCGTKVEIK
990	CD70-32_CC	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYDLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGCGTKVEIK
991	CD70-32_CCx12_C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYDLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGSGTQVVTQEPSTVSPGGTTLTTCGSGTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

992	CD70- 37_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAIGDGGGTYYYADS VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDSNYPYFDYWGQGTLLTVSS
993	CD70- 37_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQGVRSYFAWYQQKPGQAPRLLIYGASTRATGIPARF SGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIK
994	CD70- 37_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAIGDGGGTYYYADS VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDSNYPYFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQGVRSYFAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIK
995	CD70- 37_CCx12 C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAIGDGGGTYYYADS VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDSNYPYFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQGVRSYFAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
996	CD70- 38_CC	VH	EVQLLESGGGLVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSS
997	CD70- 38_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQIRSNIYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIK
998	CD70- 38_CC	scFv	EVQLLESGGGLVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQIRSNIYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIK
999	CD70- 38_CCx12 C	bispecific molecule	EVQLLESGGGLVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQIRSNIYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

1000	CD70-39_CC	VH	EVQLLESGGGVVPGRSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDSNYPYFDYWGLGLTLTVSS
1001	CD70-39_CC	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYQYGDLPFTFGCGTKVEIK
1002	CD70-39_CC	scFv	EVQLLESGGGVVPGRSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDSNYPYFDYWGLGLTLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYQYGDLPFTFGCGTKVEIK
1003	CD70-39_CCx12 C	bispecific molecule	EVQLLESGGGVVPGRSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDSNYPYFDYWGLGLTLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1004	CD70-41_CC	VH	EVQLLESGGGMVQPGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGGQGLTLTVSS
1005	CD70-41_CC	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYCYQQYQYGDLPFTFGCGTKVDIK
1006	CD70-41_CC	scFv	EVQLLESGGGMVQPGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGGQGLTLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCYQQYQYGDLPFTFGCGTKVDIK
1007	CD70-41_CCx12 C	bispecific molecule	EVQLLESGGGMVQPGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGGQGLTLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCYQQYQYGDLPFTFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

1008	CD70- 42_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1009	CD70- 42_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQGVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIK
1010	CD70- 42_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQGVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIK
1011	CD70- 42_CCx12 C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQGVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGFNYSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1012	CD70- 43_CC	VH	EVQLLESGGGLVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1013	CD70- 43_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIK
1014	CD70- 43_CC	scFv	EVQLLESGGGLVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIK
1015	CD70- 43_CCx12 C	bispecific molecule	EVQLLESGGGLVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGFNYSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

1016	CD70- 48_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSIVDSGGITDFADS VKGRFTISRDNsrNTLYLQMNslRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSS
1017	CD70- 48_CC	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGVKLLIYAASILQSGVPSKFS GSGSGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGCGTRLEIK
1018	CD70- 48_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSIVDSGGITDFADS VKGRFTISRDNsrNTLYLQMNslRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGVKLLIYAASIL QSGVPSKFSGSGSGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGCGTRLEIK
1019	CD70- 48_CCx12 C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSIVDSGGITDFADS VKGRFTISRDNsrNTLYLQMNslRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGVKLLIYAASIL QSGVPSKFSGSGSGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGCGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVTVTEPSLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVL
1020	CD70- 53_CC	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSISGSGGRTFYADS VEGRFTISRDNskNTLYLQMNslRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1021	CD70- 53_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQQKPGQAPRLLIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYFCQQYGSPPPTFGCGTRLEIK
1022	CD70- 53_CC	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSISGSGGRTFYADS VEGRFTISRDNskNTLYLQMNslRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQQKPGQAPRLLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYFCQQYGSPPPTFGCGTRLEIK
1023	CD70- 53_CCx12 C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSISGSGGRTFYADS VEGRFTISRDNskNTLYLQMNslRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQQKPGQAPRLLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYFCQQYGSPPPTFGCGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGSGTQVTVTEPSLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLGSVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVL

1024	CD70- 54_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAIGDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1025	CD70- 54_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTRLEIK
1026	CD70- 54_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAIGDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTRLEIK
1027	CD70- 54_CCx12 C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAIGDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1028	CD70- 58_CC	VH	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHYEILTGYYPDFDIWGQGTMTVSS
1029	CD70- 58_CC	VL	DIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQQKPKAPKLLIYAASNLSGVSSRFS GSGGTDFTLTISLQPEDFATYYCQQSFSSPRTFGCGTKVEIK
1030	CD70- 58_CC	scFv	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHYEILTGYYPDFDIWGQGTMTVSSG GGSGGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQQKPKAPKLLIY AASNLSGVSSRFSGSGGTDFTLTISLQPEDFATYYCQQSFSSPRTFGCGTKVEIK
1031	CD70- 58_CCx12 C	bispecific molecule	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHYEILTGYYPDFDIWGQGTMTVSSG GGSGGGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQQKPKAPKLLIY AASNLSGVSSRFSGSGGTDFTLTISLQPEDFATYYCQQSFSSPRTFGCGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSS GGSGGGGSGGGGQTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQQKPGQAPRG LIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

1032	CD70- 62_CC	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVS _Y ISSSGGYI _Y YADS VKGRFTISRDNAKNSLYLQMNSLRAEDAAVY _Y CSRGDYSN _Y AYFDYWGQGLTVTVSS
1033	CD70- 62_CC	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISN _Y LAWYQQKPGKVPKLLI _Y AASTLQSGVPSRFS GSGSGTDFTLTISSLQAEDVAVY _Y CQQY _Y STPLTFGCGTKVEIK
1034	CD70- 62_CC	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVS _Y ISSSGGYI _Y YADS VKGRFTISRDNAKNSLYLQMNSLRAEDAAVY _Y CSRGDYSN _Y AYFDYWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISN _Y LAWYQQKPGKVPKLLI _Y AASTL QSGVPSRFSGSGTDFTLTISSLQAEDVAVY _Y CQQY _Y STPLTFGCGTKVEIK
1035	CD70- 62_CCx12 C	bispecific molecule	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVS _Y ISSSGGYI _Y YADS VKGRFTISRDNAKNSLYLQMNSLRAEDAAVY _Y CSRGDYSN _Y AYFDYWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISN _Y LAWYQQKPGKVPKLLI _Y AASTL QSGVPSRFSGSGTDFTLTISSLQAEDVAVY _Y CQQY _Y STPLTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYAT _Y YADSVK DRFTISRDDSKNTAYLQMN _Y NLKTEDTAVY _Y CVRHG _Y FN _Y SG _Y IS _Y WAYWGQGLTVTVSSGGGGS GGSGGGGSGT _Y VTQEP _Y SLTVSPGGT _Y VLTCGSSTGAVTSGN _Y PNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTL _Y SGVQPEDEAEY _Y CVLWY _Y SNRWVFGG _Y TKLTVL
1036	CD70- 23_CC	VH	EVQLLES _Y GGGLVQPGGSLRLSCAASGFTF _Y SVYAMS _Y WVRQAPGKCLEWVS _Y TSISDSGGSTFYADS VKGRFTISRDN _Y SKNTLYLQMNRLRAEDTAVY _Y CARHDYSN _Y AYFDYWGQGLTVTVSS
1037	CD70- 23_CC	VL	EIVLTQSPG _Y TL _Y SLSPGERAT _Y LS _Y CRASQSV _Y RS _Y SYLAWYQQKPGQAPRLLI _Y YGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVY _Y CQQY _Y GDLPFTFGCGTKVEIK
1038	CD70- 23_CC	scFv	EVQLLES _Y GGGLVQPGGSLRLSCAASGFTF _Y SVYAMS _Y WVRQAPGKCLEWVS _Y TSISDSGGSTFYADS VKGRFTISRDN _Y SKNTLYLQMNRLRAEDTAVY _Y CARHDYSN _Y AYFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPG _Y TL _Y SLSPGERAT _Y LS _Y CRASQSV _Y RS _Y SYLAWYQQKPGQAPRLLI _Y YGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVY _Y CQQY _Y GDLPFTFGCGTKVEIK
1039	CD70- 23_CCx12 C	bispecific molecule	EVQLLES _Y GGGLVQPGGSLRLSCAASGFTF _Y SVYAMS _Y WVRQAPGKCLEWVS _Y TSISDSGGSTFYADS VKGRFTISRDN _Y SKNTLYLQMNRLRAEDTAVY _Y CARHDYSN _Y AYFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPG _Y TL _Y SLSPGERAT _Y LS _Y CRASQSV _Y RS _Y SYLAWYQQKPGQAPRLLI _Y YGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVY _Y CQQY _Y GDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYAT _Y YADSV KDRFTISRDDSKNTAYLQMN _Y NLKTEDTAVY _Y CVRHG _Y FN _Y SG _Y IS _Y WAYWGQGLTVTVSSGGGG SGGGSGGGSGT _Y VTQEP _Y SLTVSPGGT _Y VLTCGSSTGAVTSGN _Y PNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTL _Y SGVQPEDEAEY _Y CVLWY _Y SNRWVFGG _Y TKLTVL

1040	CD70-55_CC	VH	QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARGRYYGSGN YNHGMDVWGQGT TTVTVSS
1041	CD70-55_CC	VL	DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLSQSGVPSRFS GRSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKVEIK
1042	CD70-55_CC	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARGRYYGSGN YNHGMDVWGQGT TTVTVSSGG GGSGGGSGGGSDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIYA ASSLSQSGVPSRFSGRSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKVEIK
1043	CD70-55_CCx12C	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARGRYYGSGN YNHGMDVWGQGT TTVTVSSGG GGSGGGSGGGSDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIYA ASSLSQSGVPSRFSGRSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKVEIKS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVTVSSG GGSGGGSGGGGQT VVTQEP SLTVSPGGT VTLTCGSS TGA VTS GNYPNWVQKPGQAPRGL IGG TKFLAPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGG GTKLTVL
1044	CD70-13D	VH CDR1	SYAMS
1045	CD70-13D	VH CDR2	VISGSGGRPNYAESVKG
1046	CD70-13D	VH CDR3	VDYSNYLFFDY
1047	CD70-13D	VL CDR1	RAGQSVRSSLG
1048	CD70-13D	VL CDR2	GASSRAT
1049	CD70-13D	VL CDR3	QQYGYSPPT

1050	CD70- 13D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISGSGGRPNYAES VKGRFTISRDN SKNTLYLQMN SLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSS
1051	CD70- 13D_CC	VL	EIVLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIK
1052	CD70- 13D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISGSGGRPNYAES VKGRFTISRDN SKNTLYLQMN SLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIK
1053	CD70- 13D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISGSGGRPNYAES VKGRFTISRDN SKNTLYLQMN SLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1054	CD70- 13D	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSVISGSGGRPNYAES VKGRFTISRDN SKNTLYLQMN SLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSS
1055	CD70- 13D	VL	EIVLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIK
1056	CD70- 13D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSVISGSGGRPNYAES VKGRFTISRDN SKNTLYLQMN SLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIK
1057	CD70- 13Dx12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSVISGSGGRPNYAES VKGRFTISRDN SKNTLYLQMN SLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1058	CD70-	VH	IYAMS

		14D	CDR1	
1059		CD70-14D	VH CDR2	AISGGSGSTFYAESVKG
1060		CD70-14D	VH CDR3	HDYSNYPYFDY
1061		CD70-14D	VL CDR1	RASQSVRRSSYLA
1062		CD70-14D	VL CDR2	GASSRAT
1063		CD70-14D	VL CDR3	QQYGDLPFT
1064		CD70-14D_CC	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1065		CD70-14D_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGCGTKLEIK
1066		CD70-14D_CC	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGCGTKLEIK
1067		CD70-14D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGCGTKLEIK LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDS KNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGSEQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1068		CD70-14D	VH	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKLEWVSAISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS

1069	CD70-14D	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYQCQYGDLPFTFGPGTKLEIK
1070	CD70-14D	scFv	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAISGSGGSTFYAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYQCQYGDLPFTFGPGTKLEIK
1071	CD70-14Dx12C	bispecific molecule	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAISGSGGSTFYAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYQCQYGDLPFTFGPGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNIATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGSGGGGGGSGQTVVTQEPSLTVSPGGTFTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1072	CD70_6 1-D1D	VH CDR1	SYAMS
1073	CD70_6 1-D1D	VH CDR2	AISGSGGRTFYAESVEG
1074	CD70_6 1-D1D	VH CDR3	HDYSNYPYFDY
1075	CD70_6 1-D1D	VL CDR1	RASQSVRSYLA
1076	CD70_6 1-D1D	VL CDR2	GASSRAT
1077	CD70_6 1-D1D	VL CDR3	QQYGSSPFT
1078	CD70_6 1-D1D CC	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAESVEGRFTISRDNKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS

1079	CD70_6 1- D1D_CC	VL	EIVLTQSPGTL _{SL} SPGERATL _{SCR} ASQSV _{RSS} YLAWYQQKPGQAP _{RL} LIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVY _{YC} QQYGSSPFTFGCGTKLEIK
1080	CD70_6 1- D1D_CC	scFv	EVQLLESGGGMVQPGGSLRLS _{CA} ASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN _{SKNT} FLQMN _{SL} RAEDTAVY _Y CAKHDY _{SNYP} FDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTL _{SL} SPGERATL _{SCR} ASQSV _{RSS} YLAWYQQKPGQAP _{RL} LIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVY _{YC} QQYGSSPFTFGCGTKLEIK
1081	CD70_6 1- D1D_CC x12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLS _{CA} ASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN _{SKNT} FLQMN _{SL} RAEDTAVY _Y CAKHDY _{SNYP} FDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTL _{SL} SPGERATL _{SCR} ASQSV _{RSS} YLAWYQQKPGQAP _{RL} LIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVY _{YC} QQYGSSPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLS _{CA} ASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN _{NL} KTEDTAVY _Y CVRHG _N FGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP _{SL} TVSPGGTVTLT _{CG} SSGTAVTSGNYPNWVQKPGQAP _{RL} IGG TKFLAPGTPARFSGSL _{LG} GKAALTL _{SG} VQPEDEAEY _Y CVLWYSNRWVFGG _{TK} LT _{VL}
1082	CD70_6 1-D1D	VH	EVQLLESGGGMVQPGGSLRLS _{CA} ASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN _{SKNT} FLQMN _{SL} RAEDTAVY _Y CAKHDY _{SNYP} FDYWGQGLTVTVSS
1083	CD70_6 1-D1D	VL	EIVLTQSPGTL _{SL} SPGERATL _{SCR} ASQSV _{RSS} YLAWYQQKPGQAP _{RL} LIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVY _{YC} QQYGSSPFTFGPGTKLEIK
1084	CD70_6 1-D1D	scFv	EVQLLESGGGMVQPGGSLRLS _{CA} ASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN _{SKNT} FLQMN _{SL} RAEDTAVY _Y CAKHDY _{SNYP} FDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTL _{SL} SPGERATL _{SCR} ASQSV _{RSS} YLAWYQQKPGQAP _{RL} LIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVY _{YC} QQYGSSPFTFGPGTKLEIK
1085	CD70_6 1- D1Dx12 C	bispecific molecule	EVQLLESGGGMVQPGGSLRLS _{CA} ASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN _{SKNT} FLQMN _{SL} RAEDTAVY _Y CAKHDY _{SNYP} FDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTL _{SL} SPGERATL _{SCR} ASQSV _{RSS} YLAWYQQKPGQAP _{RL} LIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVY _{YC} QQYGSSPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLS _{CA} ASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN _{NL} KTEDTAVY _Y CVRHG _N FGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP _{SL} TVSPGGTVTLT _{CG} SSGTAVTSGNYPNWVQKPGQAP _{RL} IGG TKFLAPGTPARFSGSL _{LG} GKAALTL _{SG} VQPEDEAEY _Y CVLWYSNRWVFGG _{TK} LT _{VL}
1086	CD70- 16D	VH CDR1	SYAMS

1087	CD70-16D	VH CDR2	AISGSGGRTFYAESVEG
1088	CD70-16D	VH CDR3	HDYSNYPYFDY
1089	CD70-16D	VL CDR1	RASQIRSSYLA
1090	CD70-16D	VL CDR2	GASSRAT
1091	CD70-16D	VL CDR3	QQYGDLPFT
1092	CD70-16D_CC	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWMVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1093	CD70-16D_CC	VL	EIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYQYGDLPFTFGCGTKLEIK
1094	CD70-16D_CC	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWMVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYQYGDLPFTFGCGTKLEIK
1095	CD70-16D_CC x12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWMVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYQYGDLPFTFGCGTKLEIK LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWMVRQAPGKLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWMVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1096	CD70-16D	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWMVRQAPGKLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1097	CD70-16D	VL	EIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYQYGDLPFTFGPGTKLEIK

1098	CD70-16D	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQQYGDLPFTFGPGTKLEIK
1099	CD70-16Dx12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1100	CD70-17D	VH CDR1	SYAMS
1101	CD70-17D	VH CDR2	AISGSGGRTHYAESVKG
1102	CD70-17D	VH CDR3	HDYSNYPYFDY
1103	CD70-17D	VL CDR1	RASQSVRRSSYLA
1104	CD70-17D	VL CDR2	GASSRAT
1105	CD70-17D	VL CDR3	QQYGSSPFT
1106	CD70-17D_CC	VH	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTHYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1107	CD70-17D_CC	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYCCQQYGGSPFTFGCGTKLEIK
1108	CD70-17D_CC	scFv	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTHYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG

				GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLPEPEFAVYCCQYGSSPFTFGCGTKLEIK
1109	CD70- 17D _{CC} x12C	bispecific molecule		EVQLLESGGGLVQSGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLPEPEFAVYCCQYGSSPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGSQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1110	CD70- 17D	VH		EVQLLESGGGLVQSGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1111	CD70- 17D	VL		EIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTIISRLPEPEFAVYCCQYGSSPFTFGPGTKLEIK
1112	CD70- 17D	scFv		EVQLLESGGGLVQSGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLPEPEFAVYCCQYGSSPFTFGPGTKLEIK
1113	CD70- 17Dx12C	bispecific molecule		EVQLLESGGGLVQSGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLPEPEFAVYCCQYGSSPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGSQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1114	CD70- 18D	VH CDR1		SYAMS
1115	CD70- 18D	VH CDR2		LISGSGGRTHYAESVKG
1116	CD70- 18D	VH CDR3		HDYSNYPYFDY

1117	CD70-18D	VL CDR1	RASQSVRSTYLA
1118	CD70-18D	VL CDR2	DASSRAT
1119	CD70-18D	VL CDR3	QQYGSSPPT
1120	CD70-18D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSLISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1121	CD70-18D_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGCGTKLEIK
1122	CD70-18D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSLISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGCGTKLEIK
1123	CD70-18D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSLISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTVTLTCSGSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1124	CD70-18D	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSLISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1125	CD70-18D	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGCGTKLEIK
1126	CD70-18D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSLISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGCGTKLEIK
1127	CD70-	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSLISGSGGRTHYAES

	18Dx12C	c molecule	VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEIVLTQSPGTL SLSPGERATLSCRASQSVRSTYLA WYQQKPGQAPRLLIYDASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGGGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGTFN KYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGG SGGGSGGGGQT VVTQEP SLTVSPGGT VTLTCGSS TGA VTS GNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1128	CD70- 19D	VH CDR1	TYAMS
1129	CD70- 19D	VH CDR2	AISGGSGSTFYAESVKG
1130	CD70- 19D	VH CDR3	HDYSNYPYFDY
1131	CD70- 19D	VL CDR1	RASQSVRSSYLA
1132	CD70- 19D	VL CDR2	GASSRAT
1133	CD70- 19D	VL CDR3	QQYGDLPFT
1134	CD70- 19D_CC	VH	EVQLLESGGGLVQPGGSLRLS CAASGFTTFTYAMSWVRQAPGKCLEWVSAISGGSGSTFYAES VKGRFTISRDN SKNTLSLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSS
1135	CD70- 19D_CC	VL	EIVLTQSPGTL SLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYCYCQQYGDLPFTFGCGTKLEIK
1136	CD70- 19D_CC	scFv	EVQLLESGGGLVQPGGSLRLS CAASGFTTFTYAMSWVRQAPGKCLEWVSAISGGSGSTFYAES VKGRFTISRDN SKNTLSLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEIVLTQSPGTL SLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCYCQQYGDLPFTFGCGTKLEIK
1137	CD70- 19D_CC x12C	bispecific c molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTTFTYAMSWVRQAPGKCLEWVSAISGGSGSTFYAES VKGRFTISRDN SKNTLSLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEIVLTQSPGTL SLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASS

1138	CD70-19D	VH	RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1139	CD70-19D	VL	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGSTFYAES VKGRFTISRDN SKNTLSLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKLEIK
1140	CD70-19D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGSTFYAES VKGRFTISRDN SKNTLSLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKLEIK
1141	CD70-19Dx12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGSTFYAES VKGRFTISRDN SKNTLSLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSYLAWEYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTLCGSSTGAVTSNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1142	CD70-21D	VH CDR1	TYAMS
1143	CD70-21D	VH CDR2	AISGSGGRTFYAESVEG
1144	CD70-21D	VH CDR3	HDYSNYPYFDY
1145	CD70-21D	VL CDR1	RASQSVRSTYLA
1146	CD70-21D	VL	GASSRAT

		CDR2	
1147	CD70- 21D	VL CDR3	QQYGDLPFT
1148	CD70- 21D_CC	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1149	CD70- 21D_CC	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIK
1150	CD70- 21D_CC	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIK
1151	CD70- 21D_CC x12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTLCGSSGTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1152	CD70- 21D	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1153	CD70- 21D	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKLEIK
1154	CD70- 21D	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKLEIK
1155	CD70- 21Dx12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV

				KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSTLVSPGGTVTLTGSGSTGAVTSGNYPNWWQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1156	CD70- 22D	VH CDR1		SYAMS
1157	CD70- 22D	VH CDR2		AISGSGGYTYAAESVKG
1158	CD70- 22D	VH CDR3		HDYSNYPYFDY
1159	CD70- 22D	VL CDR1		RASQSVRSNYLA
1160	CD70- 22D	VL CDR2		GASSRAT
1161	CD70- 22D	VL CDR3		QQYGDLPFT
1162	CD70- 22D_CC	VH		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGYTYAAES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1163	CD70- 22D_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVEIK
1164	CD70- 22D_CC	scFv		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGYTYAAES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVEIK
1165	CD70- 22D_CC x12C	bispecific molecule		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGYTYAAES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSTLVSPGGTVTLTGSGSTGAVTSGNYPNWWQKPGQAPRGLIGG

				TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1166	CD70-22D	VH		EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGYTYAAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSS
1167	CD70-22D	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIK
1168	CD70-22D	scFv		EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGYTYAAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSSGGGSG GGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIK
1169	CD70-22Dx12C	bispecific molecule		EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGYTYAAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSSGGGSG GGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIK LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1170	CD70-24D	VH CDR1		SYAMS
1171	CD70-24D	VH CDR2		AISGSGGSTFYAESVKG
1172	CD70-24D	VH CDR3		HDYSNYPYFDY
1173	CD70-24D	VL CDR1		RASQSVRSSYLA
1174	CD70-24D	VL CDR2		GASSRAT
1175	CD70-24D	VL CDR3		QQYGDLPFT

1176	CD70- 24D_CC	VH	EVQLLESGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSS
1177	CD70- 24D_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYQCQYGDLPFTFGCGTKVEIK
1178	CD70- 24D_CC	scFv	EVQLLESGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYQCQYGDLPFTFGCGTKVEIK
1179	CD70- 24D_CC x12C	bispecific molecule	EVQLLESGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYQCQYGDLPFTFGCGTKVEIKSGGGGSEVQ LIVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYCVRHGNGFNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1180	CD70- 24D	VH	EVQLLESGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSS
1181	CD70- 24D	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYQCQYGDLPFTFGPGTKVEIK
1182	CD70- 24D	scFv	EVQLLESGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYQCQYGDLPFTFGPGTKVEIK
1183	CD70- 24Dx12C	bispecific molecule	EVQLLESGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYQCQYGDLPFTFGPGTKVEIKSGGGGSEVQ LIVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYCVRHGNGFNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1184	CD70-	VH	SYAMS

		CDR1		
1185	CD70-25D	VH CDR2		AISGSGGRTFYAESVEG
1186	CD70-25D	VH CDR3		HDYSNYPYFDY
1187	CD70-25D	VL CDR1		RASQSVRSNYLA
1188	CD70-25D	VL CDR2		GASSRAT
1189	CD70-25D	VL CDR3		QQYGDLPFT
1190	CD70-25D_CC	VH		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1191	CD70-25D_CC	VL		EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGCGTKVEIK
1192	CD70-25D_CC	scFv		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGCGTKVEIK
1193	CD70-25D_CC xl2C	bispecific molecule		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPTFTFGCGTKVEIK LVESSGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGSGTQVVTQEPSTVSPGGTFTLTCSGSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1194	CD70-25D	VH		EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS

1195	CD70- 25D	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIK
1196	CD70- 25D	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGSEIIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIK
1197	CD70- 25Dx12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGSEIIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTFTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1198	CD70- 26D	VH CDR1	SYAMS
1199	CD70- 26D	VH CDR2	AISGSGGRTFYAESVEG
1200	CD70- 26D	VH CDR3	HDYSNYPYFDY
1201	CD70- 26D	VL CDR1	RASQSVRSSYLA
1202	CD70- 26D	VL CDR2	GASSRAT
1203	CD70- 26D	VL CDR3	QQYGSSPFT
1204	CD70- 26D_CC	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1205	CD70- 26D_CC	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGSPPFTFGCGTKVEIK

1206	CD70- 26D_CC	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGSSPFTFGCGTKVEIK
1207	CD70- 26D_CC x12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGSSPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1208	CD70- 26D	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1209	CD70- 26D	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTI SRLEPEDFAVYYCQYGSSPFTFGPGTKVEIK
1210	CD70- 26D	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGSSPFTFGPGTKVEIK
1211	CD70- 26Dx12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGSSPFTFGPGTKVEIK LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1212	CD70_1- G2D	VH CDR1	SYAMS
1213	CD70_1- G2D	VH CDR2	AISGSGGSTFYAESVQG

1214		CD70_1-G2D	VH CDR3	HDYSNYPYFDY	
1215		CD70_1-G2D	VL CDR1	RASQSVRGNLYA	
1216		CD70_1-G2D	VL CDR2	GASSRAT	
1217		CD70_1-G2D	VL CDR3	QQYGYSPFT	
1218		CD70_1-G2D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGSTFYAES VQGRFTISRDNKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSS	
1219		CD70_1-G2D_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGYSPFTFGCGTKVEIK	
1220		CD70_1-G2D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGSTFYAES VQGRFTISRDNKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGYSPFTFGCGTKVEIK	
1221		CD70_1-G2D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGSTFYAES VQGRFTISRDNKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYGYSPFTFGCGTKVEIK LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTVSPGGTFTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL	
1222		CD70_1-G2D	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGSTFYAES VQGRFTISRDNKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSS	
1223		CD70_1-G2D	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYGYSPFTFGPGTKVEIK	
1224		CD70_1-G2D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGSTFYAES VQGRFTISRDNKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS	

1225	CD70_1-G2DxI2C	bispecific molecule	RATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYGYSPFTFGPGTKVEIK EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGTFFYAES VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYGYSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWSVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKLTVL
1226	CD70-27D	VH CDR1	TYAMS
1227	CD70-27D	VH CDR2	AISGSGGTFFYAESVKG
1228	CD70-27D	VH CDR3	HDYSNYPYFDY
1229	CD70-27D	VL CDR1	RASQSIRSNYLA
1230	CD70-27D	VL CDR2	GASSRAT
1231	CD70-27D	VL CDR3	QQYGSSPFT
1232	CD70-27D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKLEWVSAISGSGGTFFYAES VKGRFTISRDN SKNTLYLQMNLSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1233	CD70-27D_CC	VL	EIVLTQSPGTLSPGERATLSCRASQSIRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDTLTISRLEPEDFAVYCCQYGYSPFTFGCGTKVEIK
1234	CD70-27D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKLEWVSAISGSGGTFFYAES VKGRFTISRDN SKNTLYLQMNLSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSIRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYGYSPFTFGCGTKVEIK
1235	CD70-	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKLEWVSAISGSGGTFFYAES

		27D _{CC} x12C	c molecule	VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGSG GGSGGGGSEI VLTQSPG T LSLSPGERAT LSCRASQ SIRS NYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQYGSSPFTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGTF FNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKKAAL T LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1236		CD70- 27D	VH	EVQLLESGGGLVQPGGSLRLS CAASGTF TSTYAMSWVRQAPGKGLEWVSAISGSGGGTFYAES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSS
1237		CD70- 27D	VL	EIVLTQSPG T LSLSPGERAT LSCRASQ SIRS NYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDF TLTISRLEPEDFAVYYCQYGSSPFTFGPGTKVEIK
1238		CD70- 27D	scFv	EVQLLESGGGLVQPGGSLRLS CAASGTF TSTYAMSWVRQAPGKGLEWVSAISGSGGGTFYAES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGSG GGSGGGGSEI VLTQSPG T LSLSPGERAT LSCRASQ SIRS NYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQYGSSPFTFGPGTKVEIK
1239		CD70- 27Dx12C	bispecific c molecule	EVQLLESGGGLVQPGGSLRLS CAASGTF TSTYAMSWVRQAPGKGLEWVSAISGSGGGTFYAES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGSG GGSGGGGSEI VLTQSPG T LSLSPGERAT LSCRASQ SIRS NYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDF TLTISRLEPEDFAVYYCQYGSSPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGTF FNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKKAAL T LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1240		CD70- 28D	VH CDR1	TYAMS
1241		CD70- 28D	VH CDR2	LISGSGGRYYAESVKG
1242		CD70- 28D	VH CDR3	HDYSNYPYFDY
1243		CD70- 28D	VL CDR1	RASQSVRSNYLA

1244	CD70-28D	VL CDR2	GASNRAT
1245	CD70-28D	VL CDR3	QQYGISPPT
1246	CD70-28D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1247	CD70-28D_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASNRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGCGTKVEIK
1248	CD70-28D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGCGTKVEIK
1249	CD70-28D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNVRQAPGKLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1250	CD70-28D	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1251	CD70-28D	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASNRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGCGTKVEIK
1252	CD70-28D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGCGTKVEIK
1253	CD70-28Dx12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYSCQQYGISPPTFGCGTKVEIKSGGGSEVQ

1254	CD70-31D	VH CDR1	LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTFTLTTCGSSGTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1255	CD70-31D	VH CDR2	SYAMS AISGSGGRAQYAESVQG
1256	CD70-31D	VH CDR3	HDYSNYPYFDY
1257	CD70-31D	VL CDR1	RASQSVSSNLA
1258	CD70-31D	VL CDR2	GSSSRAT
1259	CD70-31D	VL CDR3	QQYGSSPPP
1260	CD70-31D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKCLEWVSAISGSGGRAQYAES VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1261	CD70-31D_CC	VL	EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSRATGIPDRFS GSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGCGTKVEIK
1262	CD70-31D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKCLEWVSAISGSGGRAQYAES VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGSSPPFPFGCGTKVEIK
1263	^C D70-31D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKCLEWVSAISGSGGRAQYAES VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGSSPPFPFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS

1264					GGGGGGGSGQT VVTQEP SLTVSPGGT VTLTCG SSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1265	CD70- 31D	VH			EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKGLEWVSAISGSGGRAQYAES VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1266	CD70- 31D	VL			EIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSRATGIPDRFS GSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGKVEIK
1267	CD70- 31Dx12C	scFv			EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKGLEWVSAISGSGGRAQYAES VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGKVEIK
1268	CD70- 32D	bispecific molecule			EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKGLEWVSAISGSGGRAQYAES VQGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEI VLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGQT VVTQEP SLTVSPGGT VTLTCG SSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1269	CD70- 32D	VH CDR1			SYAMS
1270	CD70- 32D	VH CDR2			AISGSGGRTFYAESVEG
1271	CD70- 32D	VH CDR3			HDYSNYPYFDY
1272	CD70- 32D	VL CDR1			RASQGVRS DYLA
1273	CD70- 32D	VL CDR2			GASSRAT
1274	CD70- 32D	VL CDR3			QQYGSTPPT

1274	CD70-32D_CC	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSS
1275	CD70-32D_CC	VL	EIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGCGTKVEIK
1276	CD70-32D_CC	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGCGTKVEIK
1277	CD70-32D_CC x12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGCGTKVEIKSGGGGSEVQ LIVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1278	CD70-32D	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSS
1279	CD70-32D	VL	EIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGCGTKVEIK
1280	CD70-32D	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGCGTKVEIK
1281	CD70-32Dx12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQQYGSTPPTFGCGTKVEIKSGGGGSEVQ LIVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1282	CD70-	VH	SYAMS

		37D	CDR1	
1283		CD70-37D	VH CDR2	AIGEGGYTYAAESVKG
1284		CD70-37D	VH CDR3	HDYSNYPYFDY
1285		CD70-37D	VL CDR1	RASQGVRRSSYFA
1286		CD70-37D	VL CDR2	GASTRAT
1287		CD70-37D	VL CDR3	QQYGSSPPT
1288		CD70-37D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWMVRQAPGKCLEWVSAIGEGGYTYAAES VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTS
1289		CD70-37D_CC	VL	EIVLTQSPGTLSPGERATLSCRASQGVRRSSYFAWYQQKPGQAPRLLIYGASTRATGIPARF SGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIK
1290		CD70-37D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWMVRQAPGKCLEWVSAIGEGGYTYAAES VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTS GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQGVRRSSYFAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIK
1291		CD70-37D_CC xl2C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWMVRQAPGKCLEWVSAIGEGGYTYAAES VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTS GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQGVRRSSYFAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIK LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWMVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTS SGGGSGGGGSGTQVVTQEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWMVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1292		CD70-37D	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWMVRQAPGKCLEWVSAIGEGGYTYAAES VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTS

1293	CD70-37D	VL	EIVLTQSPGTLSPGERATLSCRASQGVRSYFAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGGTDFTLTISRLEPEDFAVYQCQYGSSPPTFGQGTKVEIK
1294	CD70-37D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAIGEGGGYTYAAESVKGRFTISRDNKNTLSLLMNSLRAEDTAVYYCARHDYSNYPYFDYWGQGTLLTVSSGGGGSGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYFAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGGTDFTLTISRLEPEDFAVYQCQYGSSPPTFGQGTKVEIK
1295	CD70-37Dx12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAIGEGGGYTYAAESVKGRFTISRDNKNTLSLLMNSLRAEDTAVYYCARHDYSNYPYFDYWGQGTLLTVSSGGGGSGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYFAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGGTDFTLTISRLEPEDFAVYQCQYGSSPPTFGQGTKVEIKSVLVESEGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNIATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGSGGGGGGSGQTVVTQEPSLTVSPGGTFTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1296	CD70-38D	VH CDR1	SYAMS
1297	CD70-38D	VH CDR2	AISGSGGRTFYAESVEG
1298	CD70-38D	VH CDR3	HDYSNYPYFDY
1299	CD70-38D	VL CDR1	RASQSIRSNYLA
1300	CD70-38D	VL CDR2	GASSRAT
1301	CD70-38D	VL CDR3	QQYGSSPPS
1302	CD70-38D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAESVEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVSS
1303	CD70-38D_CC	VL	EIVLTQSPGTLSPGERATLSCRASQSIRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYQCQYGSSPPTFGCGTKVEIK

1304	CD70- 38D_CC	scFv	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNNYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYGSSPPSFSGGCKVEIK
1305	CD70- 38D_CC x12C	bispecific molecule	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNNYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYGSSPPSFSGGCKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1306	CD70- 38D	VH	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1307	CD70- 38D	VL	EIVLTQSPGTLSPGERATLSCRASQIRSNNYLAAYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTFTLTISRLEPEDFAVYYCQYGSSPPSFSGGCKVEIK
1308	CD70- 38D	scFv	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNNYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYGSSPPSFSGGCKVEIK
1309	CD70- 38Dx12C	bispecific molecule	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNNYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYGSSPPSFSGGCKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1310	CD70- 39D	VH CDR1	SYAMS
1311	CD70- 39D	VH CDR2	AISGSGGGTFYAESVEG

1312		CD70-39D	VH CDR3	HDYSNYPYFDY
1313		CD70-39D	VL CDR1	RASQSVRRSSYLA
1314		CD70-39D	VL CDR2	GASSRAT
1315		CD70-39D	VL CDR3	QQYGDLPFT
1316		CD70-39D_CC	VH	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGGTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGLGLTLTVSS
1317		CD70-39D_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKVEIK
1318		CD70-39D_CC	scFv	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGGTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGLGLTLTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKVEIK
1319		CD70-39D_CC x12C	bispecific molecule	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGGTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGLGLTLTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKVEIK LVESSGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTLTVSSGGG SGGGSGGGGQTVVTQEPSTVSPGGTFTLTTCGSSTGAVTSGNYPNWWQKPGQAPRGLIG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1320		CD70-39D	VH	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGGTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGLGLTLTVSS
1321		CD70-39D	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYSCQQYGDLPFTFGPGTKVEIK
1322		CD70-39D	scFv	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGGTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGLGLTLTVSSGGGSG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS

1323	CD70- 39Dx12C	bispecific molecule	RATGIPDRFSGSGGTDFTLTIISRLPEDEFAVYSCQQYGDLPFTFGPGTKVEIK EVQLLESGGGVVPGRSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGGLGLTLVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLPEDEFAVYSCQQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKCLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTLVTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTLTVL SYAMS
1324	CD70- 41D	VH CDR1	
1325	CD70- 41D	VH CDR2	AISGSGGRTFYAESVEG
1326	CD70- 41D	VH CDR3	HDYSNYPYFDY
1327	CD70- 41D	VL CDR1	RASQSVRSYLA
1328	CD70- 41D	VL CDR2	GASSRAT
1329	CD70- 41D	VL CDR3	QQYGDLPFT
1330	CD70- 41D_CC	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGLTLTVSS EIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTIISRLPEDEFAVYCCQQYGDLPFTFGCGTKVDIK
1332	CD70- 41D_CC	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGLTLVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTIISRLPEDEFAVYCCQQYGDLPFTFGCGTKVDIK
1333	CD70-	bispecific	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES

		41D _{CC} x12C	c molecule	VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1334		CD70- 41D	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLLTVSS
1335		CD70- 41D	VL	EIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGPGTKVDIK
1336		CD70- 41D	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGPGTKVDIK
1337		CD70- 41Dx12C	bispecific c molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPYFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGPGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1338		CD70- 42D	VH CDR1	TYAMS
1339		CD70- 42D	VH CDR2	LISGSGGRTYYAESVKG
1340		CD70- 42D	VH CDR3	HDYSNYPYFDY
1341		CD70- 42D	VL CDR1	RASQGVRRSSYLA

1342	CD70- 42D	VL CDR2	GASSRAT
1343	CD70- 42D	VL CDR3	QQYGSSPPT
1344	CD70- 42D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1345	CD70- 42D_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIK
1346	CD70- 42D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIK
1347	CD70- 42D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSIYSWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSGTAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1348	CD70- 42D	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1349	CD70- 42D	VL	EIVLTQSPGTLSLSPGERATLSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIK
1350	CD70- 42D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIK
1351	CD70- 42Dx12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSLSPGERATLSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIKSGGGSEVQ

1352				VH CDR1	SYAMS LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTFTLTTCGSSSTGAVTSNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1353		CD70- 43D		VH CDR2	AISGSGGRTFYAESVEG HDYSNYPYFDY
1354		CD70- 43D		VH CDR3	
1355		CD70- 43D		VL CDR1	RASQSVRSNYLA
1356		CD70- 43D		VL CDR2	GASSRAT
1357		CD70- 43D		VL CDR3	QQYGSSPPT
1358		CD70- 43D_CC		VH	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1359		CD70- 43D_CC		VL	EIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIK
1360		CD70- 43D_CC		scFv	EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGCGTKVDIKSGGGGSEVQ
1361		CD70- 43D_CC x12C		bispecific molecule	LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG

1362					SGGGSGGGGQTVVTQEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1363		CD70- 43D	VH		EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1364		CD70- 43D	VL		EIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKVDIK
1365		CD70- 43D	scFv		EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKVDIK
1366		CD70- 48D	bispecific molecule		EVQLLESGGGVVQPGRSRLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYYCQQYGSSPPTFGGGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1367		CD70- 48D	VH CDR1		SYAMS
1368		CD70- 48D	VH CDR2		VISGSGGITDFAESVKG
1369		CD70- 48D	VH CDR3		HDYSNYFFFDY
1370		CD70- 48D	VL CDR1		RASQGISNYLA
1371		CD70- 48D	VL CDR2		AASILQS
1372		CD70- 48D	VL CDR3		QQYFAYPIT

1372	CD70- 48D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSVISGSGGITDFAES VKGRFTISRDNsrntlylQmNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSS
1373	CD70- 48D_CC	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPKLLIYAASILQSGVPSKFS GSGGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGCGTRLEIK
1374	CD70- 48D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSVISGSGGITDFAES VKGRFTISRDNsrntlylQmNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPKLLIYAASIL QSGVPSKFSGSGGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGCGTRLEIK
1375	^C D70- 48D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSVISGSGGITDFAES VKGRFTISRDNsrntlylQmNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPKLLIYAASIL QSGVPSKFSGSGGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGCGTRLEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPsLTVSPGGTTLTCSGSTGAVTSNYPNWVQKPKQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1376	CD70- 48D	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSVISGSGGITDFAES VKGRFTISRDNsrntlylQmNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSS
1377	CD70- 48D	VL	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPKLLIYAASILQSGVPSKFS GSGGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGQGTREIK
1378	CD70- 48D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSVISGSGGITDFAES VKGRFTISRDNsrntlylQmNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPKLLIYAASIL QSGVPSKFSGSGGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGQGTREIK
1379	CD70- 48Dx12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSVISGSGGITDFAES VKGRFTISRDNsrntlylQmNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSGG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKVPKLLIYAASIL QSGVPSKFSGSGGTDFTLTISSLQPEDFAIYYCQQYFAYPITFGQGTREIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPsLTVSPGGTTLTCSGSTGAVTSNYPNWVQKPKQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1380	CD70-	VH	SYAMS

		53D	CDR1	
1381		CD70-53D	VH CDR2	AISGGGRTFYAESVEG
1382		CD70-53D	VH CDR3	HDYSNYPYFDY
1383		CD70-53D	VL CDR1	RASQSVRRSSYLA
1384		CD70-53D	VL CDR2	GASSRAT
1385		CD70-53D	VL CDR3	QQYGSSPPT
1386		CD70-53D_CC	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWMVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS
1387		CD70-53D_CC	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGCGTRLEIK
1388		CD70-53D_CC	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWMVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGCGTRLEIK
1389		CD70-53D_CC x12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWMVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYFCQQYGSSPPTFGCGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWMVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGSGTQVVTQEPSTVSPGGTFTLTCSGSTGAVTSGNYPNWMVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1390		CD70-53D	VH	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWMVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSS

1391	CD70-53D	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTIISRLPEDFAVYFCQQYGSSPPTFGGTRLEIK
1392	CD70-53D	scFv	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAESVEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGGGSEIIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTIISRLPEDFAVYFCQQYGSSPPTFGGTRLEIK
1393	CD70-53Dx12C	bispecific molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAESVEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGGGSEIIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTIISRLPEDFAVYFCQQYGSSPPTFGGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNIATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGSGGGSGGGGQTVVTQEPSTLTVSPGGTFTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1394	CD70-54D	VH CDR1	IYAMS
1395	CD70-54D	VH CDR2	AIGGSGGSTFYAESVKG
1396	CD70-54D	VH CDR3	HDYSNYPYFDY
1397	CD70-54D	VL CDR1	RASQSVRSSYYVA
1398	CD70-54D	VL CDR2	GASSRAT
1399	CD70-54D	VL CDR3	QQYGDLPFT
1400	CD70-54D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAIGSGGRTFYAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1401	CD70-54D_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYVAVWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTIISRLPEDFAVYYCQQYGDLPTFTFGCGTRLEIK

1402	CD70- 54D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAIGSGGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGDLPFTFGCGTRLEIK
1403	CD70- 54D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAIGSGGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGDLPFTFGCGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1404	CD70- 54D	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKLEWVSAIGSGGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSS
1405	CD70- 54D	VL	EIVLTQSPGTLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTI SRLEPEDFAVYYCQYGDLPFTFGPGTRLEIK
1406	CD70- 54D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKLEWVSAIGSGGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGDLPFTFGPGTRLEIK
1407	CD70- 54Dx12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKLEWVSAIGSGGGSTFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYVAVYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGDLPFTFGPGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL SSSYIYWG
1408	CD70- 58D	VH CDR1	
1409	CD70- 58D	VH CDR2	SIYHSGGTYFNPSLKS

1410		CD70-58D	VH CDR3	HYEILTGYYPDVFDI
1411		CD70-58D	VL CDR1	RASQSISSYLN
1412		CD70-58D	VL CDR2	AASNLSQS
1413		CD70-58D	VL CDR3	QQSFSSPRT
1414		CD70-58D_CC	VH	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARHYEILTGYYPDVFDIWGQGTMTVSS
1415		CD70-58D_CC	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASNLSQSGVSSRFS GSGGTDFTLTISSLQPEDFATYYCQQSFSSPRTFGCGTKVEIK
1416		CD70-58D_CC	scFv	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARHYEILTGYYPDVFDIWGQGTMTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIY AASNLSQSGVSSRFSGSGGTDFTLTISSLQPEDFATYYCQQSFSSPRTFGCGTKVEIK
1417		CD70-58D_CC x12C	bispecific molecule	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARHYEILTGYYPDVFDIWGQGTMTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIY AASNLSQSGVSSRFSGSGGTDFTLTISSLQPEDFATYYCQQSFSSPRTFGCGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWAYWGQGTMLTVSS GGSGGGGGGGGQTVVTEPSLTSPGGTTLTTCGSGTAVTSNYPNWWVQQKPGQAPRG LIGGTFKFLAPGTPARFSGSLGGKAALTLGVPQDEAEYYCVLWYSNRWVFGGKTLTVL
1418		CD70-58D	VH	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARHYEILTGYYPDVFDIWGQGTMTVSS
1419		CD70-58D	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASNLSQSGVSSRFS GSGGTDFTLTISSLQPEDFATYYCQQSFSSPRTFGQGTKEIK
1420		CD70-58D	scFv	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARHYEILTGYYPDVFDIWGQGTMTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIY

1421	CD70- 58Dx12C	bispecific molecule	AASNLSQSGVSSRFSGSGGTFTLTISSLQPEDFATYYCQQSFSSPRTFGGQTKVEIK QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKGLEWIGSIYHSGGTYNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYCARHYEILTGYYPDVFDIWGQGTMTVTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIY AASNLSQSGVSSRFSGSGGTFTLTISSLQPEDFATYYCQQSFSSPRTFGGQTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTLLTVSS GGSGGGGGGGGQTVVTPQEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRG LIGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGQTKLTVL SYSMN
1422	CD70- 62D	VH CDR1	
1423	CD70- 62D	VH CDR2	YISSGGYIYYAESVKG
1424	CD70- 62D	VH CDR3	GDYSNYAYFDY
1425	CD70- 62D	VL CDR1	RASQGISNYLA
1426	CD70- 62D	VL CDR2	AASTLQS
1427	CD70- 62D	VL CDR3	QQYYSTPLT
1428	CD70- 62D_CC	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYISSSGGYIYYAES VKGRFTISRDNAKNSLYLQMNLSLRAEDAAVYYCSRGDYSNYAYFDYWGQGTLLTVSS
1429	CD70- 62D_CC	VL	DIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFS GSGGTFTLTISSLQAEADVAYYCQQYYSTPLTFGCGTKVEIK
1430	CD70- 62D_CC	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYISSSGGYIYYAES VKGRFTISRDNAKNSLYLQMNLSLRAEDAAVYYCSRGDYSNYAYFDYWGQGTLLTVSSGGGGSG GGSGGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTL QSGVPSRFSGSGGTFTLTISSLQAEADVAYYCQQYYSTPLTFGCGTKVEIK
1431	CD70-	bispecific	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYISSSGGYIYYAES

		62D _{CC} x12C	c molecule	VKGRFTISRDNAKNSLYLQMNLSLRAEDAAVYCSRGDYSNYAYFDYWGQGTLLTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKPKLLIYAASTL QSGVPSRFSGSGTDFTLTISLQAEADVAVYCCQYYSTPLTFGGGKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGTLLTVSSGGGG GGSGGGGSGTQVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1432		CD70- 62D	VH	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYSISSSGGYIYYAES VKGRFTISRDNAKNSLYLQMNLSLRAEDAAVYCSRGDYSNYAYFDYWGQGTLLTVSS
1433		CD70- 62D	VL	DIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKPKLLIYAASTLQSGVPSRFS GSGGTDFTLTISLQAEADVAVYCCQYYSTPLTFGGGKVEIK
1434		CD70- 62D	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYSISSSGGYIYYAES VKGRFTISRDNAKNSLYLQMNLSLRAEDAAVYCSRGDYSNYAYFDYWGQGTLLTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKPKLLIYAASTL QSGVPSRFSGSGTDFTLTISLQAEADVAVYCCQYYSTPLTFGGGKVEIK
1435		CD70- 62Dx12C	bispecific c molecule	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYSISSSGGYIYYAES VKGRFTISRDNAKNSLYLQMNLSLRAEDAAVYCSRGDYSNYAYFDYWGQGTLLTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPGKPKLLIYAASTL QSGVPSRFSGSGTDFTLTISLQAEADVAVYCCQYYSTPLTFGGGKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGTLLTVSSGGGG GGSGGGGSGTQVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1436		CD70- 23D	VH CDR1	VYAMS
1437		CD70- 23D	VH CDR2	TISGSGGSTFYAESVKG
1438		CD70- 23D	VH CDR3	HDYSNYAYFDY
1439		CD70- 23D	VL CDR1	RASQSVRRSSYLA

1440	CD70- 23D	VL CDR2	GASSRAT
1441	CD70- 23D	VL CDR3	QQYGDLPFT
1442	CD70- 23D_CC	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSS
1443	CD70- 23D_CC	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAQYQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGCGTKVEIK
1444	CD70- 23D_CC	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAQYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGCGTKVEIK
1445	CD70- 23D_CC x12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAQYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGCGTKVEIKSGSGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNRLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSGTGAVTSGNYPNWWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1446	CD70- 23D	VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSS
1447	CD70- 23D	VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAQYQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGPGTKVEIK
1448	CD70- 23D	scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAQYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGPGTKVEIK
1449	CD70- 23Dx12C	bispecific molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVRSYLAQYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGPGTKVEIKSGSGGSEVQ

				LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1450	CD70- 55D	VH CDR1		SYGMH
1451	CD70- 55D	VH CDR2		VISYEGSNKYAESEVKG
1452	CD70- 55D	VH CDR3		GRYYGSGNHNHGMMDV
1453	CD70- 55D	VL CDR1		RASQISSYLN
1454	CD70- 55D	VL CDR2		AASSLQS
1455	CD70- 55D	VL CDR3		QQSYSTPFT
1456	CD70- 55D_CC	VH		QVQLVESGGGVVQPGRSRLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYEGSNKYAAES VKGRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARGRYYGSGNHNHGMMDVWGQGTTVTVSS
1457	CD70- 55D_CC	VL		DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFS GRSGTDFTLTISLQPEDFATYYCQQSYSTPFTFGCGTKVEIK
1458	CD70- 55D_CC	scFv		QVQLVESGGGVVQPGRSRLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYEGSNKYAAES VKGRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARGRYYGSGNHNHGMMDVWGQGTTVTVSSGG GGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQSYSTPFTFGCGTKVEIK
1459	CD70- 55D_CC x12C	bispecific molecule		QVQLVESGGGVVQPGRSRLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYEGSNKYAAES VKGRFTISRDNKNTLYLQMNLSLRAEDTAVYYCARGRYYGSGNHNHGMMDVWGQGTTVTVSSGG GGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQSYSTPFTFGCGTKVEIKSGGGGS

				EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGSGGGGGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYCYLWYSNRWVFGGGLTKLTVL
1460	CD70- 55D	VH		QVQLVESGGGVVQPGRSRLSCLASAGFMFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYAAES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARGRYGSGNHNHGMVDVWGQGTITVTVSS
1461	CD70- 55D	VL		DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLSQSGVPSRFS GRSGGDTFTLTISLQPEDFATYYCQSYSTPFTFGPGTKVEIK
1462	CD70- 55D	scFv		QVQLVESGGGVVQPGRSRLSCLASAGFMFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYAAES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARGRYGSGNHNHGMVDVWGQGTITVTVSSG GGSGGGGGGGGDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGGTDFTLTISLQPEDFATYYCQSYSTPFTFGPGTKVEIK
1463	CD70- 55Dx12C	bispecific molecule		QVQLVESGGGVVQPGRSRLSCLASAGFMFSSYGMHWVRQAPGKGLEWVAVISYEGSNKYAAES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARGRYGSGNHNHGMVDVWGQGTITVTVSSG GGSGGGGGGGGDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGGTDFTLTISLQPEDFATYYCQSYSTPFTFGPGTKVEIK EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGSGGGGGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYCYLWYSNRWVFGGGLTKLTVL
1464	CD70- 3.001	VH CDR1		SYGMH
1465	CD70- 3.001	VH CDR2		VTWYDASNKYYGDAVKG
1466	CD70- 3.001	VH CDR3		DLLRGVKGYAMDV
1467	CD70- 3.001	VL CDR1		RASQSLRRIYLA
1468	CD70- 3.001	VL		DVFDRAIT

		CDR2		
1469	CD70-3.001	VL CDR3	QQYSESPFT	
1470	CD70-3.001_C C	VH	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVTWYDASNKYYGDA VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMD VWGQGT TTVTVSS	
1471	CD70-3.001_C C	VL	EIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLA WYQQKPGQAPRLLIYDV FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSESPFTFGCGTKVDIK	
1472	CD70-3.001_C C	scFv	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVTWYDASNKYYGDA VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMD VWGQGT TTVTVSSGGGG SGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLA WYQQKPGQAPRLLIYDV FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSESPFTFGCGTKVDIK	
1473	CD70-3.001_C Cx12C	bispecific molecule	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVTWYDASNKYYGDA VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMD VWGQGT TTVTVSSGGGG SGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLA WYQQKPGQAPRLLIYDV FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSESPFTFGCGTKVDIKSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYAWYWGQGT LTVTVSSGGGGSGGGSGTQVVTQEP SLTVSPGGT VTLTCGSS TGA VTS GNYPNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYVCVLWYSNRWVFGG TKLTVL	
1474	CD70-3.001	VH	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVTWYDASNKYYGDA VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMD VWGQGT TTVTVSS	
1475	CD70-3.001	VL	EIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLA WYQQKPGQAPRLLIYDV FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSESPFTFGPGTKVDIK	
1476	CD70-3.001	scFv	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVTWYDASNKYYGDA VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMD VWGQGT TTVTVSSGGGG SGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLA WYQQKPGQAPRLLIYDV FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSESPFTFGPGTKVDIK	
1477	CD70-3.001x12 C	bispecific molecule	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAVTWYDASNKYYGDA VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMD VWGQGT TTVTVSSGGGG SGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSLRRIYLA WYQQKPGQAPRLLIYDV	

1478	CD70- 4.007	VH CDR1	FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYQCQYSESPFTFGPGTKVDIKSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGLTVTVSSGG GGGGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLI GGTKFLAPGTPARFSGSLGGKAAITLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL SYGIS
1479	CD70- 4.007	VH CDR2	WISAYQGYTHYAQLQG
1480	CD70- 4.007	VH CDR3	DYGGNDYYGMDV
1481	CD70- 4.007	VL CDR1	SGSSSNIGINYVY
1482	CD70- 4.007	VL CDR2	RSDQRPS
1483	CD70- 4.007	VL CDR3	AAFDESLGVV
1484	CD70- 4.007_C C	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWI SAYQGYTHYAQK LQGRVTMTTDTSTSTAYMELRSLRSDDTAVYICARDYGGNDY YGMDVWGQGT TTVTVSS
1485	CD70- 4.007_C C	VL	QSVLTQPPSASGTPGQRTVITSCSGSSSNIGINYVYVYQQLPGTAPKLLIYRSDQRPSPGVPDRF SGSKSGTSASLALSGLRSEDEADY YCAAFDESLGVVFGCGTKLTVL
1486	CD70- 4.007_C C	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWI SAYQGYTHYAQK LQGRVTMTTDTSTSTAYMELRSLRSDDTAVYICARDYGGNDY YGMDVWGQGT TTVTVSSGGGS GGGGGGGGGQSGLTQPPSASGTPGQRTVITSCSGSSSNIGINYVYVYQQLPGTAPKLLIYRSD QRPSPGVPDRFSGSKSGTSASLALSGLRSEDEADY YCAAFDESLGVVFGCGTKLTVL
1487	CD70- 4.007_C Cx12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWI SAYQGYTHYAQK LQGRVTMTTDTSTSTAYMELRSLRSDDTAVYICARDYGGNDY YGMDVWGQGT TTVTVSSGGGS GGGGGGGGGQSGLTQPPSASGTPGQRTVITSCSGSSSNIGINYVYVYQQLPGTAPKLLIYRSD

				QRPSPVDRFSGSKSGTSASLALSGLRSEDEADYYCAAFDESLSGVVFSGGTKLTVLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNYSI SYWAYWGQGLTVTVSSG GGSGGGGGGGGQTVVTQEPSTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGL IGGTFKFLAPGTPARFSGSLLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1488	CD70- 4.007	VH		QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWISAYQGYTHYAQK LQGRVTMTTDTSTSTAYMELSLRSDDTAVYCCARDYGGNDYGMVDVWGQGTVTVTSS
1489	CD70- 4.007	VL		QSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVYVYQQLPGTAPKLLIYRSDQRPSPGVPDRF SGSKSGTSASLALSGLRSEDEADYYCAAFDESLSGVVFSGGTKLTVL
1490	CD70- 4.007	scFv		QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWISAYQGYTHYAQK LQGRVTMTTDTSTSTAYMELSLRSDDTAVYCCARDYGGNDYGMVDVWGQGTVTVTSSGGGGS GGSGGGGGGQSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVYVYQQLPGTAPKLLIYRSD QRPSPVDRFSGSKSGTSASLALSGLRSEDEADYYCAAFDESLSGVVFSGGTKLTVL
1491	CD70- 4.007x12 C	bispecific molecule		QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWMGWISAYQGYTHYAQK LQGRVTMTTDTSTSTAYMELSLRSDDTAVYCCARDYGGNDYGMVDVWGQGTVTVTSSGGGGS GGSGGGGGGQSVLTQPPSASGTPGQQRVTISCSGSSSNIGINIVYVYQQLPGTAPKLLIYRSD QRPSPVDRFSGSKSGTSASLALSGLRSEDEADYYCAAFDESLSGVVFSGGTKLTVLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNYSI SYWAYWGQGLTVTVSSG GGSGGGGGGGGQTVVTQEPSTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQKPGQAPRGL IGGTFKFLAPGTPARFSGSLLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1492	CD70- 12.013	VH CDR1		YYGMH
1493	CD70- 12.013	VH CDR2		VIWYDASNKYYADAVKG
1494	CD70- 12.013	VH CDR3		DREMGSRGDFDY
1495	CD70- 12.013	VL CDR1		RASQGINNYIA
1496	CD70- 12.013	VL		AVSILQS

		CDR2	
1497	CD70- 12.013	VL CDR3	QQYNFYFVS
1498	CD70- 12.013_ CC	VH	QAQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKCLEWVAVIWDASNKYYADA VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDREMGSRGDFDYWGQGLT LVTVSS
1499	CD70- 12.013_ CC	VL	DIQMTQSPSSLSASVGD RVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSILQSGVPSKFS GSGGTDFTLTISNLQPEDFATYQCQQYNFYFVSFGCGTKVDIK
1500	CD70- 12.013_ CC	scFv	QAQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKCLEWVAVIWDASNKYYADA VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDREMGSRGDFDYWGQGLT LVTVSSGGGGS GGGSGGGGSDIQMTQSPSSLSASVGD RVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSI LQSGVPSKFSGSGGTDFTLTISNLQPEDFATYQCQQYNFYFVSFGCGTKVDIK
1501	^C D70- 12.013 CCx12C	bispecific molecule	QAQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKCLEWVAVIWDASNKYYADA VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDREMGSRGDFDYWGQGLT LVTVSSGGGGS GGGSGGGGSDIQMTQSPSSLSASVGD RVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSI LQSGVPSKFSGSGGTDFTLTISNLQPEDFATYQCQQYNFYFVSFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN LKTEDTAVYYCVRHGNFNSYISYWAYWGQGLT LVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGTVTLTCGSSGTAVTSNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1502	CD70- 12.013	VH	QAQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKLEWVAVIWDASNKYYADA VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDREMGSRGDFDYWGQGLT LVTVSS
1503	CD70- 12.013	VL	DIQMTQSPSSLSASVGD RVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSILQSGVPSKFS GSGGTDFTLTISNLQPEDFATYQCQQYNFYFVSFGCGTKVDIK
1504	CD70- 12.013	scFv	QAQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKLEWVAVIWDASNKYYADA VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDREMGSRGDFDYWGQGLT LVTVSSGGGGS GGGSGGGGSDIQMTQSPSSLSASVGD RVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSI LQSGVPSKFSGSGGTDFTLTISNLQPEDFATYQCQQYNFYFVSFGCGTKVDIK
1505	CD70- 12.013x1 2C	bispecific molecule	QAQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKLEWVAVIWDASNKYYADA VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDREMGSRGDFDYWGQGLT LVTVSSGGGGS GGGSGGGGSDIQMTQSPSSLSASVGD RVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSI

1506	CD70- 75.002.0 08	VH CDR1	LQGVPSKFGSGGTDFTLTISNLQPEDFATYYCQQYNFYFFSGQGKVDIKSGGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GFYWS
1507	CD70- 75.002.0 08	VH CDR2	EIYHSGHATNNPSLKS
1508	CD70- 75.002.0 08	VH CDR3	GGNSGYIFDY
1509	CD70- 75.002.0 08	VL CDR1	RTSQYIGRYLN
1510	CD70- 75.002.0 08	VL CDR2	GASTLQQ
1511	CD70- 75.002.0 08	VL CDR3	QQTYSTPRT
1512	CD70- 75.002.0 08 CC	VH	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGFYWSWIRQPPGKCLEWIGEIIYHSGHATNNPSL KSRVTISLDTSKNQFSLKLSVTAADTAVYYCARGGNSGYIFDYWGQGLTVTVSS
1513	CD70- 75.002.0 08 CC	VL	DVQMTQSPSSLSASVGDRTVITTCRTSQYIGRYLNWYQQKPKAPKVLIIYGASTLQQGVPSRFS GSGGTDFTLTITSLQPEDFASYCQQTYSTPRTFGCGTKVEIK
1514	CD70- 75.002.0 08 CC	scFv	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGFYWSWIRQPPGKCLEWIGEIIYHSGHATNNPSL KSRVTISLDTSKNQFSLKLSVTAADTAVYYCARGGNSGYIFDYWGQGLTVTVSSGGGGGGG SGGGGSDVQMTQSPSSLSASVGDRTVITTCRTSQYIGRYLNWYQQKPKAPKVLIIYGASTLQQ GVPSRFSGSGGTDFTLTITSLQPEDFASYCQQTYSTPRTFGCGTKVEIK

1515	CD70- 75.002.0 08_CcXI 2C	bispecific molecule	QVQLQQWAGALLKPSETLSLTCAVYGGSFSGFYWSWIRQPPGKCLEWIGEIIYHSGHATNNPSL KSRVTISLDTSKNQFSLKLNSTAAADTAAYYCARGGNSGYIFDYWGQGTLLTVSSGGGGGGG GSGGGSDVQMTQSPSSLSASVGDRTITCRTSQYIGRYLNWYQQKPKAPKVLIIYGASTLQQ GVPSRFSGSGGTDFTLTITSLQPEDFASYCQQTYSTPRTFGGKVEIKSGGGGSEVQLVE SGGLVQPGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGTLLTVSSGGGGGG GSGGGGSGTQVVTQEPSTVSPGGTTLTLCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFK LAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGKTLTVL
1516	CD70- 75.002.0 08	VH	QVQLQQWAGALLKPSETLSLTCAVYGGSFSGFYWSWIRQPPGKLEWIGEIIYHSGHATNNPSL KSRVTISLDTSKNQFSLKLNSTAAADTAAYYCARGGNSGYIFDYWGQGTLLTVSS
1517	CD70- 75.002.0 08	VL	DVQMTQSPSSLSASVGDRTITCRTSQYIGRYLNWYQQKPKAPKVLIIYGASTLQQGVPSRFS GSGGTDFTLTITSLQPEDFASYCQQTYSTPRTFGGKVEIK
1518	CD70- 75.002.0 08	scFv	QVQLQQWAGALLKPSETLSLTCAVYGGSFSGFYWSWIRQPPGKLEWIGEIIYHSGHATNNPSL KSRVTISLDTSKNQFSLKLNSTAAADTAAYYCARGGNSGYIFDYWGQGTLLTVSSGGGGGGG GSGGGSDVQMTQSPSSLSASVGDRTITCRTSQYIGRYLNWYQQKPKAPKVLIIYGASTLQQ GVPSRFSGSGGTDFTLTITSLQPEDFASYCQQTYSTPRTFGGKVEIK
1519	CD70- 75.002.0 08xI2C	bispecific molecule	QVQLQQWAGALLKPSETLSLTCAVYGGSFSGFYWSWIRQPPGKLEWIGEIIYHSGHATNNPSL KSRVTISLDTSKNQFSLKLNSTAAADTAAYYCARGGNSGYIFDYWGQGTLLTVSSGGGGGGG GSGGGSDVQMTQSPSSLSASVGDRTITCRTSQYIGRYLNWYQQKPKAPKVLIIYGASTLQQ GVPSRFSGSGGTDFTLTITSLQPEDFASYCQQTYSTPRTFGGKVEIKSGGGGSEVQLVE SGGLVQPGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGTLLTVSSGGGGGG GSGGGGSGTQVVTQEPSTVSPGGTTLTLCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFK LAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGKTLTVL
1520	CD70- 1.005	VH CDR1	TYGMH
1521	CD70- 1.005	VH CDR2	VIWYEGSNKYGESVKG
1522	CD70- 1.005	VH CDR3	DNSHYYYGMDV

1523	CD70- 1.005	VL CDR1	TGSSSNIGAGYDVN
1524	CD70- 1.005	VL CDR2	VNNNRPS
1525	CD70- 1.005	VL CDR3	QSYDTSLSASV
1526	CD70- 1.005_C	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFTSTYGMHWVRQAPGKCLEWVAWIWEGSNKYYGES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDNSHYYYGMDVWGQGT TTVTVSS
1527	CD70- 1.005_C	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNNNRPSGVPDR FSGSTSGTSASLAI TGLQAEDEADYYCQSYDTSLSASVFGCGTRLTVL
1528	CD70- 1.005_C	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFTSTYGMHWVRQAPGKCLEWVAWIWEGSNKYYGES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDNSHYYYGMDVWGQGT TTVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSGTSASLAI TGLQAEDEADYYCQSYDTSLSASVFGCGTRLTVL
1529	CD70- 1.005_C Cx12C	bispecific molecule	QVQLVESGGGVVQPGRSLRLSCAASGFTFTSTYGMHWVRQAPGKCLEWVAWIWEGSNKYYGES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDNSHYYYGMDVWGQGT TTVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSGTSASLAI TGLQAEDEADYYCQSYDTSLSASVFGCGTRLTVLSSGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGFGNSYISYWAYWGQGT LTVTVSSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN IGGTFKFLAPGTPARFSGSLGKKAAL TSGVQPEDEAEYCYLVWYSNRWVFGGKTLTVL
1530	CD70- 1.005	VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFTSTYGMHWVRQAPGKCLEWVAWIWEGSNKYYGES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDNSHYYYGMDVWGQGT TTVTVSS
1531	CD70- 1.005	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNNNRPSGVPDR FSGTSGTSASLAI TGLQAEDEADYYCQSYDTSLSASVFGGTRLTVL
1532	CD70- 1.005	scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFTSTYGMHWVRQAPGKLEWVAWIWEGSNKYYGES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDNSHYYYGMDVWGQGT TTVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN

1533	CD70- 1.005x12 C	bispecific molecule	NRPSGVPDRFSGSTSGTSASLAITGLQAEDEADYYCQSYDTLSASVFGGGTRLTVL QVQLVESGGGVVQPGRSLRLSCLASAGFTFTSYGMHWVRQAPGKLEWVAVIWIWEGSNKYYGES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDNSHYIYGMDVWGQGTITVTVSSGGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFGTAPKLLIYVNN NRPSGVPDRFSGSTSGTSASLAITGLQAEDEADYYCQSYDTLSASVFGGGTRLTVLSGGGGS EVQLVESGGGLVQPGGSLKLSCLASAGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLSRAEDTAVYYCVRHGNGFNYSYISWAYWGQGTITVTVSSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFGTAPKLLIYVNN IGGTFKFLAPGTPARFSGSLGKAAALTLGSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL
1534	CD70- 1.009	VH CDR1	TYGMH
1535	CD70- 1.009	VH CDR2	VIWYEGSNKYYGESVKG
1536	CD70- 1.009	VH CDR3	DNSHYIYGMDV
1537	CD70- 1.009	VL CDR1	TGSSSNIGAGYDVN
1538	CD70- 1.009	VL CDR2	VNNRPS
1539	CD70- 1.009	VL CDR3	QSYETSLASV
1540	CD70- 1.009_C C	VH	QVQLVESGGGVVQPGRSLRLSCLASAGFTFTSYGMHWVRQAPGKLEWVAVIWIWEGSNKYYGES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDNSHYIYGMDVWGQGTITVTVSS
1541	CD70- 1.009_C C	VL	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFGTAPKLLIYVNNRPSGVPDR FSGKSGTSASLAITGLQAEDEADYYCQSYETSLASVFGGGTRLTVL
1542	CD70- 1.009_C C	scFv	QVQLVESGGGVVQPGRSLRLSCLASAGFTFTSYGMHWVRQAPGKLEWVAVIWIWEGSNKYYGES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDNSHYIYGMDVWGQGTITVTVSSGGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVNWYQQFGTAPKLLIYVNN

1543	CD70- 1.009_C Cx12C	bispecific molecule	NRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYETSLSASFVGGGTRLTVL QVQLVESGGGVVQPGRSRLRLSCAASGFTFTSTYGMHWVRQAPGKCLEWVAVIWEYSNKKYYGES VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCARDNSHYHYGMDVWGQGLTVTVSSGGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYDVNWYQQLPGTAPKLLIYVNN NRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYETSLSASFVGGGTRLTVLSSGGGS EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLSRAEDTAVYYCVRHGNGFNYSYISWAYWGQGLTVTVSSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYDVNWYQQLPGTAPKLLIYVNN IGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCYLWYSNRWVFGGGLTTLVL
1544	CD70- 1.009	VH	QVQLVESGGGVVQPGRSRLRLSCAASGFTFTSTYGMHWVRQAPGKCLEWVAVIWEYSNKKYYGES VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCARDNSHYHYGMDVWGQGLTVTVSS
1545	CD70- 1.009	VL	QSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYDVNWYQQLPGTAPKLLIYVNNNRPSGVPDR FSGSKSGTSASLAITGLQAEDEADYYCQSYETSLSASFVGGGTRLTVL
1546	CD70- 1.009	scFv	QVQLVESGGGVVQPGRSRLRLSCAASGFTFTSTYGMHWVRQAPGKCLEWVAVIWEYSNKKYYGES VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCARDNSHYHYGMDVWGQGLTVTVSSGGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYDVNWYQQLPGTAPKLLIYVNN NRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYETSLSASFVGGGTRLTVL
1547	CD70- 1.009x12 C	bispecific molecule	QVQLVESGGGVVQPGRSRLRLSCAASGFTFTSTYGMHWVRQAPGKCLEWVAVIWEYSNKKYYGES VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCARDNSHYHYGMDVWGQGLTVTVSSGGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYDVNWYQQLPGTAPKLLIYVNN NRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYETSLSASFVGGGTRLTVL EVQLVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLSRAEDTAVYYCVRHGNGFNYSYISWAYWGQGLTVTVSSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYDVNWYQQLPGTAPKLLIYVNN IGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCYLWYSNRWVFGGGLTTLVL
1548	CD70- 76.008	VH CDR1	SGVYYWS
1549	CD70- 76.008	VH CDR2	YIYSGSTSYNPSLKS
1550	CD70- 76.008	VH CDR3	SGYSYALFDY

1551	CD70- 76.008	VL CDR1	RASQSVDRYFN
1552	CD70- 76.008	VL CDR2	AASSLQS
1553	CD70- 76.008	VL CDR3	QQSYSTPWT
1554	CD70- 76.008_ CC	VH	QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYYWSWIRQPPGKCLEWIGIYIYSGSTSYP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGLTVTVSS
1555	CD70- 76.008_ CC	VL	DIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQQKPKGKAPKVLIFAASSLQSGVPSRFS GSGSGTDFTLTISSLPEDFATYYCQQSYSTPWTFGCGTKVEVK
1556	CD70- 76.008_ CC	scFv	QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYYWSWIRQPPGKCLEWIGIYIYSGSTSYP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQQKPKGKAPKVLIFAASSL QSGVPSRFSGSGGTDFTLTISSLPEDFATYYCQQSYSTPWTFGCGTKVEVK
1557	CD70- 76.008_ CCxI2C	bispecific molecule	QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYYWSWIRQPPGKCLEWIGIYIYSGSTSYP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQQKPKGKAPKVLIFAASSL QSGVPSRFSGSGGTDFTLTISSLPEDFATYYCQQSYSTPWTFGCGTKVEVKSGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQQKPKGKAPKVLIFAASSL KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVL
1558	CD70- 76.008	VH	QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYYWSWIRQPPGKCLEWIGIYIYSGSTSYP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGLTVTVSS
1559	CD70- 76.008	VL	DIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQQKPKGKAPKVLIFAASSLQSGVPSRFS GSGSGTDFTLTISSLPEDFATYYCQQSYSTPWTFGCGTKVEVK
1560	CD70- 76.008	scFv	QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYYWSWIRQPPGKCLEWIGIYIYSGSTSYP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQQKPKGKAPKVLIFAASSL

1561	CD70- 76.008xI 2C	bispecific molecule	QSGVPSRFSGSGTDFTLTISSLPEDFATYYCQQSYSTPWTFGQGTKVEVK QMLQESGPGLVKPSQTLSTCTVSGGSIESGVYYSWIRQPPGKGLEWIGYIYSGSTSYNP SLKSRILTMSVDTSKNQFSLKLSSTAAADTAVYCARSGYSYALFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASLGDRTITCRASQSDRYFNWYQQKPGKAPKVLIFAASSL QSGVPSRFSGSGTDFTLTISSLPEDFATYYCQQSYSTPWTFGQGTKVEVKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWNVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPSTVSPGGTTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1562	CD70- 5.008	VH CDR1	SGGYYS
1563	CD70- 5.008	VH CDR2	YIFYSGSTDYNPSLKS
1564	CD70- 5.008	VH CDR3	SGYSYALFDA
1565	CD70- 5.008	VL CDR1	RASQFIGRYFN
1566	CD70- 5.008	VL CDR2	AESSLQS
1567	CD70- 5.008	VL CDR3	QQSYSTPWT
1568	CD70- 5.008_C C	VH	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSSTAAADTAVYCARSGYSYALFDAGWGQGLTVTVSS
1569	CD70- 5.008_C C	VL	DIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQKPGKAPKVLIIYAESSLQSGVPSRFS GSGGTEFTLTISLPEDFATYYCQQSYSTPWTFGCGTKVEIK
1570	CD70- 5.008_C C	scFv	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSSTAAADTAVYCARSGYSYALFDAGWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRVTISCRASQFIGRYFNWYQQKPGKAPKVLIIYAESSL

1571	CD70- 5.008_C Cx12C	bispecific molecule	QSGVPSRFSGSGTEFTLTIISSLOPEDFATYYCQQSYSTPWTFGCGTKVEIK QVQLQESGPGLVKPSQTLSTCTVSGDSIIISGGYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLASVGDRTVTSRASCQFGRYFNWYQKPKAPKVLIIYAESSL QSGVPSRFSGSGTEFTLTIISSLOPEDFATYYCQQSYSTPWTFGCGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL QVQLQESGPGLVKPSQTLSTCTVSGDSIIISGGYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGWGQGLTVTVSS DIQMTQSPSSLASVGDRTVTSRASCQFGRYFNWYQKPKAPKVLIIYAESSLQSGVPSRFS GSGGTEFTLTIISSLOPEDFATYYCQQSYSTPWTFGQGTKVEIK QVQLQESGPGLVKPSQTLSTCTVSGDSIIISGGYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLASVGDRTVTSRASCQFGRYFNWYQKPKAPKVLIIYAESSL QSGVPSRFSGSGTEFTLTIISSLOPEDFATYYCQQSYSTPWTFGQGTKVEIK QVQLQESGPGLVKPSQTLSTCTVSGDSIIISGGYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLASVGDRTVTSRASCQFGRYFNWYQKPKAPKVLIIYAESSL QSGVPSRFSGSGTEFTLTIISSLOPEDFATYYCQQSYSTPWTFGQGTKVEIK VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1572	CD70- 5.008	VH	QVQLQESGPGLVKPSQTLSTCTVSGDSIIISGGYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGWGQGLTVTVSS
1573	CD70- 5.008	VL	DIQMTQSPSSLASVGDRTVTSRASCQFGRYFNWYQKPKAPKVLIIYAESSLQSGVPSRFS GSGGTEFTLTIISSLOPEDFATYYCQQSYSTPWTFGQGTKVEIK
1574	CD70- 5.008	scFv	QVQLQESGPGLVKPSQTLSTCTVSGDSIIISGGYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLASVGDRTVTSRASCQFGRYFNWYQKPKAPKVLIIYAESSL QSGVPSRFSGSGTEFTLTIISSLOPEDFATYYCQQSYSTPWTFGQGTKVEIK QVQLQESGPGLVKPSQTLSTCTVSGDSIIISGGYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLASVGDRTVTSRASCQFGRYFNWYQKPKAPKVLIIYAESSL QSGVPSRFSGSGTEFTLTIISSLOPEDFATYYCQQSYSTPWTFGQGTKVEIK VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1575	CD70- 5.008x12 C	bispecific molecule	QVQLQESGPGLVKPSQTLSTCTVSGDSIIISGGYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLASVGDRTVTSRASCQFGRYFNWYQKPKAPKVLIIYAESSL QSGVPSRFSGSGTEFTLTIISSLOPEDFATYYCQQSYSTPWTFGQGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1576	CD70- 13x12C- scFc	bispecific HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSISGSGGRPNYADS VKGRFTISRDNKNTLYLQMNSLRDEDTAVYYCAKVDYSNYLFFFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGEGATLSRAGQSVRSYLGWYQKPKAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGYSPPTFGGQTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGGS SGGGSGGGGSGTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT

1577	CD70- 13_CcXl2 C-scFc	bispecific c HLE molecule	<p>TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKCLEWVSIVISGSGGRPNYADS VKGRFTISRDN SKNTLYLQMNLSRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGEGATLSCRAGQSVRRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGYSPPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK</p>
1578	CD70- 14x12C- scFc	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLKLSCAASGFTTFSSYAMSWVRQAPGKLEWVSIVISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPTFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p>

[illegible]

[illegible]

1583	CD70-16_Cc x12 C-scFc	bispecific HLE molecule	GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGKEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADSV EGRFTISRDN SKNTLYIQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGT LVTVSSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQISRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPTFTGCGTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGT LVTVSSGGGGSGGGSGGSQT VVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGKGSDKTHTCP CPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK
1584	CD70-17 x12C-scFc	bispecific HLE molecule	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTHYADSVKGRFTISRDN SKNTLYIQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGT LVTVSSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGS SPTTFGPGTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGT LVTVSSGGGGSGGGSGGSQT VVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK

1585	CD70- 17_CcX12 C-scFc	bispecific c HLE molecule	YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQSGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYCCQYGSSPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKTLVLGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1586	CD70- 18x12C- scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSRSTYLAHYQQKPGQAPRLLIYDASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYCCQYGSSPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKTLVLGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1587	CD70-	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSISGSGGRTHYADS

	18_CCx12 C-scFc	c HLE molecule	VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPG T LSLSPGERAT LSCRASQSVRSTYLA WYQKPGQAPRLLIYDASS RATGIPDRFSGSGGTDF TLTISRLEPEDFAVYFCQYGSSPPTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAA SGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGG SGGGSGGGSQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVFGG TKLTVLGGGDK TKFLAPGTPARFSGSL LGKAA LTL SGVQPEDEAEY YCVLWYSNRWVFGG TKLTVLGGGDK THTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1588	CD70- 19x12C- scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKGLEWVS AISGGSGSTFYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPG T LSLSPGERAT LSCRASQSVRSTYLA WYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDF TLTISRLEPEDFAVYFCQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAA SGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGG SGGGSGGGSQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVFGG TKLTVLGGGDK TKFLAPGTPARFSGSL LGKAA LTL SGVQPEDEAEY YCVLWYSNRWVFGG TKLTVLGGGDK THTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1589	CD70- 19_CCx12 C-scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKCLEWVS AISGGSGSTFYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPG T LSLSPGERAT LSCRASQSVRSTYLA WYQKPGQAPRLLIYGASS

1590	CD70- 21x2C- scFc	bispecific c HLE molecule	<p>RATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTSCSSTGAVTSGNPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKLEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTSCSSTGAVTSGNPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1591	CD70- 21_CCx12 C-scFc	bispecific c HLE molecule	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV</p>

1592	CD70- 22x12C- scFc	bispecific c HLE molecule	KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGYTYIYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGDLPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGYTYIYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGDLPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG
1593	CD70- 22_Cc12 C-scFc	bispecific c HLE molecule	KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGYTYIYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGDLPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG

1594	CD70- 24x12C- scFc	bispecific c HLE molecule	<p>TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLAQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSATISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYFCAKHDYSNYPFDYWGQGTITVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYQCQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYCVRHGNGFNSYISYWAYWGQGTITVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK</p>
1595	CD70- 24_CCx12 C-scFc	bispecific c HLE molecule	<p>EVQLLESGGGLAQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKCLEWVSATISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYFCAKHDYSNYPFDYWGQGTITVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYQCQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYCVRHGNGFNSYISYWAYWGQGTITVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p>

1596	CD70-25x12C-scFc	bispecific HLE molecule	NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYVDSKRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1597	CD70-25_CCx12C-scFc	bispecific HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTFYADSV

[illegible]

1600	CD70_1- G2x12C- scFc	bispecific c HLE molecule	<p>GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADSVQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNPYFDYWGQGTLLTVSSGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGSPFTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLLTVSSGGGSGGGSGGGSGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>
1601	CD70_1- G2_CCx1 2C-scFc	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGSTFYADSVQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNPYFDYWGQGTLLTVSSGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGSPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLLTVSSGGGSGGGSGGGSGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>

1602	CD70- 27x12C- scFc	bispecific c HLE molecule	<p>YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGGTFTYADS</p> <p>VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG</p> <p>GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNIYAWYQQKPGQAPRLLIYGASS</p> <p>RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKVEIKSGGGGSEVQ</p> <p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV</p> <p>KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG</p> <p>SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG</p> <p>TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKTLTVLGGGDK</p> <p>THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p> <p>NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV</p> <p>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLT</p> <p>VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG</p> <p>GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD</p> <p>GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ</p> <p>REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFL</p> <p>YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1603	CD70- 27_CCx12 C-scFc	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGGTFTYADS</p> <p>VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG</p> <p>GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNIYAWYQQKPGQAPRLLIYGASS</p> <p>RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGSSPFTFGCGTKVEIKSGGGGSEVQ</p> <p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV</p> <p>KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG</p> <p>SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG</p> <p>TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKTLTVLGGGDK</p> <p>THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p> <p>NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV</p> <p>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLT</p> <p>VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG</p> <p>GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD</p> <p>GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ</p> <p>REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFL</p> <p>YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1604	CD70-	bispecific	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGGTFTYADS</p>

1605	CD70-28_CCx12 C-scFc	c HLE molecule	VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDY SNYPFDYWGQGLVTVTSSGGGGSGGGGGSEIVLTQSPG TLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYSCQQYGISPTFGGGTKVEIKSGGGSEVQ LVESSGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLVTVTSSGGGG SGGGGGGGSQT VVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPEEYQGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
1606	CD70-31x12C-scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTTSTYAMSWVRQAPGKCLEWVSLISGSGGRITYYADS VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDY SNYPFDYWGQGLVTVTSSGGGGSGGGGGSEIVLTQSPG TLSLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYSCQQYGISPTFGGGTKVEIKSGGGSEVQ LVESSGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLVTVTSSGGGG SGGGGGGGSQT VVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPEEYQGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFIPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK

1607	CD70- 31_CCxI2 C-scFc	bispecific c HLE molecule	<p>ATGIPDRFSGSGTDFTLTISRLEPEDFAVYCYCQYQSSPPFPFGGKTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCYVRHGFNGSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGKTKLTVLGGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPSSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKCLEWVSATSGSGGRAQYADS VQGRFTVSRDNSKNTLYLQMNLSRAEDTAVYCYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGGGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQKPKGQAPRLLIYGSSSR ATGIPDRFSGSGTDFTLTISRLEPEDFAVYCYCQYQSSPPFPFGGKTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCYVRHGFNGSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGKTKLTVLGGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPSSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1608	CD70- 32xI2C- scFc	bispecific c HLE molecule	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSATSGSGRFTFYADS VEGRFTISRDNKNTLYLQMNLSRAEDTAVYCYCTKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYHCQYQYGSTPTFTFGGKTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV</p>

1609	CD70- 32_CcX12 C-scFc	bispecific c HLE molecule	<p>KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGG GGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCTKHDYSNYPYFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQVRSYDLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYHCQQYGSTPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGG GGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1610	CD70- 37x12C- scFc	bispecific c HLE molecule	<p>EVQLLESGGGIVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAIGDGGGYTYIYADS VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPYFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQVRSYFAWYQKPGQAPRLLIYGAST RATGIPARFSGSGGTFTLTISRLEPEDFAVYHCQQYGSTPTFGQGTKEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG</p>

1611	CD70- 37_CcXl2 C-scFc	bispecific c HLE molecule	<p>TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKCLEWVSATIGDGGGYTYIYADS VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGTLLTVSSGGGGSG GGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRRSSYFAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPPTFGCGTKVEIKSGGGGSEVQ LIVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGGGGGSQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPGK</p>
1612	CD70- 38xI2C- scFc	bispecific c HLE molecule	<p>EVQLLESGGGVVPGRSLRLSCAASGFTTFSSYAMSWVRQAPGKLEWVSATISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGGGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPSPFGQGTKEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGGGGGSQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVVDGVEVH</p>

1613	CD70-38_CCx12C-scFc	bispecific HLE molecule	NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1614	CD70-39x12C-scFc	bispecific HLE molecule	EVQLLESGGGVVQPGSRSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTFYADSV

[illegible]

1617	CD70-41_CcX12C-scFc	bispecific HLE molecule	GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKEVQLLESGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSIAISGSGGRRTFYADSV EGRFTISRDN SKNTLYIQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGLTVTVSSGGGGSGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPTFTGCGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGGGGGQTVVTOEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK
1618	CD70-42x12C-scFc	bispecific HLE molecule	EVQLLESGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSLSISGSGGRRTYYADSVKGRFTISRDN SKNTLYIQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTINRLEPEDFAVYYCQYGSPPFTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGGGGGQTVVTOEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKEVQLLESGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSLSISGSGGRRTYYADSVKGRFTISRDN SKNTLYIQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTINRLEPEDFAVYYCQYGSPPFTFGGGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGGSGGGGGGGGQTVVTOEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK

1619	CD70- 42_CcX12 C-scFc	bispecific c HLE molecule	YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQVRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTINRLEPEDFAVYYCQQYGSSPTFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTFTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKTLVLGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1620	CD70- 43x12C- scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQVRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTINRLEPEDFAVYYCQQYGSSPTFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTFTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKTLVLGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1621	CD70-	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKLEWVSAISGSGGRTFYADS

	43_CCx12 C-scFc	c HLE molecule	VEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEIVLTQSPG TSLSPGERATLS CRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYCCQYGSSPPTFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGSLKLS CAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLTTCGSS TGAVTSGNYPNWVFGG TKT LTVLGGGDK TKFLAPGTPARFSGLLGGKAAL T LSGVQPEDEAEYYCVLWYSNRWVFGG TKT LTVLGGGDK THTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1622	CD70- 48x12C- scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSYAMSWVRQAPGKLEWVSISDSGGITDFADS VKGRFTISRDN SRNTLYLQMN SLRAEDTAVYFCARHDYSNYFFFDYWGQGT LVTVSSGGGGSG GGSGGGGSDIQMTQSPSSL SASVGDRTITCRASQGISNYLAWYQQKPKVPKLLIYAASIL QSGVPSKFSGSGGTDFTLTISLQPEDFAIYCCQYFAYPI TFGQGRLEIKSGGGSEVQL VESGGGLVQPGGSLKLS CAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGGS GGSGGGGSGQTVVTQEP SLTVSPGGT VTLTTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGLLGGKAAL T LSGVQPEDEAEYYCVLWYSNRWVFGG TKT LTVLGGGDKT HTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1623	CD70- 48_CCx12 C-scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSYAMSWVRQAPGKLEWVSISDSGGITDFADS VKGRFTISRDN SRNTLYLQMN SLRAEDTAVYFCARHDYSNYFFFDYWGQGT LVTVSSGGGGSG GGSGGGGSDIQMTQSPSSL SASVGDRTITCRASQGISNYLAWYQQKPKVPKLLIYAASIL

1624	CD70- 53x12C- scFc	bispecific c HLE molecule	QSGVPSKFSGSGSGTDFTLTISSSQPEDFAIYYCQQYFAYPITFGCGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCVLWYSNRWVFGGGLTVLGGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLPSSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVFCQYGGSSPTFGGGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCVLWYSNRWVFGGGLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY YKLTITVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVFCQYGGSSPTFGCGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV
1625	CD70- 53_Cc12 C-scFc	bispecific c HLE molecule	QSGVPSKFSGSGSGTDFTLTISSSQPEDFAIYYCQQYFAYPITFGCGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCVLWYSNRWVFGGGLTVLGGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLPSSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVFCQYGGSSPTFGCGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV

1626	CD70-54x12C-scFc	bispecific HLE molecule	KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGFGNSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGSQTVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
1627	CD70-54_CcX12C-scFc	bispecific HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAIGDSGGSTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYVAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGPTRLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGFGNSYISYWAYWGQGTTLTVSSGGGGSGGGSGGGSQTVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK

1628	CD70- 58x12C- scFc	bispecific c HLE molecule	TKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
1629	CD70- 58_CCx12 C-scFc	bispecific c HLE molecule	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWI RQPPGKGLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTA VYCARHYEILTGYYPDFDIWGQGTMTVTVSSG GGSGGGSGGGSDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPKAPKLLIY AASNLSQSGVSSRFSGSGGTDFTLTISSLQPEDFATYYCQQSFSSPRTFGQGTKEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNILKTEDTA VYCVRHGNGFSYISYWAYWGQGTMTVTVSS GGSGGGSGGGGQT VVTQEP SLTVSPGGT VTLTCSGSTGAVTSGNYPNWVQQKPGQAPRG LIGGTFKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGG GGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGG GGSGGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG SFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
1629	CD70- 58_CCx12 C-scFc	bispecific c HLE molecule	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWI RQPPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTA VYCARHYEILTGYYPDFDIWGQGTMTVTVSSG GGSGGGSGGGSDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPKAPKLLIY AASNLSQSGVSSRFSGSGGTDFTLTISSLQPEDFATYYCQQSFSSPRTFGQGTKEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNILKTEDTA VYCVRHGNGFSYISYWAYWGQGTMTVTVSS GGSGGGSGGGGQT VVTQEP SLTVSPGGT VTLTCSGSTGAVTSGNYPNWVQQKPGQAPRG LIGGTFKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGG GGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG

1630	CD70- 62x12C- scFc	bispecific c HLE molecule	<p>VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK</p> <p>GGGGGGSDIQMTQSPSSLSASVGRVITTCRASQGISNYLAWYQQKPKVPKLLIYAASL QSGVPSRFSGSGGTFTLTISSLQAEDVAVYCCQYISTPLTGGGTKEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTQVVTQEPSTLTVSPGGTFTLTCGSSTGAVTSNYPNWVQKPGQAPRGLIGGT KFLAPGTAPRFSGLLGKKAALTLGSGVQPEDEAEYICVLWYSNRWVFGGTGKLTVLGGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK</p> <p>EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKLEWVSYSISSSGGYIYYADS VKGRFTISRDNKNSLYLQMNSLRAEDAAVYYCSRGDYSNYAYFDYWGQGLTVTVSSGGGGSG GGGGGGGSDIQMTQSPSSLSASVGRVITTCRASQGISNYLAWYQQKPKVPKLLIYAASL QSGVPSRFSGSGGTFTLTISSLQAEDVAVYCCQYISTPLTGGGTKEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTQVVTQEPSTLTVSPGGTFTLTCGSSTGAVTSNYPNWVQKPGQAPRGLIGGT KFLAPGTAPRFSGLLGKKAALTLGSGVQPEDEAEYICVLWYSNRWVFGGTGKLTVLGGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK</p>
1631	CD70- 62_CCx12 C-scFc	bispecific c HLE molecule	<p>EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKLEWVSYSISSSGGYIYYADS VKGRFTISRDNKNSLYLQMNSLRAEDAAVYYCSRGDYSNYAYFDYWGQGLTVTVSSGGGGSG GGGGGGGSDIQMTQSPSSLSASVGRVITTCRASQGISNYLAWYQQKPKVPKLLIYAASL QSGVPSRFSGSGGTFTLTISSLQAEDVAVYCCQYISTPLTGGGTKEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSGTQVVTQEPSTLTVSPGGTFTLTCGSSTGAVTSNYPNWVQKPGQAPRGLIGGT KFLAPGTAPRFSGLLGKKAALTLGSGVQPEDEAEYICVLWYSNRWVFGGTGKLTVLGGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV</p>

[illegible]

1634	CD70- 55x12C- scFc	bispecific c HLE molecule	<p>GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>QVQLVESGGGVVQPGRLSLRLSCAASGFMFSSYGMHWVRQAPGKGLEWVAIVSYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGNHNHGMVWVGQGTTVTVSSGG GSGGGSGGGSDIQMTQSPSSLSASVGDRTITTCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQSYSTPFTFGPTKVEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSG GSGGGSGGGSGQTVVTEPSLTVSPGGTVTLTCGSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLGGAALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>QVQLVESGGGVVQPGRLSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAIVSYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGNHNHGMVWVGQGTTVTVSSGG GSGGGSGGGSDIQMTQSPSSLSASVGDRTITTCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQSYSTPFTFGPTKVEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSG GSGGGSGGGSGQTVVTEPSLTVSPGGTVTLTCGSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLGGAALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS</p>
1635	CD70- 55_CCx12 C-scFc	bispecific c HLE molecule	<p>QVQLVESGGGVVQPGRLSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAIVSYDGSNKYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGNHNHGMVWVGQGTTVTVSSGG GSGGGSGGGSDIQMTQSPSSLSASVGDRTITTCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQSYSTPFTFGPTKVEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSG GSGGGSGGGSGQTVVTEPSLTVSPGGTVTLTCGSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLGGAALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS</p>

				FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1636	CD70- 13x12C- scFc_del GK	bispecific c HLE molecule		<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGRPNYADS VKGRFTISRDN SKNTLYLQMNSLRDEDTAVYYCAKVDYSNYLFDDYWGQGTLTVTSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGEGATLSCRAGQSVRRSSYLGWYQKQPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGGGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGTLTVTSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTCGSSTGAVTSGNYPNWVQKQPGQAPRGLIGG TKFLAPGTPARFSGSLGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1637	CD70- 13_CCx12 C- scFc_del GK	bispecific c HLE molecule		<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSVISGSGGRPNYADS VKGRFTISRDN SKNTLYLQMNSLRDEDTAVYYCAKVDYSNYLFDDYWGQGTLTVTSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGEGATLSCRAGQSVRRSSYLGWYQKQPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGGGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGTLTVTSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTCGSSTGAVTSGNYPNWVQKQPGQAPRGLIGG TKFLAPGTPARFSGSLGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>

1638	CD70- 14x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTFTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGSGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
1639	CD70- 14_CCx12 C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTFTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGSGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
1640	CD70- 15x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG

1641	CD70- 15_CcX12 C- scFc_del GK	bispecific c HLE molecule	GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYCCQYGSSPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGSTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGGGGGGG VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1642	CD70- 16x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYCCQYGSSPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGSTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYS VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

	GK	<p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTTLTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLSGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK</p>
1643	<p>CD70- 16_CcX12 C- scFc_del GK</p> <p>bispecific c HLE molecule</p>	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTTLTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLSGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK</p>
1644	<p>CD70- 17x12C- scFc_del GK</p> <p>bispecific c HLE molecule</p>	<p>EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQYGSPTFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG</p>

1645	CD70- 17_CcX12 C- scFc_del GK	bispecific c HLE molecule	<p>SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLIESGGGLVQSGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGSSPTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLIESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGSSPTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGGDK</p>
1646	CD70- 18x12C- scFc_del GK	bispecific c HLE molecule	<p>SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLIESGGGLVQSGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGSSPTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGGDK</p>

1647	CD70- 18_Cx12 C- scFc_del GK	bispecific c HLE molecule	<p> THTCPPCPAPELLGGPSVFLFPPKPKD TLMI SRTPVETCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK SDKTHTCPAPELLGGPSVFLFPPKPKD TLMI SRTPVETCVVVDVSHEDPEVKFNWYVDGVEVH EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKCLEWVSLSISGSGGRTHYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGT LTVTVSSGGGSGG GGGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSTYLA WYQQKPGQAPRLLIYDASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYFCQYGS SPTTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVTVSSGGGG SGGGGGGGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEY YCVLWYSNRWVFGG GTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKD TLMI SRTPVETCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPAPELLGGPSVFLFPPKPKD TLMI SRTPVETCVVVDVSHEDPEVKFNWYVDGVEVH EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK </p>
1648	CD70- 19x12C- scFc_del GK	bispecific c HLE molecule	<p> EVQLLESGGGLVQPGGSLRLSCAASGFTTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VKGRFTISRDN SKNTLSLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGT LTVTVSSGGGSGG GGGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSTYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYCCQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVTVSSGGGG SGGGGGGGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGGKAALTL SGVQPEDEAEY YCVLWYSNRWVFGG GTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKD TLMI SRTPVETCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV </p>

				YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLT VDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTI LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYS KLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK
1649	CD70- 19_CCx12 C- scFc_del GK	bispecific c HLE molecule	EVQLLESGLLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVS AISGSGGSTRFYADS VKGRFTISRDN SKNTLSLQMNLSRAEDTA VYYCAKHDYSNYPFDYWGQGTLLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLLTVTVSSGGGG SGGGSGGGSQTVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLT VDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTI LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYS KLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK	
1650	CD70- 21x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGLLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVS AISGSGGSTRFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTA VYYCAKHDYSNYPFDYWGQGTLLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYSCQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLLTVTVSSGGGG SGGGSGGGSQTVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLT VDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGGSGGGSGGGSGGGSGGGSGGGSGGGG	

1651	CD70- 21_CCx12 C- scFc_del GK	bispecific c HLE molecule	<p>SDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSATISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGTITVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYSCQQYGDLPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFGNSYISYWAYWGQGTITVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSGTAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>
1652	CD70- 22x12C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAMSWVRQAPGKLEWVSATISGSGGYTYIADS VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGTITVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFGNSYISYWAYWGQGTITVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSGTAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE</p>

1653	CD70- 22_CCx12 C- scFc_del GK	bispecific c HLE molecule	PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKCLEWVSATISGSGGYTYIYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1654	CD70- 24x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGLAQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKLEWVSATISGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

1655	CD70- 24_CCx12 C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNPYFDYWGQGTLLTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLAQYQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWRVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1656	CD70- 25x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNPYFDYWGQGTLLTVSSGGGSGG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLAQYQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWRVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1657	CD70- 25_CCx12	bispecific c HLE	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNPYFDYWGQGTLLTVSSGGGSGG

	C- scFc_del GK	molecule	GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYCCQQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGG SGGGSGGGSQTIVTQEPSLTVSPGGTVTLTCGSSGTAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1658	CD70- 26x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYCCQQYGSPTFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGG SGGGSGGGSQTIVTQEPSLTVSPGGTVTLTCGSSGTAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1659	CD70- 26_Cx12 C-	bispecific c HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYCCQQYGSPTFTFGCGTKVEIKSGGGGSEVQ

	scFc_del GK		<p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTCGSSGTAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK</p>
1660	CD70_1- G2x12C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTFYADS VQGRFTISRDNKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGYSPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTCGSSGTAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK</p>
1661	CD70_1- G2_CCXl 2C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGSTFYADS VQGRFTISRDNKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGYSPFTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG</p>

1662	CD70- 27x12C- scFc_del GK	bispecific c HLE molecule	<p>SGGGSGGGGQTVVTQEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLIESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGGTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGSSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLIESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGGTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGSSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK</p>
1663	CD70- 27_CCx12 C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLIESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGGTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYYCQYGSSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNIATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK</p>

1664	CD70- 28x12C- scFc_del GK	bispecific c HLE molecule	<p>THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRITYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFLTISRLEPEDFAVYSCQYGISPTTFGGGTKEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSI SYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRITYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFLTISRLEPEDFAVYSCQYGISPTTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSI SYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOV</p>
1665	CD70- 28_CCx12 C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRITYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFLTISRLEPEDFAVYSCQYGISPTTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSI SYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOV</p>

1666	CD70-31x12C-scFc_delGK	bispecific HLE molecule	YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK
1667	CD70-31_CCx12C-scFc_delGK	bispecific HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKCLEWVSATISGSGGRAQYADSVQGRFTVSIRDNSKNTLYLQMNSLRAEDTAVYCAKHDYSNYPFDYWGQGTTLVTVSSGGGGSGGGGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPKGQAPRLLIYGSSSRATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGSSPPFPFGGKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNIATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCYVRHGFNGNSYISYWAYWGQGTTLTVSSGGGSGGGGGGGSGGTIVTQTEPSSLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQQKPKGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYICVLWYSNRWVFGGKTKLTVLGGGDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK

1668	CD70- 32x12C- scFc_del GK	bispecific c HLE molecule	DKTHTCPPCPAPELGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCTKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQVRS DYLA WYQ QKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQYGSTPTTFGGGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCTKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQVRS DYLA WYQ QKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQYGSTPTTFGGGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
1669	CD70- 32_Cc12 C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCTKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQVRS DYLA WYQ QKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQYGSTPTTFGGGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE

1670	CD70- 37x12C- scFc_del GK	bispecific c HLE molecule	PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAIGDGGGYTYIYADS VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRRSSYFAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1671	CD70- 37_CCx12 C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAIGDGGGYTYIYADS VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRRSSYFAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

1672	CD70- 38x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGVVQPGRLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNPYFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGSSPPSFSGGQTKVEIKSGGGGSEVQ LVESGGGLVQPGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGQTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
1673	CD70- 38_CCx12 C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGVVQPGRLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNPYFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGSSPPSFSGGQTKVEIKSGGGGSEVQ LVESGGGLVQPGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGQTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
1674	CD70- 39x12C-	bispecific c HLE	EVQLLESGGGVVQPGRLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNPYFDYWGGLGLTVTVSSGGGGSG

	scFc_del GK	molecule	GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYSCQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGSTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGGGGGG VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1675	CD70- 39_CCx12 C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGVVPGRSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGGTFFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGGLTTLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYSCQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGSTVVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1676	CD70- 41x12C- scFc_del	bispecific c HLE molecule	EVQLLESGGMVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYSCQYGDLPFTFGPGTKVDIKSGGGGSEVQ

	GK	<p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTTLTCGSSGTAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1677	<p>CD70- 41_Cc x12 C- scFc_del GK</p> <p>bispecific c HLE molecule</p>	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYQYGDLPFTFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSLTVSPGGTTLTCGSSGTAVTSGNYPNWWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1678	<p>CD70- 42x12C- scFc_del GK</p> <p>bispecific c HLE molecule</p>	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEI VLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTINRLEPEDFAVYYCQYQYGSPPFTFGGGLTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG</p>

1679	CD70- 42_CcX12 C- scFc_del GK	bispecific c HLE molecule	<p>SGGGSGGGGQTVVTQEPSTLVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLIESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTINRLEPEDFAVYYCQYGSSPTFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLIESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTINRLEPEDFAVYYCQYGSSPTFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK</p>
1680	CD70- 43x12C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLIESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTINRLEPEDFAVYYCQYGSSPTFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK</p>

1681	CD70- 43_Cc12 C- scFc_del GK	bispecific c HLE molecule	<p> THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTINRLEPEDFAVYCCQYGSSTPTFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNGNSYISYWAYWGQGTLLTVSSGGGG SGGGGGGGQTVVTEPSLTVSPGGTTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYICVLWYSNRWVFGGKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK </p>
1682	CD70- 48x12C- scFc_del GK	bispecific c HLE molecule	<p> EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATISDGGITDFADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCARHDYSNYFFDYWGQGTLLTVSSGGGSG GGGGGGSDIQMTQSPSSLSASVGRVTITCRASQGISNYLAWYQQKPKVPKLLIYAASIL QSGVPSKFSGSGGTDFLTITISLQPEDFAIYCCQYFAYPIITFGQGTREIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNGNSYISYWAYWGQGTLLTVSSGGGG GGGGGGGGQTVVTEPSLTVSPGGTTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYICVLWYSNRWVFGGKLTVLGGGDKT HTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY </p>

[illegible]

1685	CD70- 53_CCx12 C- scFc_del GK	bispecific c HLE molecule	<p>SDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTFYADS VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYFCQQYGSSPTFGCGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK</p>
1686	CD70- 54x12C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKLEWVSATIGDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYVAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYCCQQYGDLPFTFGPGRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSKAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE</p>

1687	CD70- 54_CCx12 C- scFc_del GK	bispecific c HLE molecule	PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAGDSGGSTFYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGTLTIVSSGGGGSG GGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYVAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPFTFGCGTRLEIKSGGGSEVQ LIVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLTIVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKLTIVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1688	CD70- 58x12C- scFc_del GK	bispecific c HLE molecule	QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWI RQPPGKGLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHYEILTGYYPDFDIWGQGTMTVTVSSG GGGGGGGGGGGDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIY AASNLSGVSSRFSGSGGTDFLTITISLQPEDFATYYCQQSFSSPRTFGQGTKEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLTIVSS GGGGGGGGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRG LIGGTFKFLAPGTPARFSGSLGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKLTIVLGG GGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

1689	CD70- 58_CCx12 C- scFc_del GK	bispecific c HLE molecule	<p>QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYYWGWIQQPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHYEILTGYPDFDIWGQGMVTVSSG GGSGGGGGGGSDIQMTQSPSSLASVGDRTITCRASQSISSYLNWYQKPGKAPKLLIY AASNLSGVSSRFSGSGGTDTLTITISLQPEDFATYCCQSFSSPRTFCGCTKVEIKSGGGG SEVQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS GGSGGGGGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRG LIGGTFKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGG GGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR EPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1690	CD70- 62x12C- scFc_del GK	bispecific c HLE molecule	<p>EVQLVESGGGLVKPGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSYISSSGGIYYADS VKGRFTISRDNKNSLYLQMNSLRAEDAAVYYCSRGDYSNYAFDYWGQGLTVTVSSGGGSG GGSGGGGGSDIQMTQSPSSLASVGDRTITCRASQGISNLYAWYQKPGKVPKLLIYAASLT QSGVPSRFSGSGGTDTLTITISLQAEADVAVYYCQYQYSTPLTFGGGCTKVEIKSGGGSEVQL VESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY ITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1691	CD70- 62_CCx12	bispecific c HLE	<p>EVQLVESGGGLVKPGGSLRLSCAASGFTTFSSYSMNWVRQAPGKLEWVSYISSSGGIYYADS VKGRFTISRDNKNSLYLQMNSLRAEDAAVYYCSRGDYSNYAFDYWGQGLTVTVSSGGGSG</p>

	C- scFc_del GK	molecule	GGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPKVPKLLIYAAS TL QSGVPSRFSGSGTDFTLTIISSLQAEADVAYYCQQYYSTPLTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYCYVRHGNFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPSTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGLTVLGGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPDSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYSKLT DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYSK LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1692	CD70- 23x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKGLEWVSTISDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYCARHDYSNYAFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCYQQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYCYVRHGNFNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGSGTQVVTQEPSTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGLTVLGGGGDK THTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGSGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGGSFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1693	CD70- 23_CCx12 C-	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISDSGGSTFYADS VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYCARHDYSNYAFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCYQQYGDLPFTFGCGTKVEIKSGGGGSEVQ

	scFc_del GK	<p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLGGGDK THTCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK</p>
1694	CD70- 55xI2C- scFc_del GK	<p>QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARGRYGSGNHNHGMVWQGTITVTVSSGG GGGGGGGGGSDIQMTQSPSSLSASVGDRTITTCRASQSISSYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGRGSGTDFTLTITSSLPEDFATYYCQSYSTPFTFGPGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGGGGGGGGQTVVTQEPSTLVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGKFLAPGTPARFSGLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLGGG GDKTHTCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGG GGGDKTHTCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK</p>
1695	CD70- 55_CCxI2 C- scFc_del GK	<p>QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAVISYDGSNKYYADS VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARGRYGSGNHNHGMVWQGTITVTVSSGG GGGGGGGGGSDIQMTQSPSSLSASVGDRTITTCRASQSISSYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGRGSGTDFTLTITSSLPEDFATYYCQSYSTPFTFGCGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG</p>

1696	CD70- 13D _{CC} - x12C- scFc	bispecific c HLE molecule	GGGGGGGGGGGGQTVVTQEPSTLVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGL IGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1697	CD70- 13Dx12C -scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISGSGGPRNYAES VKGRFTISRDN SKNTLYLQMNSLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSVISGSGGPRNYAES VKGRFTISRDN SKNTLYLQMNSLRDEDTAVYYCAKVDYSNYLFFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGEGATLSCRAGQSVRSYLGWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGGGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIG

1698	C D70- 14D ₂ CC x12C- scFc	bispecific c HLE molecule	TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKCLEWVSATISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPFTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1699	CD70- 14Dx12C -scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLKLSCAASGFTFSIYAMSWVRQAPGKLEWVSATISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPFTFGPGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH

1700	CD70_6 1-D1D_CC xI2C- scFc	bispecific c HLE molecule	NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKEVQLLESGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAESVEGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGGGSEIVLTQSPGTTLSLSPGERATLSCRASQSVRS SYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPFTFGCGTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNGNSIYSWAYWGQGTLLTVSSGGGGSGGGSGGSQT VVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK
1701	CD70_6 1-D1DxI2 C-scFc	bispecific c HLE molecule	EVQLLESGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAESVEGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGGGSEIVLTQSPGTTLSLSPGERATLSCRASQSVRS SYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPFTFGPGTKLEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNGNSIYSWAYWGQGTLLTVSSGGGGSGGGSGGSQT VVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK

[illegible]

1704	CD70- 17D ₂ CC x12C- scFc	bispecific c HLE molecule	<p>GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQSGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTHYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNPYFDYWGQGTLLTVSSGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGSYISYWAYWGQGTLLTVSSGGGGSGGGSGGSQTAVTQEPSLTVSPGGTFTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVPQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>
1705	CD70- 17Dx12C -scFc	bispecific c HLE molecule	<p>EVQLLESGGGLVQSGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTHYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNPYFDYWGQGTLLTVSSGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGSYISYWAYWGQGTLLTVSSGGGGSGGGSGGSQTAVTQEPSLTVSPGGTFTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVPQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>

1706	CD70- 18D _{CC} - x12C- scFc	bispecific c HLE molecule	YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSLISGSGGRTHYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVFCQQYGSPPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1707	CD70- 18Dx12C -scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSLISGSGGRTHYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYDASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVFCQQYGSPPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1708	CD70-	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGSTFYAES

	19D _{CC} -xI2C-scFc	c HLE molecule	VKGRFTISRDN SKNTLSLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSGGGGGGGSEI VLTQSPG TSLSPGERATLS CRASQSVRRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGSLKLSCAA SGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGGSGGGSGGSQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGG TKLTVLGGGDKTHTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNV FSCVMHEALHNHYTQKSLSLSPGK
1709	CD70-19DxI2C-scFc	bispecific HLE molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKGLEWVS AISGGSGSTFYAESVKGRFTISRDN SKNTLSLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSGGGGGGGSEI VLTQSPG TSLSPGERATLS CRASQSVRRSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGSLKLSCAA SGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGGSGGGSGGSQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGG TKLTVLGGGDKTHTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNV FSCVMHEALHNHYTQKSLSLSPGK
1710	CD70-21D _{CC} -xI2C-	bispecific HLE molecule	EVQLLESGGGMVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKCLEWVS AISGGSGRTFYAESVEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSGGGGGGGSEI VLTQSPG TSLSPGERATLS CRASQSVRRSYLAWYQQKPGQAPRLLIYGASS

1711	CD70- 21Dx12C -scFc	bispecific c HLE molecule	<p>RATGIPDRFSGSGGTDTLTISRLEPEDFAVYSCQYGDLPFTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYYCVRHGFNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTSCSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFTYAMSWVRQAPGKGLEWVSASISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAHYQKPKGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYSCQYGDLPFTFGPGTKLEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYYCVRHGFNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTSCSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1712	CD70- 22D ₂ CC x12C- scFc	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSASISGSGGYTYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAHYQKPKGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYSCQYGDLPFTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV</p>

1713	CD70- 22Dx12C -scFc	bispecific c HLE molecule	KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRRHGFNGNSIYSWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY YSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGYTYAAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRRHGFNGNSIYSWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY YSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK EVQLLESGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGSTFYAAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRRHGFNGNSIYSWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG
1714	CD70- 24D _{CC} x12C- scFc	bispecific c HLE molecule	KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRRHGFNGNSIYSWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY YSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK EVQLLESGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGSTFYAAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRRHGFNGNSIYSWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG

1715	CD70- 24Dx12C -scFc	bispecific c HLE molecule	TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLAQPGGSLRLSCAASGFTTSSYAMSWVRQAPGKGLEWVSATISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYFCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYQCQYGDLPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYCVRHGNGFNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK
1716	CD70- 25D _{CC} - x12C- scFc	bispecific c HLE molecule	EVQLLESGGMVQPGGSLRLSCAASGFTTSSYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYQCQYGDLPFTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYCVRHGNGFNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH

1717	CD70- 25Dx12C -scFc	bispecific c HLE molecule	<p>NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGKGSSGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFL YSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLGVQVPEDEAEYICVLWYSNRWVFGGGLTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGKGSSGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFL YSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>
1718	CD70- 26D _{CC} x12C- scFc	bispecific c HLE molecule	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGSPPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLGVQVPEDEAEYICVLWYSNRWVFGGGLTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT</p>

[illegible]

1721	CD70_1- G2DxI2 C-scFc	bispecific c HLE molecule	<p>GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGSTFYAESVQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNPYFDYWGQGTLLTVSSGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSPFTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGSGGGSGGGSGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVPQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>
1722	CD70- 27D_CC xI2C- scFc	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGSTFYAESVQGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNPYFDYWGQGTLLTVSSGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGSGGGSGGGSGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVPQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>

1723	CD70- 27DxI2C -scFc	bispecific c HLE molecule	YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSALISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSNIYAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGSPPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLVGQPEDEAEYYCVLWYSNRWVFGGDKTLVLGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1724	CD70- 28D _{CC} xI2C- scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNIYAWYQQKPGQAPRLLIYGASN RATGIPDRFSGSGGTFTLTISRLEPEDFAVYSCQQYGISPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLVGQPEDEAEYYCVLWYSNRWVFGGDKTLVLGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1725	CD70-	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYAES

	28DxI2C -scFc	c HLE molecule	VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPG T LSLSPGERAT LSCRASQSVRSNYLAWYQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYSCQYGISPPTFGGKVEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAAAGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGG SGGGSGGGSQTVVTQEP SLTVSPGGT VTLTTCG SSTGAVTSGNYPNWRVFGGKTLTVLGGGDK TKFLAPGTPARFSGLLGGKAAL T LSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1726	C D70- 31D_CC xI2C- scFc	bispecifi c HLE molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTFSYAMSWVRQSPGKCLEWVS AISGGGRAQYAES VQGRFTVSRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPATLSVSPGERAT LSCRASQSVSSNLAWYQKPGQAPRLLIYGSSSR ATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSPPFPFGCGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAAAGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMN LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGGS GGSGGGGSGQTVVTQEP SLTVSPGGT VTLTTCG SSTGAVTSGNYPNWRVQKPGQAPRLLIGGT KFLAPGTPARFSGLLGGKAAL T LSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDKT HTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPEL LGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1727	CD70- 31DxI2C -scFc	bispecifi c HLE molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTFSYAMSWVRQSPGKLEWVS AISGGGRAQYAES VQGRFTVSRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPATLSVSPGERAT LSCRASQSVSSNLAWYQKPGQAPRLLIYGSSSR

1728	CD70- 32D ₂ CC xI2C ⁻ scFc	bispecific c HLE molecule	<p>ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCYCQYQSSPPFPFGGKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCYCVRHGFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYLWYSNRWVFGGKTLTVLGGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSASISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNLSRAEDTAVYCYCTKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQYGYSTPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYCYCVRHGFNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYLWYSNRWVFGGKTLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTV VDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLY YKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSASISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNLSRAEDTAVYCYCTKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQYGYSTPTFGGKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV</p>
1729	CD70- 32DxI2C -scFc	bispecific c HLE molecule	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSASISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNLSRAEDTAVYCYCTKHDYSNYPFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVSRDYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYHCQYGYSTPTFGGKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV</p>

1730	CD70- 37D_CC xI2C- scFc	bispecific c HLE molecule	<p>KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGGSGQTVVTQEPSLTVSPGGTTLTSCGSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAIGE GGGYTYAAES VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPYFDYWGQGLTVTVSSGGGGSG GGGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYFAWYQKPGQAPRLLIYGAST RATGIPARFSGSGGTFTLTISRLEPEDFAVYYCQYGSSPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGGSGQTVVTQEPSLTVSPGGTTLTSCGSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1731	CD70- 37DxI2C -scFc	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAIGE GGGYTYAAES VKGRFTISRDN SKNTLSLLMNSLRAEDTAVYYCARHDYSNYPYFDYWGQGLTVTVSSGGGGSG GGGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRSYFAWYQKPGQAPRLLIYGAST RATGIPARFSGSGGTFTLTISRLEPEDFAVYYCQYGSSPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGGSGQTVVTQEPSLTVSPGGTTLTSCGSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>

1732	CD70- 38D ₂ CC xI2C- scFc	bispecific c HLE molecule	<p>TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGVVQPGRSRLRSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPPSFSGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSGTA VTSNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK</p>
1733	CD70- 38DxI2C -scFc	bispecific c HLE molecule	<p>EVQLLESGGGVVQPGRSRLRSCAASGFTFSYAMSWVRQAPGKLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSI RSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPPSFSGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLVSPGGTTLTTCGSSGTA VTSNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p>

1734	CD70-39D_CCxI2C-scFc	bispecific HLE molecule	NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKEVQLLESQGGVVQPGRSRLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGGTFFYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGLGTLTVTVSSGGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPKGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYSCQYGDLPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSI SYWAYWGQGT LTVTVSSGGGGSGGGSGGGSGGSGQTVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPKGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPPELLGGPSVFLFPPKPKD TLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGKEVQLLESQGGVVQPGRSRLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAISGSGGGTFFYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGLGTLTVTVSSGGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPKGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYSCQYGDLPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSI SYWAYWGQGT LTVTVSSGGGGSGGGSGGGSGGSGQTVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPKGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPPELLGGPSVFLFPPKPKD TLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPG
1735	CD70-39DxI2C-scFc	bispecific HLE molecule	EVQLLESQGGVVQPGRSRLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGGGTFFYAESVEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGLGTLTVTVSSGGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPKGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYSCQYGDLPFTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSI SYWAYWGQGT LTVTVSSGGGGSGGGSGGGSGGSGQTVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPKGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPPELLGGPSVFLFPPKPKD TLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPG

[illegible]

1738	CD70- 42D ₂ CC xI2C- scFc	bispecific c HLE molecule	<p>GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTYAMSWMVRQAPGKCLEWVSLSISGSGGRTYYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTINRLEPEDFAVYYCQYGSSPPTFGCGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWMVRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNFGNSYISYWAYWGQGTLLTVSSGGGSGGGGSGGSGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>
1739	CD70- 42DxI2C -scFc	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTYAMSWMVRQAPGKCLEWVSLSISGSGGRTYYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTINRLEPEDFAVYYCQYGSSPPTFGCGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWMVRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNFGNSYISYWAYWGQGTLLTVSSGGGSGGGGSGGSGQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>

1740	CD70- 43D _{CC} - x12C- scFc	bispecific c HLE molecule	YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGVVPGRSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTINRLEPEDFAVYYCQQYGSSPTFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1741	CD70- 43Dx12C -scFc	bispecific c HLE molecule	EVQLLESGGGVVPGRSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTINRLEPEDFAVYYCQQYGSSPTFGCGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1742	C	bispecific	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSISGSGGITDFAES

	D70- 48D ₋ CC xI2C ₋ scFc	c HLE molecule	VKGRFTISRDNsrntlylQmnsLraEDTAVyFCARHDYsNYFFFDYWGQGTlVTVSSGGGGSG GGSGGGSDIqMTQSPSSLSASvGDRVTITCRASQGISNYLAWYQqKPKVpKLLIYAASIL QSGVPSKfSGSGSGTDFTLTlTlSSLPEDFAIYcQqYFAYPItFGCGTRlEIKSGGGSEVQl VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYlQmnnlKtEDTAVYcVRHGnFGNSYISYWAYWGQGTlVTVSSGGGG GGSGGGGSQTvVTQEPsLTVSPGGTVTLTCGSSTGAVTSgNYPNWVfQKPGQAPRGLIGGT KFLAPGTPARfSGSLlGGKAALTLsGVQPEDEAEYcVLWYSNRWfVfGGGTklTVlGGGGDKT HTCPCPAPeLLGGPSVfLFPpKpKDTlMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSYRCVSVLTVLHQDwLNGKEYKCKVSNKALPAPIEKtISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKtTPPVLDSGSFFLYSKLTlV DKSRWQqGNVfSCSVmHEALHNHYtQKSLSlSPGKGGGGGGGGGGGGGGGGGGGGGGGG GSDKtHTCPCPAPeLLGGPSVfLFPpKpKDTlMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSYRCVSVLTVLHQDwLNGKEYKCKVSNKALPAPIEKtISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKtTPPVLDSGSFFLY SKLTVDKSRWQqGNVfSCSVmHEALHNHYtQKSLSlSPGK
1743	CD70- 48DxI2C -scFc	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTfSSyAMSWVRQAPGKLEWVSISGGGITDFAES VKGRFTISRDNsrntlylQmnsLraEDTAVyFCARHDYsNYFFFDYWGQGTlVTVSSGGGGSG GGSGGGSDIqMTQSPSSLSASvGDRVTITCRASQGISNYLAWYQqKPKVpKLLIYAASIL QSGVPSKfSGSGSGTDFTLTlTlSSLPEDFAIYcQqYFAYPItFGCGTRlEIKSGGGSEVQl VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYlQmnnlKtEDTAVYcVRHGnFGNSYISYWAYWGQGTlVTVSSGGGG GGSGGGGSQTvVTQEPsLTVSPGGTVTLTCGSSTGAVTSgNYPNWVfQKPGQAPRGLIGGT KFLAPGTPARfSGSLlGGKAALTLsGVQPEDEAEYcVLWYSNRWfVfGGGTklTVlGGGGDKT HTCPCPAPeLLGGPSVfLFPpKpKDTlMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSYRCVSVLTVLHQDwLNGKEYKCKVSNKALPAPIEKtISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKtTPPVLDSGSFFLYSKLTlV DKSRWQqGNVfSCSVmHEALHNHYtQKSLSlSPGKGGGGGGGGGGGGGGGGGGGGGGGG GSDKtHTCPCPAPeLLGGPSVfLFPpKpKDTlMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSYRCVSVLTVLHQDwLNGKEYKCKVSNKALPAPIEKtISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKtTPPVLDSGSFFLY SKLTVDKSRWQqGNVfSCSVmHEALHNHYtQKSLSlSPGK
1744	CD70- 53D ₋ CC xI2C ₋	bispecific c HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTfSSyAMSWVRQAPGKLEWVSISGGGRtFYAES VEGRFTISRDNskntlylQmnsLraEDTAVYcAKHDYsNYPFYDYWGQGTlVTVSSGGGGSG GGSGGGGSEIvLTQSPGTLslSPGERATlSCRASQSVrSSYLAWYQqKPGQAPRlLIYGASS

1745	CD70- 53Dx12C -scFc	bispecific c HLE molecule	<p>RATGIPDRFSGSGGTDTLTISRLEPEDFAVFCQQYGSPPFTFGCGTRLEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYCVRHGFGNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGSGQTVVTQEPSTVSPGGTTLTSCSSTGAVTSGNPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVFCQQYGSPPFTFGCGTRLEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYCVRHGFGNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGSGQTVVTQEPSTVSPGGTTLTSCSSTGAVTSGNPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1746	CD70- 54D ₂ CC x12C- scFc	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAIGSGGGSTFYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRRSYAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYGDLPFTFGCGTRLEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV</p>

1747	C D70- 54Dx12C -scFc	bispecific c HLE molecule	<p>KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGSQT VVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGGVQPEDEAEYYCVLWYSNRWVFGGGLTVLGGGDK THTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFL YSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAIGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYVAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYQDLPFTFGPGTRLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGSQT VVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGGVQPEDEAEYYCVLWYSNRWVFGGGLTVLGGGDK THTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFL YSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK</p> <p>QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSSYWGWIRQPPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHYEILTGYYPDFDIWGQGMVTVSSG GGSGGGGGGGGSDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPKGAPKLLIY AASNLIQSGVSSRFSGSGGTDFLTITSSLPEDFATYYCQQSFSFSPRTFGCGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSS GGSGGGGGGGGSGQT VVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPR</p>
1748	CD70- 58D ₂ CC x12C- scFc	bispecific c HLE molecule	<p>QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSSYWGWIRQPPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHYEILTGYYPDFDIWGQGMVTVSSG GGSGGGGGGGGSDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPKGAPKLLIY AASNLIQSGVSSRFSGSGGTDFLTITSSLPEDFATYYCQQSFSFSPRTFGCGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSS GGSGGGGGGGGSGQT VVTQEPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPR</p>

1749	C D70- 58DxI2C -scFc	bispecific c HLE molecule	LIGGKFLAPGTPARFSGSLIGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGG GGDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLY SKLTVDKSRWQOGNMFSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGG GSGGGGSKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSG SFFLYSKLTVDKSRWQOGNMFSCVMHEALHNHYTQKSLSLSPGK QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSSSYYWGWI RQPPGKGLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHYEILTGYDPDFDIWGQGTMTVTVSSG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKGKAPKLLIY AASNLSGVSSRFSGSGGTDFTLTISLQPEDFATYYCQQSFSPRTFGQGQTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSS GGGGGGGGGGGQTIVTQEPSLTVSPGGTVTLTCGSGTGAVTSGNYPNWVQQKPGQAPRG LIGGKFLAPGTPARFSGSLIGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGG GGDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLY SKLTVDKSRWQOGNMFSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGG GSGGGGSKTHTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSG SFFLYSKLTVDKSRWQOGNMFSCVMHEALHNHYTQKSLSLSPGK EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYSISSSGGYIYYAES VKGRFTISRDNAKNSLYLQMNSLRAEDAAVYYCVRGDSYSNYAFDYWGQGTITVTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGKPKLLIYAASTL QSGVPSRFSGSGGTDFTLTISLQAEADVAVYYCQQYYSTPLTFGCGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSGGGS GGGGGGGGGQTIVTQEPSLTVSPGGTVTLTCGSGTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLIGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKT HTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
1750	CD70- 62D_CC xI2C- scFc	bispecific c HLE molecule	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKCLEWVSYSISSSGGYIYYAES VKGRFTISRDNAKNSLYLQMNSLRAEDAAVYYCVRGDSYSNYAFDYWGQGTITVTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPKGKPKLLIYAASTL QSGVPSRFSGSGGTDFTLTISLQAEADVAVYYCQQYYSTPLTFGCGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITVTVSSGGGS GGGGGGGGGQTIVTQEPSLTVSPGGTVTLTCGSGTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLIGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKT HTCPPCPAPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN

1751	CD70- 62Dx12C -scFc	bispecific c HLE molecule	AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQÖQGNVFCSCVMHEALHNHYTQKSLSLSPGK GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQÖQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSYSISSSGGYIYYAES VKGRFTISRDNKNSLYLQMNSLRAEDAAVYYCSRGDYSNYAYFDYWGQGTLLTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGRVTITCRASQGISNYLAWYQÖQKPKVPKLLIYAASTL QSGVPSRFSGSGGTDTLTITSSLAEDVAVYYCQYYSTPLTFGGGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGS GGSGGGGSGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQÖQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYICVLWYSNRWVFGGGTKLTVLGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQÖQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSGGGGSGGGGSGGG GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQÖQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISGSGGSTFYAES VKGRFTISRDNKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQÖQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQYQYDLPFTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQÖQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYICVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
1752	CD70- 23D _{CC} x12C- scFc	bispecific c HLE molecule	AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQÖQGNVFCSCVMHEALHNHYTQKSLSLSPGK GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQÖQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKCLEWVSTISGSGGSTFYAES VKGRFTISRDNKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQÖQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQYQYDLPFTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQÖQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYICVLWYSNRWVFGGGTKLTVLGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV

[illegible]

1755	CD70- 55Dx12C -scFc	bispecific c HLE molecule	<p>PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGG SGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKGLEWAVISYEGSNKYAE VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYYGSGNHNHGMVWGQGT TTVTVSSGG GGGGSGGGSDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPKAPKLLIYA ASSLQSGVPSRFSGRGSGDTLTISLQPEDFATYYCQSYSTPFTFGPGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGLTVTVSSG GGGGSGGGSGGQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGKTKLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGG SGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1756	CD70- 3.001 C Cx12C- scFc	bispecific c HLE molecule	<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWAVTWYDASNKYIGDA VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGYAMDVGQGT TTVTVSSGGG SGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSLRRIYLA WYQKPGQAPRLLIYDV FDRATGIPDRFSGGGSGDTLTISRLEPEDFAVYYCQQSYSESPFTFGCGTKVDIKSGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGLTVTVSSGG GGGGSGGGSGQTVVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLI GGTKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGKTKLTVLGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGG</p>

1757	CD70- 3.001x12 C-scFc	bispecific c HLE molecule	<p>GGGSDKTHTCPPAPPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWAVATWYDASNKYYGDA VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDLLRGVKGAMDVWGQGTITVTVSSGGGG SGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSLRRIYLAWYQQKPGQAPRLIYDV FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSESPFTFGPGTKVDIKSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGFSYISYWAYWGQGTITVTVSSGG GGGGSGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQQKPGQAPRLI GGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1758	CD70- 4.007_C Cx12C- scFc	bispecific c HLE molecule	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWISAYQGYTHYAQK LQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDYGGNDYIGMDVWGQGTITVTVSSGGGG GGGGSGGGGQSVLTQPPSASGTPGQRTVISCSSSSNIGINYVYWYQQLPGTAPKLLIYRSD QRPSPVDRFSGSKGTSASIALSGLRSEADYYCAAFDELSGVVFGCGTKLTVLSGGGG EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGFSYISYWAYWGQGTITVTVSSG GGGGSGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSGTGAVTSGNYPNWVQQKPGQAPRLI IGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGG SGGGSDKTHTCPPCPAPPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK</p>

1759	CD70- 4.007x12 C-scFc	bispecific c HLE molecule	<p> GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK </p> <p> QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWI SAYQGYTHYAQK LQGRVTMTTDTSTAYMELRLSRDDTAVYYCARDYGGNDYYGMDVWGQGT VTVTVSSGGGGS GGGSGGGSQSVLTQPPSASGTPGQRTVITSCSGSSNIGINYVYQQLPGTAPKLLIYRSD QRP SGVPDRFSGSKGTSASLALSGLRSEADYYCAAFDESLGVVFGGGTKLT VLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFGNSYI SYWAYWGQGT LVTVSSG GGGSGGGSQSVLTQPPSASGTPGQRTVITSCSGSSNIGINYVYQQLPGTAPKLLIYRSD IGGTKFLAPGTPARFSGSLGKKAALTL SGVQPEDEAEYCVLWYSNRWVFGGGTKLT VLG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGG SGGGSKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK </p>
1760	^C D70- 12.013 ₋ CCxI2C- scFc	bispecific c HLE molecule	<p> QAQLVESGGGVVQPGRSRLSLSCAASGFTFSYYGMHWVRQAPGKCLEWVAWIWYDASNKYADA VKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCARDREMGSRGDFDYWGQGT LVTVSSGGGGS GGGSGGGSDIQMTQSPSSLSASVGDRTVITCRASQGINNYLAWFQQPGKAPKSLIYAVSI LQGVPSKFSGGSGGTDFTLTISNLQPEDFATYYCQQYNFYPSFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFGNSYI SYWAYWGQGT LVTVSSGGG SGGSGGGGSQSVLTQPPSASGTPGQRTVITSCSGSSNIGINYVYQQLPGTAPKLLIYRSD TKFLAPGTPARFSGSLGKKAALTL SGVQPEDEAEYCVLWYSNRWVFGGGTKLT VLG THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGG GSKDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK </p>

1761	CD70- 12.013xI 2C-scFc	bispecific c HLE molecule	QAQLVESGGGVVQPRSLRLSCAASGFTFSYYGMHWVRQAPGKGLEWVAVIWYDASNKYIYADA VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDREMGSRGDFDYWGQGTLLTVSSGGGGG GGGGGGGGSDIQMTQSPSSLSASVGRVTITCRASQGINNYLAWFQQKPGKAPKSLIYAVSI LQGVPSKFSGSGTDFTLTISNLQPEDFATYCCQYNYFPFSFGQGTKVDIKSGGGGSEVQ LVESGGVLVQPGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGGGGGGQTVVTQEPSTLVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1762	CD70- 75.002.0 08_CCxI 2C-scFc	bispecific c HLE molecule	QVQLQQWGAGLLKPSETLSLTCAVYGGSGFGYFWSWIRQPPGKCLEWIGEIIYHSGHATNPNPSL KSRVTISLDTSKNQFSLKLNSTAAATAVYYCARGGNSGYIFDYWGQGTLLTVSSGGGGGGG GGGGGSDVQMTQSPSSLSASVGRVTITCRTSQYIGRYLNWYQKPGKAPKVLIIYGASTLQQ GVPSRFSGSGGTDFTLTITSLQPEDFAFYCCQYTYSTPRTFGCGTKVEIKSGGGGSEVQLVE SGGLVQPGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGGGG GGGGGGGQTVVTQEPSTLVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFK LAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHT CPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1763	CD70- 75.002.0	bispecific c HLE	QVQLQQWGAGLLKPSETLSLTCAVYGGSGFGYFWSWIRQPPGKCLEWIGEIIYHSGHATNPNPSL KSRVTISLDTSKNQFSLKLNSTAAATAVYYCARGGNSGYIFDYWGQGTLLTVSSGGGGGGG

	08xI2C-scFc	molecule	<p>GSGGGSDVQMTQSPSSLASVGDVRVTITCRTSQYIGRYLNWYQQKPGKAPKVLIIYGASTLQQ GVPFRFSGSGGTDFTLITISLQPEDFASYCQQTYSYTPRTFGQGTKEIKSGGGGSEVQLVE SGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGLTVTVSSGGGGGG GGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFK LAPGTPARFSGSLGGKAALTLSGVQPEDEAEYICVLWYSNRWVFGGKTLTVLGGGGDKTHT CPCPAPPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKHTCPCPAPPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1764	CD70-1.005_C CxI2C-scFc	bispecific HLE molecule	<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFTSYGMHWVRQAPGKCLEWAVAIWYEGSNKYIGES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYCARDNSHYIYGMVDWGQGTITVTVSSGGGGSG GGGGGGGSQSVLTQPPSVSGAPGQRTVTSCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSASLAITGLQAEDEADYICQSYDTLSASVFGCGTRLTVLSSGGGGG EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGLTVTVSSG GGGGGGGGSGGQTVVTQEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYICVLWYSNRWVFGGKTLTVLGGG GDKHTCPCPAPPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGG SGGGGDKTHTCPCPAPPELLGGPSVFLFPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGS FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1765	CD70-1.005xI2C-scFc	bispecific HLE molecule	<p>QVQLVESGGGVVQPGRSLRLSCAASGFTFTSYGMHWVRQAPGKCLEWAVAIWYEGSNKYIGES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYCARDNSHYIYGMVDWGQGTITVTVSSGGGGSG GGGGGGGSQSVLTQPPSVSGAPGQRTVTSCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSASLAITGLQAEDEADYICQSYDTLSASVFGGTRLTVLSSGGGGG</p>

1766	CD70- 1.009_C Cx12C- scFc	bispecific c HLE molecule	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSI SYWAYWGQGLTVTVSSG GGSGGGGGGSQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYCYLVWYSNRWVFGGKTLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGG SGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK GQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGS FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1767	CD70- 1.009x12 C-scFc	bispecific c HLE molecule	QVQLVESGGGVVQPGRSRLRLSCAASGFTFTSTYGMHWVRQAPGKCLEWVAWIWEGSNKYIGES VKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDNSHYIYGMVDVWGQGLTVTVSSGGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRTVTSCTGSSSNIGAGYDVNWYQQLPGTAPKLLIYVNN NRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYCYQSYETLSASVFGCGTRLTLSLGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNYSI SYWAYWGQGLTVTVSSG GGSGGGGGGSQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYCYLVWYSNRWVFGGKTLTVLGGG GDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGG SGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK GQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGS FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

1768	CD70- 76.008xI CCxI2C- scFc	bispecific c HLE molecule	<p>GGSGGGGGGGGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG SDDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG YVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGS FFLYSKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK</p> <p>QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYYSWIRQPPGKCLEWIGIYIYSGSTSYNP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGTTLTVSSGGGGSG GGSGGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQKPKGAPKVLIFAASSL QSGVPSRFSGSGGTDFTLTITSSLPEDFATYCYQSYSTPWTFCGCTKVEKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCYVRHGNFGNSYISYWAYWGQGTTLTVSSGGGG GGSGGGGGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK</p> <p>QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYYSWIRQPPGKCLEWIGIYIYSGSTSYNP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGTTLTVSSGGGGSG GGSGGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQKPKGAPKVLIFAASSL QSGVPSRFSGSGGTDFTLTITSSLPEDFATYCYQSYSTPWTFCGCTKVEKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCYVRHGNFGNSYISYWAYWGQGTTLTVSSGGGG GGSGGGGGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKT</p>
1769	CD70- 76.008xI 2C-scFc	bispecific c HLE molecule	<p>QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYYSWIRQPPGKCLEWIGIYIYSGSTSYNP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGTTLTVSSGGGGSG GGSGGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQKPKGAPKVLIFAASSL QSGVPSRFSGSGGTDFTLTITSSLPEDFATYCYQSYSTPWTFCGCTKVEKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCYVRHGNFGNSYISYWAYWGQGTTLTVSSGGGG GGSGGGGGQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKT</p>

1770	CD70- 5.008_C Cx12C- scFc	bispecific c HLE molecule	HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK
1771	CD70- 5.008x12 C-scFc	bispecific c HLE molecule	QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSSTAAADTAVYCARSGYSYALFDAGQGTLTVTVSSGGGGSG GGGGGGGSDIQMTQSPSSLSASVGRVTISCRASQFIGRYFNWYQQKPKAPKVLIIYAESSL QSGVPSRFSGSGTEFTLTITSSLPEDFATYYCQQSISTPTWTFGCGTKVEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGSYISYWAYWGQTLTVTVSSGGGGSG GGGGGGGSGTQVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCYLVWSNRWVFGGGLTTLVLGGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK

1772	CD70-13D_CCxI2C-scFc_delGK	bispecific HLE molecule	TLPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1773	CD70-13DxI2C-scFc_delGK	bispecific HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSIVSGSGGRPNYAESVKGRFTISRDN SKNTLYIQMNSLRDEDTAVYYCAKVDYSNLYFFDYWGQGTLTVTSSGGGSGGGSGGGSEIVLTQSPGTLSPGEGATLSCRAGQSVRSYLGWYQQPKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGYSPPTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGTLTVTSSGGGGSGGGSGGGQTVVQTQEP SLT VSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPETCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

[illegible]

1776	CD70_6 1- D1D_CC xI2C- scFc_del GK	bispecific c HLE molecule	EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGSSPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTTQEPSTLTVSPGGTTLTTCGSSTGAVTSNYPNWWQQKPGQAPRGLIG TKFLAPGTPARFSGSLGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK
1777	CD70_6 1- D1DxI2 C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGSSPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNFGNSYISYWAYWGQGTLLTVSSGGG SGGGSGGGGQTVVTTQEPSTLTVSPGGTTLTTCGSSTGAVTSNYPNWWQQKPGQAPRGLIG TKFLAPGTPARFSGSLGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK

1778	CD70- 16D_CC xI2C- scFc_del GK	bispecific c HLE molecule	<p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTFYAES</p> <p>VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG</p> <p>GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS</p> <p>RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGCGTKLEIKSGGGGSEVQ</p> <p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV</p> <p>KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG</p> <p>SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG</p> <p>TKFLAPGTPARFSGSLGKKAALTLVGQPEDEAEYCYVLWYSNRWVFGGDKLTVLGGGDK</p> <p>THTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p> <p>NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV</p> <p>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT</p> <p>VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG</p> <p>SDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV</p> <p>EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE</p> <p>PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS</p> <p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1779	CD70- 16DxI2C - scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGRTFYAES</p> <p>VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGSG</p> <p>GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQIRSSYLAWYQQKPGQAPRLLIYGASS</p> <p>RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKLEIKSGGGGSEVQ</p> <p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV</p> <p>KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG</p> <p>SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG</p> <p>TKFLAPGTPARFSGSLGKKAALTLVGQPEDEAEYCYVLWYSNRWVFGGDKLTVLGGGDK</p> <p>THTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p> <p>NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV</p> <p>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT</p> <p>VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG</p> <p>SDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV</p> <p>EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE</p> <p>PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS</p> <p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1780	CD70-	bispecific	<p>EVQLLESGGGLVQSGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATSGSGGRTHYAES</p>

	17D_CC x12C- scFc_del GK	c HLE molecule	VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPGT LSLSPGERAT LSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPFTFGCGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLTLCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKAA LTL SGVQPEDEAEYVCVLWYSNRWVFGG TKLTVLGGGDK THTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPETCVVDVSHEDPEVKFNWYVDGVEVH THTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPETCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPAPEL LGPSVFLFPKPKD TLMISRTPETCVVDVSHEDPEVKFNWYVDGVEVH EVHNAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1781	CD70- 17Dx12C - scFc_del GK	bispecifi c HLE molecule	EVQLLESGGGLVQSGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISGSGGRTHYAES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPGT LSLSPGERAT LSCRASQSVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGG SGGGSGGGGQTVVTQEP SLTVSPGGT VTLTLCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSL LGKAA LTL SGVQPEDEAEYVCVLWYSNRWVFGG TKLTVLGGGDK THTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPETCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPAPEL LGPSVFLFPKPKD TLMISRTPETCVVDVSHEDPEVKFNWYVDGVEVH EVHNAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1782	CD70- 18D_CC x12C-	bispecifi c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSLISGSGGRTHYAES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPGT LSLSPGERAT LSCRASQSVRRSTYLA WYQQKPGQAPRLLIYDASS

		scFc_del GK	<p>RATGIPDRFSGSGGTDFTLTISRLEPEDFAVFCQQYGGSPPTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTSGSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK</p>
1783	CD70- 18DxI2C - scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSLISGSGGRTHYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAHYQKPKGQAPRLLIYDASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVFCQQYGGSPPTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTSGSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK</p>
1784	CD70- 19D_CC xI2C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGGSTFYAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAHYQKPKGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV</p>

1785	CD70- 19Dx12C - scFc_del GK	bispecific c HLE molecule	<p>KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH NAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGSTFYAES VKGRFTISRDN SKNTLSLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH NAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGSTFYAES VKGRFTISRDN SKNTLSLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH NAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGSTFYAES VKGRFTISRDN SKNTLSLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG</p>
1786	CD70- 21D_CC x12C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLSLQMNLSRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGG SGGGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG</p>

1787	CD70- 21Dx12C - scFc_del GK	bispecific c HLE molecule	TKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPEEQYSTYRCVSVLTVLHQDLWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGSEFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK SDKTHTCPPCPAPELLGGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH EVHNAKTKPEEQYSTYRCVSVLTVLHQDLWLNKGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGSEFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK EVQLLESGGGGVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGT LTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSTYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYSCQQYGDLPFTFGPGTKLEIKSGGGGSEVQ LVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHHGFGNSYISYWAYWGQGT LTVTVSSGGGG SGGGSGGGGQTVVTEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPEEQYSTYRCVSVLTVLHQDLWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGSEFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH EVHNAKTKPEEQYSTYRCVSVLTVLHQDLWLNKGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGSEFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK EVQLLESGGGGVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGYTYYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGT LTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYSCQQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHHGFGNSYISYWAYWGQGT LTVTVSSGGGG SGGGSGGGGQTVVTEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
1788	CD70- 22D_CC x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGGVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKCLEWVSAISGSGGYTYYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGT LTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTI SRLEPEDFAVYSCQQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHHGFGNSYISYWAYWGQGT LTVTVSSGGGG SGGGSGGGGQTVVTEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH

1789	CD70- 22DxI2C - scFc_del GK	bispecific c HLE molecule	NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1790	CD70- 24D_CC xI2C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGLAQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSATISGSGGSTFYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKHDYSNYPFDYWGQGTTLTVTSVSSGGGGSGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPFTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNGSYISYWAYWGQGTTLTVTSVSSGGGGTKFLAPGTPARFSGSLGGAALTLGSGVQPEDEAEYCYLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

[illegible]

1793	CD70-25DxI2C - scFc_del GK	bispecific HLE molecule	EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1794	CD70-26D_CCxI2C-scFc_del GK	bispecific HLE molecule	EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

1795	CD70- 26DxI2C - scFc_del GK	bispecific c HLE molecule	<p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGRTFYAES</p> <p>VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG</p> <p>GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSRSSYLAWYQQKPGQAPRLLIYGASS</p> <p>RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKVEIKSGGGGSEVQ</p> <p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV</p> <p>KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG</p> <p>SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTAVTSGNYPNWVQQKPGQAPRGLIG</p> <p>TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGDK</p> <p>THTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p> <p>NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV</p> <p>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLT</p> <p>VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGG</p> <p>SDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG</p> <p>EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE</p> <p>PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYS</p> <p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1796	CD70_1- G2D_CC xI2C- scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGRTFYAES</p> <p>VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSG</p> <p>GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRGNYLAWYQQKPGQAPRLLIYGASS</p> <p>RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGSPFTFGCGTKVEIKSGGGGSEVQ</p> <p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV</p> <p>KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG</p> <p>SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTAVTSGNYPNWVQQKPGQAPRGLIG</p> <p>TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGDK</p> <p>THTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p> <p>NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV</p> <p>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLT</p> <p>VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGG</p> <p>SDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG</p> <p>EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE</p> <p>PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYS</p> <p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1797	CD70_1-	bispecific	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATSGSGGRTFYAES</p>

	G2DxI2 C- scFc_del GK	c HLE molecule	VQGRFTISRDN SKNTLYLQVNSLRAEDTAVYYCARHDYSNYPYFDYWGQGTLLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTL SLSPGERATLSRASQSVRGNYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGYSPFTFGPGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVTVSSGGGG SGGGSGGGSQTVVTQEP SLTVSPGGTVTLT CGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGKAAALTL SGVQPEDEAEYCYVLWYSNRWVFGGKTLTVLGGGGDK THTCPPCPARFSGSLGKAAALTL SGVQPEDEAEYCYVLWYSNRWVFGGKTLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPAPPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1798	CD70- 27D_CC xI2C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKCLEWVS AISGGGGTFFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTL SLSPGERATLSRASQSVIRSNYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGYSSPFTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVTVSSGGGG SGGGSGGGSQTVVTQEP SLTVSPGGTVTLT CGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGKAAALTL SGVQPEDEAEYCYVLWYSNRWVFGGKTLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1799	CD70- 27DxI2C -	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLS CAASGFTFTSYAMSWVRQAPGKLEWVS AISGGGGTFFYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPYFDYWGQGTLLTVTVSSGGGGSG GGSGGGGSEIVLTQSPGTL SLSPGERATLSRASQSVIRSNYLA WYQQKPGQAPRLLIYGASS

	scFc_del GK	RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTSGSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1800	CD70- 28D_CC x12C- scFc_del GK bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKCLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGISPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTSGSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1801	CD70- 28Dx12C - scFc_del GK bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVSLISGSGGRTYYAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQKPGQAPRLLIYGASN RATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGISPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV

1802	CD70- 31D_CC xI2C- scFc_del GK	bispecific c HLE molecule	<p>KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSQTVVTQEPLSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDK THTCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKCLEWVSATSGSGGRAQYAES VQGRFTVSRDNSKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGTDFTLTISRLEPEDFAVYCYQQYSSPPFPFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG GGSGGGGSGTVVTQEPLSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGS</p> <p>DKTHTCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK</p>
1803	CD70- 31DxI2C - scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQSPGKLEWVSATSGSGGRAQYAES VQGRFTVSRDNSKNTLYLQMNLSRAEDTAVYYCAKHDYSNYPYFDYWGGQGLTVTVSSGGGGSG GGSGGGGSEIVLTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGSSSR ATGIPDRFSGSGTDFTLTISRLEPEDFAVYCYQQYSSPPFPFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG GGGGSGGGSQTVVTQEPLSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGS</p> <p>DKTHTCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK</p>

1804	CD70- 32D_CC xI2C- scFc_del GK	bispecific c HLE molecule	<p>KFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRS DYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYHCQQYGSTPTPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGGGGGGQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTV VDSRWQQGNVFCVMHEALHNHYTQKSLSLSPGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK</p>
1805	CD70- 32DxI2C - scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKLEWVSATISGSGGRTFYAES VEGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGGGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRS DYLA WYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYHCQQYGSTPTPTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGGG SGGGGGGGGQTVVTQEP SLTVSPGGT VTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p>

1806	CD70- 37D_CC x12C- scFc_del GK	bispecific c HLE molecule	<p>NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAIGEAGGYYTYAES VKGRFTISRDNKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRRSSYFAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGGTFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p> <p>SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK</p>
1807	CD70- 37Dx12C - scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSAIGEAGGYYTYAES VKGRFTISRDNKNTLSLLMNSLRAEDTAVYYCARHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQGVRRSSYFAWYQQKPGQAPRLLIYGAST RATGIPARFSGSGGTFTLTISRLEPEDFAVYYCQQYGSSPPTFGCGTKVEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYCVLWYSNRWVFGGGLTKLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT</p>

[illegible]

1810	CD70- 39D _{CC} xI2C- scFc _{del} GK	bispecific c HLE molecule	EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK EVQLLESGGGVVQPGRLSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSASISGSGGGTFFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGGLGLTLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYSCQYGDLPFTFGCGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTLTVTVSSGGGG SGGGSGGGGQTVVTVQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGK
1811	CD70- 39DxI2C - scFc _{del} GK	bispecific c HLE molecule	EVQLLESGGGVVQPGRLSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSASISGSGGGTFFYAES VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHDYSNYPFDYWGGLGLTLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAHYQQKPGQAPRLLIYGASS RATGIPDRFSGSGTDFTLTISRLEPEDFAVYSCQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTLTVTVSSGGGG SGGGSGGGGQTVVTVQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVFCSTMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS

1812	CD70- 41D_CC xI2C- scFc_del GK	bispecific c HLE molecule	<p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGMVQPGGSLRLSCAASGFTTSSYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES</p> <p>VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGSGG</p> <p>GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSRSSYLAWYQQKPGQAPRLLIYGASS</p> <p>RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGDLPFTFGCGTKVDIKSGGGGSEVQ</p> <p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV</p> <p>KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG</p> <p>SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTAVTSGNYPNWWVQQKPGQAPRGLIGG</p> <p>TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGDK</p> <p>THTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p> <p>NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV</p> <p>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLT</p> <p>VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG</p> <p>SDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV</p> <p>EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE</p> <p>PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYS</p> <p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1813	CD70- 41DxI2C - scFc_del GK	bispecific c HLE molecule	<p>EVQLLESGGGMVQPGGSLRLSCAASGFTTSSYAMSWVRQAPGKLEWVSATISGSGGRTFYAES</p> <p>VEGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKHDYSNYPFDYWGQGTLLTVSSGGGSGG</p> <p>GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSRSSYLAWYQQKPGQAPRLLIYGASS</p> <p>RATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQQYGDLPFTFGPGTKVDIKSGGGGSEVQ</p> <p>LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV</p> <p>KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVSSGGG</p> <p>SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTAVTSGNYPNWWVQQKPGQAPRGLIGG</p> <p>TKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGDKLTVLGGGDK</p> <p>THTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH</p> <p>NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV</p> <p>YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLT</p> <p>VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG</p> <p>SDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGV</p> <p>EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE</p> <p>PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYS</p> <p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1814	CD70-	bispecific	<p>EVQLLESGGGLVQPGGSLRLSCAASGFTTSTYAMSWVRQAPGKCLEWVSATISGSGGRTFYAES</p>

	42D_CC x12C- scFc_del GK	c HLE molecule	VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPGT LSLSPGERAT LSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDF LTI NRLEPEDFAVYYCQYGS SPPTFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGG SGGGSGGGSQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSL LGKAA LTL SGVQPEDEAEYYCVLWYSNRWVFGG T KLTVLGGGDK THTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH THTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGGSGSGSGSGSGSGSGSGSGSGSGGGG SDKTHTCPAPEL LGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK
1815	CD70- 42Dx12C - scFc_del GK	bispecifi c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKLEWVSLISGSGGRITYYAES VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPGT LSLSPGERAT LSCRASQGVRRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDF LTI NRLEPEDFAVYYCQYGS SPPTFGGGTKVDIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGG SGGGSGGGSQTVVTQEP SLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSL LGKAA LTL SGVQPEDEAEYYCVLWYSNRWVFGG T KLTVLGGGDK THTCPPCPAPEL LGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGGSGSGSGSGSGSGSGSGSGSGSGGGG SDKTHTCPAPEL LGPSVFLFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK
1816	CD70- 43D_CC x12C-	bispecifi c HLE molecule	EVQLLESGGGVVPGRSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGRITYYAES VEGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKHDYSNYPYFDYWGQGT LVTVSSGGGGSG GGSGGGGSEI VLTQSPGT LSLSPGERAT LSCRASQSVRSNYLAWYQQKPGQAPRLLIYGASS

	scFc_del GK	RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYCCQYGGSPPTFGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTAVTSGNPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGKTLTVLGGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1817	CD70- 43DxI2C - scFc_del GK	EVQLLESGGGVVPGRSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGGRTFYAES VEGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKHDYSNYPFDYWGQGTTLTVSSGGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSNYLAWYQKPKGQAPRLLIYGASS RATGIPDRFSGSGGTDFTLTINRLEPEDFAVYCCQYGGSPPTFGGKTKVDIKSGGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLTVSSGGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTAVTSGNPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGVQPEDEAEYCVLWYSNRWVFGGKTLTVLGGGGDK THTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
1818	CD70- 48D_CC xI2C- scFc_del GK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAISGSGGITDFAES VKGRFTISRDNKNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGTTLTVSSGGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWYQKPKGKVPKLLIYAASIL QSGVPSKFSGSGSGTDFTLTISLQPEDFAIYCCQYFAYPITFGCGTRLEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK

			DRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTVLGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK DKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1819	CD70- 48Dx12C - scFc_del GK	bispecific c HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSISGSGGITDFAES VKGRFTISRDNSTNTLYLQMNSLRAEDTAVYFCARHDYSNYFFFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGRVTITCRASQGISNYLAWYQQKPKVPKLLIYAASIL QSGVPSKFSGSGGTFTLTISSLQPEDFAIYCCQQYFAYPIITFGQGRLEIKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGS GGGGGGGSQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGLTVLGGGDKT HTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGS DKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1820	CD70- 53D_CC x12C- scFc_del GK	bispecific c HLE molecule	EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKCLEWVSISGSGGRTFYAES VEGRFTISRDNSTNTLYLQMNSLRAEDTAVYCAKHDYSNYPFDYWGQGLTVTVSSGGGSG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVFCQQYGGSSPPTFGCGTRLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNHLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGG

1821	CD70-53DxI2C - scFc_del GK	bispecific HLE molecule	TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDSHEDPEVKFNWYVDGVEVH NAKTKPEEQYSTYRCVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDSHEDPEVKFNWYVDGV EVHNAKTKPEEQYSTYRCVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EVQLLESGGGMVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSAISGSGGRTFYAES VEGRFTISRDN SKNTLYIQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTTLSLSPGERATLSCRASQSVRSYLAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYFCQQYGSPPFTFGGTRLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDSHEDPEVKFNWYVDGVEVH NAKTKPEEQYSTYRCVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDSHEDPEVKFNWYVDGV EVHNAKTKPEEQYSTYRCVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
1822	CD70-54D_CC xI2C- scFc_del GK	bispecific HLE molecule	EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKCLEWVSAIGSGGRTFYAES VKGRFTISRDN SKNTLYIQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLLTVSSGGGGSG GGSGGGGSEIVLTQSPGTTLSLSPGERATLSCRASQSVRSYVAAYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGDLPFTFGCGTRLEIKSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFGNSYISYWAYWGQGTLLTVSSGGGG SGGGSGGGGQTVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDSHEDPEVKFNWYVDGVEVH

1823	CD70-54DxI2C - scFc_del GK	bispecific HLE molecule	NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK
			EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYAMSWVRQAPGKGLEWVSAIGSGSGSTFYAESVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHDYSNYPFDYWGQGTLTITVSSGGGGSGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSSYVAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTI SRLEPEDFAVYYCQYGDLPFTFGPGRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTLTITVSSGGGGSGGGGGSGGSGQTIVTQEP SLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK
1824	CD70-58D_CCxI2C- scFc_del GK	bispecific HLE molecule	QVQLQESGGPGLVKPSQTLSTLTCTVSGGSISSSYWGWI RQPPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHYEILTGYPDPFDIWGQGTMTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGD RVTITCRASQSISSYLNWYQQKPKAPKLLIYAASNLQSGVSSRFSGSGGTDFLTISSLQPEDFATYYCQQSFSPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTLTITVSSGGGGGGGGGGGSGQTIVTQEP SLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK
			QVQLQESGGPGLVKPSQTLSTLTCTVSGGSISSSYWGWI RQPPGKCLEWIGSIYHSGGTYFNP SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHYEILTGYPDPFDIWGQGTMTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGD RVTITCRASQSISSYLNWYQQKPKAPKLLIYAASNLQSGVSSRFSGSGGTDFLTISSLQPEDFATYYCQQSFSPRTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTLTITVSSGGGGGGGGGGGSGQTIVTQEP SLT VSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK

[illegible]

1827	CD70-62Dx12C - scFc_del GK	bispecific HLE molecule	VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
1828	CD70-23D_CCx12C - scFc_del GK	bispecific HLE molecule	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSSMNWVRQAPGKGLEWVSYISSSGGYIYYAESVKGRFTISRDNKNTLYLQMNRLRAEDTAVYYCARHDYSNAYAFDYWGQGLTVTVSSGGGGSGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVRSSYLAAYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGDLPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNRLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGGSGGGGGSGGSGQTVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN

1829	CD70- 23Dx12C - scFc_del GK	bispecific c HLE molecule	<p>KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYAMSWVRQAPGKLEWVSTISGSGGSTFYAES VKGRFTISRDN SKNTLYLQMNRLRAEDTAVYYCARHDYSNYAYFDYWGQGLTVTVSSGGGSGG GGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSRSSYLAWYQQKPGQAPRLLIYGASS RATGIPDRFSGSGGTFTLTISRLEPEDFAVYCCQYGDLPFTFGPGTKVEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNRLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGG SGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTAVTSGNYPNWVQQKPGQAPRGLIG TKFLAPGTPARFSGSLGKKAALTLVGQPEDEAEYYCVLWYSNRWVFGGGLKTLVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1830	CD70- 55D_CC x12C- scFc_del GK	bispecific c HLE molecule	<p>QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKCLEWVAIVSYEGSNKYIAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGNHNHGMVWQGTITVTSSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITICRASQSISSYLWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQSYSTPFTFGCGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNRLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGSGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTAVTSGNYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGKKAALTLVGQPEDEAEYYCVLWYSNRWVFGGGLKTLVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1831	CD70-	bispecific	<p>QVQLVESGGGVVQPGRSLRLSCAASGFMFSSYGMHWVRQAPGKLEWVAIVSYEGSNKYIAES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGRYGSGNHNHGMVWQGTITVTSSGG GGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITICRASQSISSYLWYQQKPGKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQSYSTPFTFGCGTKVEIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNRLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGSGGGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTAVTSGNYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGKKAALTLVGQPEDEAEYYCVLWYSNRWVFGGGLKTLVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFF LYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>

	55DxI2C - scFc_del GK	c HLE molecule	VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARGRYGSGN YNHGMDVWGQGT TTVTVSSGG GGSGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYA ASSLQSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQSYSTPFTFGPTKVEIKSGGGGS EVQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGT LTVTVSSG GGSGGGGGGSGQTVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGAALTL SGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGEVHNNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1832	CD70- 3.001_C CxI2C- scFc_del GK	bispecific c HLE molecule	QVQLVESGGGVVQPGRSRLRLS CAASGFTFSSYGMHWVRQAPGKCLEWAVTWYDASNKY YGDA VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDLLRGVKGYAMDVGQGT TTVTVSSGGGG SGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSLRRIYLA WYQQKPGQAPRLLIYDV FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQSYSESPFTFGCGTKVDIKSGGGGSE VQLVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGT LTVTVSSGG GGSGGGGGGSGQTVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLGGAALTL SGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGG DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
1833	CD70- 3.001xI2 C-	bispecific c HLE molecule	QVQLVESGGGVVQPGRSRLRLS CAASGFTFSSYGMHWVRQAPGKGLEWAVTWYDASNKY YGDA VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDLLRGVKGYAMDVGQGT TTVTVSSGGGG SGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSLRRIYLA WYQQKPGQAPRLLIYDV

	scFc_del GK	<p>FDRATGIPDRFSGGGSGTDFTLTISRLEPEDFAVYYCQQYSESPFTFGPGTKVDIKSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGLTVTVSSGG GGGGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLI GGTKFLAPGTPARFSGLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGTTKLTVLGGG DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1834	CD70- 4.007_C Cx12C- scFc_del GK	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWI SAYQGYTHYAQK LQGRVTMTTDTSTSTAYMELRLSRDDTAVYYCARDYGGNDY YGMDVWGQGT TTVTVSSGGGGS GGGGGGGGGQS VLTQPPSASGTPGQRVTISCSGSSNIGINYYWYQQLPGTAPKLLIYRSD QRP SGVPDRFSGSKGTSASLALSGLRSEADYYCAAFDESLGVVFGCGTKLT VLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGLTVTVSSG GGGGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGKFLAPGTPARFSGSLGGAALTLSGVQPEDEAEYCVLWYSNRWVFGGTTKLT VLG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1835	CD70- 4.007x12 C- scFc_del GK	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQCLEWMGWI SAYQGYTHYAQK LQGRVTMTTDTSTSTAYMELRLSRDDTAVYYCARDYGGNDY YGMDVWGQGT TTVTVSSGGGGS GGGGGGGGGQS VLTQPPSASGTPGQRVTISCSGSSNIGINYYWYQQLPGTAPKLLIYRSD QRP SGVPDRFSGSKGTSASLALSGLRSEADYYCAAFDESLGVVFGGTTKLT VLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYA</p>

				<p>DSVKDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSG GGSGGGGGSGQTVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGL IGGKFLAPGTPARFSGLLGGKAAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGKTLTVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1836	CD70- 12.013 CCx12C- scFc_del GK	bispecifi c HLE molecule		<p>QAQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAIVWDASNKYYADA VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDREMGSRGDFDYWGQGLTVTVSSGGGGS GGSGGGGGSDIQMTQSPSSLSASVGRVTITCRASQGINNYLAWFQKPGKAPKSLIYAVSI LQSGVPSKFGSGSGTDFTLTISNLQPEDFATYYCQYNYFPFSGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSGQTVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGLLGGKAAALTLGSGVQPEDEAEYCYVLWYSNRWVFGGKTLTVLGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1837	CD70- 12.013xI 2C- scFc_del GK	bispecifi c HLE molecule		<p>QAQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIVWDASNKYYADA VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDREMGSRGDFDYWGQGLTVTVSSGGGGS GGSGGGGGSDIQMTQSPSSLSASVGRVTITCRASQGINNYLAWFQKPGKAPKSLIYAVSI LQSGVPSKFGSGSGTDFTLTISNLQPEDFATYYCQYNYFPFSGCGTKVDIKSGGGGSEVQ LVESGGGLVQPGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNKLKTEDTAVYYCVRHGFNGNSYISYWAYWGQGLTVTVSSGGGG SGGGSGGGSGQTVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGG</p>

1838	CD70- 75.002.0 08_CCxI 2C- scFc_del GK	bispecific c HLE molecule	TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
1839	CD70- 75.002.0 08xI2C- scFc_del GK	bispecific c HLE molecule	QVQLQQWAGALLKPKSETLSLTCAVYGGSFSGFYWISWIRQPPGKCLEWIGEIIYHSGHATNNPSL KSRVTISLDTSKNQFSLKLNSTAAATAVYYCARGGNSGYIFDYWGQGTLLTVSSGGGGSGGG GGGGSDVQMTQSPSSLSASVGDRTITCRTSQYIGRYLNWYQQKPKAPKVLIIYGASTLQQ GVPSRFSGGSGTDFTLTITSLQPEDFAFYCYCQTYSTPRTFGCGTKVEIKSGGGSEVQLVE SGGLVQPGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGNSYISYWAYWGQGTLLTVSSGGGGSGG GGGGGSGTQVVTQEPSTVSPGGTTLTSCGSTGAVTSGNYPNWVQKQKPGQAPRGLIGGTFK LAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHT CPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDK SRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGSDK THTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLT VDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

1840	CD70- 1.005_C Cx12C- scFc_del GK	bispecific HLE molecule	TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGS THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK QVQLVESGGGVVQPGRSLRLSCAASGFTTFSTYGMHWVRQAPGKCLEWVAIVIEWGSNKYYGES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGTITVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSASLAITGLQAEDEADYCYQSYDTLSASVFGCGTRLTIVLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGTITVTVSSG GGSGGGSGGGGSQSVLTQEPSTLTVSPGGTTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLSNRWVFGGGLTIVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGSGGGSGGGSGGGSG GGGSKDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFF LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK QVQLVESGGGVVQPGRSLRLSCAASGFTTFSTYGMHWVRQAPGKLEWVAIVIEWGSNKYYGES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGTITVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSASLAITGLQAEDEADYCYQSYDTLSASVFGGTRLTIVLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGTITVTVSSG GGSGGGSGGGGSQSVLTQEPSTLTVSPGGTTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLSNRWVFGGGLTIVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS
1841	CD70- 1.005x12 C- scFc_del GK	bispecific HLE molecule	TKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGS THTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH NAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK QVQLVESGGGVVQPGRSLRLSCAASGFTTFSTYGMHWVRQAPGKCLEWVAIVIEWGSNKYYGES VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDNSHYYYGMDVWGQGTITVTVSSGGGSG GGSGGGGSQSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYDVNWYQQFPGTAPKLLIYVNN NRPSGVPDRFSGTSASLAITGLQAEDEADYCYQSYDTLSASVFGGTRLTIVLSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGTITVTVSSG GGSGGGSGGGGSQSVLTQEPSTLTVSPGGTTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLSNRWVFGGGLTIVLGGG GDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYS

[illegible]

1844	CD70- 76.008- CCxI2C- scFc_del GK	bispecific c HLE molecule	DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF LYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYVWSWIRQPPGKCLEWIGYIYSGSTSYNP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQQKPKGKAPKVLIFAASSL QSGVPSRFSGSGTDFTLTITSSLPEDFATYCYCQSYSTPWTFCGKVEKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPSTLTVSPGGTTLTTCGSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLYSNRWVFGGKTKLTVLGGGDKT HTCPFCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYVWSWIRQPPGKCLEWIGYIYSGSTSYNP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQQKPKGKAPKVLIFAASSL QSGVPSRFSGSGTDFTLTITSSLPEDFATYCYCQSYSTPWTFCGKVEKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPSTLTVSPGGTTLTTCGSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLYSNRWVFGGKTKLTVLGGGDKT HTCPFCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
1845	CD70- 76.008xI 2C- scFc_del GK	bispecific c HLE molecule	QMQLQESGPGLVKPSSETLSLTCTVSGGSIESGVYVWSWIRQPPGKCLEWIGYIYSGSTSYNP SLKSRLTMSVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDYWGQGLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASLGDRVTITCRASQSVDRYFNWYQQKPKGKAPKVLIFAASSL QSGVPSRFSGSGTDFTLTITSSLPEDFATYCYCQSYSTPWTFCGKVEKSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTQVVTQEPSTLTVSPGGTTLTTCGSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCYVLYSNRWVFGGKTKLTVLGGGDKT HTCPFCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK

1846	CD70- 5.008_C CxI2C- scFc_del GK	bispecific c HLE molecule	<p>LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGQGTLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTVTSRSGQFGRYFNWYQQKPKAPKVLIIYAESSL QSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCQSYSTPWTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTVVTEPSLTVSPGGTVTLTCGSSTGAVTSNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPDSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
1847	CD70- 5.008x12 C- scFc_del GK	bispecific c HLE molecule	<p>QVQLQESGPGLVKPSQTLSTCTVSGDSISGGYYWSWIRQPPGKCLEWIGYIFYSGSTDYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAVYCARSGYSYALFDAGQGTLTVTVSSGGGSG GGSGGGGSDIQMTQSPSSLSASVGDRTVTSRSGQFGRYFNWYQQKPKAPKVLIIYAESSL QSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCQSYSTPWTFGCGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISYWAYWGQGLTVTVSSGGGGS GGSGGGGSGTVVTEPSLTVSPGGTVTLTCGSSTGAVTSNYPNWVQQKPGQAPRGLIGGT KFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGGDKT HTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPDSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGGGGGGGGGGGG DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>

1848	Fc 1 monome r +c/-g	DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSK LTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK
1849	Fc 2 monome r +c/-g/ delGK	DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSK LTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSP
1850	Fc 3 monome r -c/+g	DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSK LTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK
1851	Fc 4 monome r -c/+g/ delGK	DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSK LTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSP
1852	Fc 5 monome r -c/-g	DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSK LTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK
1853	Fc 6 monome r -c/-g/ delGK	DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSK LTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSP
1854	Fc 7 monome r +c/+g	DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSK LTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK
1855	Fc 8 monome r +c/+g/	DKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFFLYSK LTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSP

	delGK	
1856	scFc-1	DKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGKGSGGSGGGSGGGSGGGSGGGSGGG GGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK
1857	scFc-2	DKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGKGSGGSGGGSGGGSGGGSGGGSGGG GGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSP
1858	scFc-3	DKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGKGSGGSGGGSGGGSGGGSGGGSGGG GGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK
1859	scFc-4	DKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGKGSGGSGGGSGGGSGGGSGGGSGGG GGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSP
1860	scFc-5	DKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE

1861		scFc-6		<p>VHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP</p>
1862		scFc-7		<p>DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP</p>
1863		scFc-8		<p>DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP</p>
1864		(G ₄ S) ₄ linker		GGGGGGGGGGGGGGGGGGGG

1865	(G ₄ S) ₅ linker		GGGGGGGGGGGGGGGGGGGGGGGGG	
1866	(G ₄ S) ₆ linker		GGGGGGGGGGGGGGGGGGGGGGGGG	
1867	(G ₄ S) ₇ linker		GGGGGGGGGGGGGGGGGGGGGGGGG	
1868	(G ₄ S) ₈ linker		GGGGGGGGGGGGGGGGGGGGGGGGG	
1869	consensus	VH- CDR1	X ₁ YX ₂ MX ₃	X ₁ is S, T or V, X ₂ is A or S, and X ₃ is S or N
1870	consensus	VH- CDR2	X ₁ I SX ₂ SGGX ₃ X ₄ X ₅ X ₆ AESVX ₇ G	X ₁ is A, Y, V, L, or T, X ₂ is G or S, X ₃ is R, Y, S, G or I, X ₄ is T, I, P, or A, X ₅ is F, Y, N, Q or D, X ₆ is Y or F, and X ₇ is E, K or Q
1871	consensus	VH- CDR3	X ₁ DYSNYX ₂ X ₃ FDY	X ₁ is H, G or V, X ₂ is P, A, L or F, and X ₃ is Y or F
1872	consensus	VL- CDR1	RAX ₁ QX ₂ X ₃ X ₄ X ₅ X ₆ X ₇ LX ₈	X ₁ is S or G, X ₂ is S or G, X ₃ is I or V, X ₄ is R, S or no amino acid, X ₅ is S or G, X ₆ is S, N, T or D, X ₇ is Y or no amino acid, and X ₈ is A or G
1873	consensus	VL- CDR2	X ₁ X ₂ SX ₃ X ₄ X ₅ X ₆	X ₁ is G or A, X ₂ is A or S, X ₃ is S, T, N or I, X ₄ is R or L, X ₅ is A or Q, and X ₆ is T or S
1874	consensus	VL- CDR3	QQYX ₁ X ₂ X ₃ PX ₄ X ₅	X ₁ is G, Y or F, X ₂ is D, S, Y, I or A, X ₃ is L, T, S or Y, X ₄ is F, L, P or I, and X ₅ is T or P
1875	consensus	VH- CDR1	X ₁ YAMS	X ₁ is S, T or V
1876	consensus	VH- CDR2	X ₁ ISGGGGX ₂ X ₃ X ₄ YAESVX ₅ G	X ₁ is A, V, L or T, X ₂ is R, S, or G, X ₃ is T, P or A, X ₄ is F, N, Y or Q, and X ₅ is E, K, or Q
1877	consensus	VH- CDR3	X ₁ DYSNYX ₂ X ₃ FDY	X ₁ is H or V, X ₂ is P, L or A, and X ₃ is Y or F
1878	consensus	VL- CDR1	RAX ₁ QX ₂ X ₃ X ₄ X ₅ X ₆ YLX ₇	X ₁ is S or G, X ₂ is S or G, X ₃ is I or V, X ₄ is R or S, X ₅ is S or G, X ₆ is S, T, N or D, and X ₇ is A or G
1879	consensus	VL- CDR2	AASXLQS	X is T or I

1880		consensus	VL- CDR2	GX ₁ SX ₂ RAT	X ₁ is A or S, and X ₂ is S or N
1881		consensus	VL- CDR3	QQYGX ₁ X ₂ PX ₃ X ₄	X ₁ is D, Y, S or I, X ₂ is L, S or T, X ₃ is F or P, and X ₄ is T or P

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<151> 2015-07-31

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<151> 2016-02-03

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100

105

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Gly Thr Thr Val Thr Val Ser Ser

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Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly

20 25 30

Tyr Asp Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu

35 40 45

Leu Ile Tyr Val Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe

50 55 60

Ser Gly Ser Thr Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser

85 90 95

Leu Ser Ala Ser Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu

100 105 110

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165 170 175

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

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210

215

220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly

225

230

235

240

Thr Arg Leu Thr Val Leu Ser

245

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1

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10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe
165 170 175

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

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala
195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
210 215 220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly
225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu

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Ser Tyr Gly Met His

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Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Phe Ala Asp Ser Val Lys

1 5 10 15

Gly

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Asp Gly Ile Ala Gly Ala Arg Tyr Val Tyr Phe Asp Tyr

1 5 10

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<400> 14

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala

1 5 10

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Ala Ala Ser Ser Leu Gln Gly

1 5

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Gln Gln Tyr Tyr Asn Tyr Pro Phe Thr

1 5

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<400> 17

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Gly Ile Ala Gly Ala Arg Tyr Val Tyr Phe Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

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<400> 18

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Lys Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Thr Val Asp Ile Lys
100 105

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Gly Ile Ala Gly Ala Arg Tyr Val Tyr Phe Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser

130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys

145 150 155 160

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Phe Gln Gln Lys

165 170 175

Pro Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Ala Ser Ser Leu Gln

180

185

190

Gly Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe

195

200

205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr

210

215

220

Cys Gln Gln Tyr Tyr Asn Tyr Pro Phe Thr Phe Gly Pro Gly Thr Thr

225

230

235

240

Val Asp Ile Lys

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Gly Ile Ala Gly Ala Arg Tyr Val Tyr Phe Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Phe Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Ala Ser Ser Leu Gln
180 185 190

Gly Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Tyr Tyr Asn Tyr Pro Phe Thr Phe Gly Pro Gly Thr Thr
225 230 235 240

Val Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
245 250 255

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys

260 265 270

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg

275 280 285

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys

290 295 300

Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe

305 310 315 320

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn

325 330 335

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly

340 345 350

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly

355 360 365

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

370 375 380

Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu

385 390 395 400

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr

405 410 415

Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro

420 425 430

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro

435 440 445

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala

450 455 460

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys

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Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu

485 490 495

Thr Val Leu

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Ser Tyr Gly Met His

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<400> 22

Val Thr Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val Lys

1 5 10 15

Gly

<210> 23

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<400> 23

Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val

1 5 10

<210> 24

<211> 12

<212> PRT

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Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala

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Asp Val Phe Asp Arg Ala Thr

1 5

<210> 26

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Gln Gln Tyr Ser Asp Ser Pro Phe Thr

1 5

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Gln Glu Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100

105

110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Arg Arg Ile

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Asp Val Phe Asp Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Asp Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

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Gln Glu Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln
 165 170 175

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

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp
 195 200 205

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

Tyr Cys Gln Gln Tyr Ser Asp Ser Pro Phe Thr Phe Gly Pro Gly Thr
225 230 235 240

Lys Val Asp Ile Lys
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Gln Glu Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys

145 150 155 160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln

165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Val Phe Asp Arg

180 185 190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp

195 200 205

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr

210 215 220

Tyr Cys Gln Gln Tyr Ser Asp Ser Pro Phe Thr Phe Gly Pro Gly Thr

225 230 235 240

Lys Val Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val

245 250 255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser

260 265 270

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val

275 280 285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser

290 295 300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg

305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met

325 330 335

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His

340 345 350

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln

355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

370 375 380

Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser

385 390 395 400

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser

405 410 415

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys

420 425 430

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala

435 440 445

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala

450 455 460

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr

465 470 475 480

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys

485 490 495

Leu Thr Val Leu

500

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<400> 31

Ser Tyr Gly Ile Ser

1 5

<210> 32

<211> 17

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<400> 32

Trp Ile Ser Ala Tyr Asn Gly Tyr Thr His Tyr Ala Gln Lys Leu Gln

1 5 10 15

Gly

<210> 33

<211> 12

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<400> 33

Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val

1 5 10

<210> 34

<211> 13

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<223> Synthetic peptide

<400> 34

Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr

1 5 10

<210> 35

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 35

Arg Ser Asp Gln Arg Pro Ser

1 5

<210> 36

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 36

Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Val

1 5 10

<210> 37

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 37

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 38

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 38

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn

20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

35 40 45

Ile Tyr Arg Ser Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Leu Ser Gly Leu Arg

65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu

85 90 95

Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105 110

<210> 39

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 39

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro
130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly
145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu
165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro
180 185 190

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

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr
210 215 220

Cys Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Val Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Thr Val Leu

245

<210> 40

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 40

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro
 130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly
145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu
 165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro
 180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Val Phe Gly Gly Gly

225 230 235 240

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465

470

475

480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu

500

<210> 41

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 41

Ser Gly Gly Tyr Tyr Trp Ser

1 5

<210> 42

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 42

Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 43

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 43

Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His

1 5 10

<210> 44

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 44

Arg Ala Ser Gln Phe Ile Gly Arg Tyr Phe Asn

1 5 10

<210> 45

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 45

Ala Glu Ser Ser Leu Gln Ser

1 5

<210> 46

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 46

Gln Gln Ser Tyr Ser Thr Pro Trp Thr

1 5

<210> 47

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 47

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 48

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 48

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Phe Ile Gly Arg Tyr

20 25 30

Phe Asn Trp Tyr Gln Gln Gln Pro Gly Lys Ala Pro Lys Val Leu Ile

35 40 45

Tyr Ala Glu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Arg Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 49

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 49

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

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

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Gln Pro Gly
165 170 175

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Arg Tyr Tyr Cys Gln
210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 50

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 50

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

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

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Gln Pro Gly
165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Arg Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 51

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 51

Ser Gly Gly Tyr Tyr Trp Ser

1 5

<210> 52

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 52

Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 53

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 53

Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His

1 5 10

<210> 54

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 54

Arg Ala Ser Gln Phe Ile Gly Arg Tyr Phe Asn

1 5 10

<210> 55

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 55

Ala Glu Ser Ser Leu Gln Ser

1 5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 56

Gln Gln Ser Tyr Ser Thr Pro Phe Thr

1 5

<210> 57

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 57

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 58

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 58

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Phe Ile Gly Arg Tyr

20 25 30

Phe Asn Trp Tyr Gln Gln Gln Pro Gly Lys Ala Pro Lys Val Leu Ile

35 40 45

Tyr Ala Glu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Arg Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 59

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 59

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Gln Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Arg Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 60

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 60

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Cys Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

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

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Gln Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Arg Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 61

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 61

Ser Tyr Tyr Leu His

1 5

<210> 62

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 62

Ile Val Asp Pro Ser Gly Gly Ser Thr Ser Tyr Asp Gln Lys Phe Gln

1 5 10 15

Gly

<210> 63

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 63

Asp Tyr Gly Asp Tyr Val Phe Asp Tyr

1 5

<210> 64

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 64

Ser Gly Ser Ser Ser Asn Ile Gly Thr Asn Thr Val Asn

1 5 10

<210> 65

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 65

Ile Asn Asn Gln Arg Pro Ser

1 5

<210> 66

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 66

Ala Thr Trp Asp Asp Ser Leu Asn Gly Pro Val

1 5 10

<210> 67

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 67

Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Ile Val Asp Pro Ser Gly Gly Ser Thr Ser Tyr Asp Gln Lys Phe

50 55 60

Gln Gly Arg Phe Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Asp Tyr Val Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 68

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 68

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Thr Asn

20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Gln Leu Leu

35 40 45

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

50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln

65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu

85 90 95

Asn Gly Pro Val Val Gly Cys Gly Thr Lys Leu Thr Val Leu

100 105 110

<210> 69

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 69

Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Ile Val Asp Pro Ser Gly Gly Ser Thr Ser Tyr Asp Gln Lys Phe

50 55 60

Gln Gly Arg Phe Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Asp Tyr Val Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser

130 135 140

Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser

145 150 155 160

Asn Ile Gly Thr Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr

165 170 175

Ala Pro Gln Leu Leu Ile Tyr Ile Asn Asn Gln Arg Pro Ser Gly Val

180

185

190

Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala

195

200

205

Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr

210

215

220

Trp Asp Asp Ser Leu Asn Gly Pro Val Val Gly Cys Gly Thr Lys Leu

225

230

235

240

Thr Val Leu

<210> 70

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 70

Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Ile Val Asp Pro Ser Gly Gly Ser Thr Ser Tyr Asp Gln Lys Phe

50 55 60

Gln Gly Arg Phe Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Asp Tyr Val Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser

130 135 140

Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser

145 150 155 160

Asn Ile Gly Thr Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr

165 170 175

Ala Pro Gln Leu Leu Ile Tyr Ile Asn Asn Gln Arg Pro Ser Gly Val

180 185 190

Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala

195 200 205

Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr

210 215 220

Trp Asp Asp Ser Leu Asn Gly Pro Val Val Gly Cys Gly Thr Lys Leu

225 230 235 240

Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 71

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 71

Ser Tyr Gly Met His

1 5

<210> 72

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 72

Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Phe Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 73

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 73

Asp Gly Ile Ala Gly Ala Arg Tyr Val Tyr Phe Asp Tyr

1 5 10

<210> 74

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 74

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala

1 5 10

<210> 75

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 75

Ala Ala Ser Ser Leu Gln Gly

1 5

<210> 76

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 76

Gln Gln Tyr Tyr Asn Tyr Pro Phe Thr

1 5

<210> 77

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 77

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Gly Ile Ala Gly Ala Arg Tyr Val Tyr Phe Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 78

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 78

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Lys Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Phe

85

90

95

Thr Phe Gly Cys Gly Thr Thr Val Asp Ile Lys

100

105

<210> 79

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 79

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Phe Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ile Ala Gly Ala Arg Tyr Val Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys

145 150 155 160

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Phe Gln Gln Lys

165 170 175

Pro Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Ala Ser Ser Leu Gln

180 185 190

Gly Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe

195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr

210 215 220

Cys Gln Gln Tyr Tyr Asn Tyr Pro Phe Thr Phe Gly Cys Gly Thr Thr

225 230 235 240

Val Asp Ile Lys

<210> 80

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 80

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asp Lys Tyr Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Gly Ile Ala Gly Ala Arg Tyr Val Tyr Phe Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser

130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys

145 150 155 160

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Phe Gln Gln Lys

165 170 175

Pro Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Ala Ser Ser Leu Gln

180 185 190

Gly Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe

195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr

210 215 220

Cys Gln Gln Tyr Tyr Asn Tyr Pro Phe Thr Phe Gly Cys Gly Thr Thr

225 230 235 240

Val Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu

245 250 255

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys

260 265 270

Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg

275 280 285

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys

290 295 300

Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe

305 310 315 320

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn

325 330 335

Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly

340

345

350

Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly

355

360

365

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

370

375

380

Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu

385

390

395

400

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr

405

410

415

Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro

420

425

430

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro

435

440

445

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala

450

455

460

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

Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu
 485 490 495

Thr Val Leu

<210> 81

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 81

Ser Tyr Gly Ile Ser

1 5

<210> 82

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 82

Trp Ile Ser Ala Tyr Asn Gly Tyr Thr His Tyr Ala Gln Lys Leu Gln

1 5 10 15

Gly

<210> 83

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 83

Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val

1 5 10

<210> 84

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 84

Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr

1 5 10

<210> 85

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 85

Arg Ser Asp Gln Arg Pro Ser

1 5

<210> 86

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 86

Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Val

1 5 10

<210> 87

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 87

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 88

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 88

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn

20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

35 40 45

Ile Tyr Arg Ser Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Leu Ser Gly Leu Arg

65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu

85 90 95

Ser Gly Val Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu

100 105 110

<210> 89

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 89

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Val Phe Gly Cys Gly

225 230 235 240

Thr Lys Leu Thr Val Leu

245

<210> 90

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 90

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Val Phe Gly Cys Gly

225 230 235 240

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465

470

475

480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu

500

<210> 91

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 91

Ser Gly Gly Tyr Tyr Trp Ser

1 5

<210> 92

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 92

Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 93

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 93

Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His

1 5 10

<210> 94

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 94

Arg Ala Ser Gln Phe Ile Gly Arg Tyr Phe Asn

1 5 10

<210> 95

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 95

Ala Glu Ser Ser Leu Gln Ser

1 5

<210> 96

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 96

Gln Gln Ser Tyr Ser Thr Pro Trp Thr

1 5

<210> 97

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 97

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 98

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 98

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Phe Ile Gly Arg Tyr

20 25 30

Phe Asn Trp Tyr Gln Gln Gln Pro Gly Lys Ala Pro Lys Val Leu Ile

35 40 45

Tyr Ala Glu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Arg Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 99

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 99

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Gln Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Arg Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 100

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 100

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp His Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Gln Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Arg Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
485 490 495

Leu

<210> 101

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 101

Thr Tyr Gly Met His

1 5

<210> 102

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 102

Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val Lys

1 5 10 15

Gly

<210> 103

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 103

Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val

1 5 10

<210> 104

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 104

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn

1 5 10

<210> 105

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 105

Val Asn Asn Asn Arg Pro Ser

1 5

<210> 106

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 106

Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val

1 5 10

<210> 107

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 107

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 108

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 108

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly

20 25 30

Tyr Asp Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu

35 40 45

Leu Ile Tyr Val Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe

50 55 60

Ser Gly Ser Thr Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Thr Ser

85 90 95

Leu Ser Ala Ser Val Phe Gly Cys Gly Thr Arg Leu Thr Val Leu

100 105 110

<210> 109

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 109

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165 170 175

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

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly

225 230 235 240

Thr Arg Leu Thr Val Leu

245

<210> 110

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 110

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Gly Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165 170 175

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

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly

225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260

265

270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275

280

285

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

290

295

300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305

310

315

320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325

330

335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340

345

350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

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

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu
 500

<210> 111

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 111

Tyr Tyr Gly Met His

1 5

<210> 112

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 112

Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 113

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 113

Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr

1 5 10

<210> 114

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 114

Arg Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala

1 5 10

<210> 115

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 115

Ala Val Ser Ile Leu Gln Ser

1 5

<210> 116

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 116

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser

1 5

<210> 117

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 117

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

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100

105

110

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 118

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 118

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asn Asn Tyr

20

25

30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile

35

40

45

Tyr Ala Val Ser Ile Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Gly Asn Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Phe Tyr Pro Phe

85 90 95

Ser Phe Gly Cys Gly Thr Lys Val Asp Ile Lys

100 105

<210> 119

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 119

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

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro

130 135 140

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

145 150 155 160

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro

165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser

180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Gly Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys

210 215 220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys

<210> 120

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 120

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

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro

130 135 140

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

145 150 155 160

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro

165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser

180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Gly Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys

210 215 220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 121

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 121

Ser Tyr Ala Met Ser

1

5

<210> 122

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 122

Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 123

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 123

Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr

1 5 10

<210> 124

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 124

Arg Ala Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly

1 5 10

<210> 125

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 125

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 126

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 126

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr

1 5

<210> 127

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 127

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 128

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 128

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

1 5 10 15

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

20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 129

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 129

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115	120	125			
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly					
130	135	140			
Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala					
145	150	155	160		
Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro					
	165	170	175		
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr					
	180	185	190		
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr					
	195	200	205		
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys					
	210	215	220		
Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu					
225	230	235	240		

Glu Ile Lys

<210> 130

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 130

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 131

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 131

Ile Tyr Ala Met Ser

1

5

<210> 132

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 132

Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 133

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 133

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 134

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 134

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 135

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 135

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 136

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 136

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 137

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 137

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 138

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 138

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 139

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 139

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 140

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 140

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 141

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 141

Ser Tyr Ala Met Ser

1 5

<210> 142

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 142

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 143

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 143

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 144

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 144

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 145

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 145

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 146

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 146

Gln Gln Tyr Gly Ser Ser Pro Phe Thr

1 5

<210> 147

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 147

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 148

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 148

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85

90

95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 149

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 149

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 150

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 150

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 151

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 151

Ser Tyr Ala Met Ser

1 5

<210> 152

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 152

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 153

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 153

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 154

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 154

Arg Ala Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 155

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 155

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 156

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 156

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 157

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 157

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 158

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 158

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 159

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 159

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 160

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 160

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 161

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 161

Ser Tyr Ala Met Ser

1 5

<210> 162

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 162

Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 163

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 163

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 164

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 164

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 165

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 165

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 166

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 166

Gln Gln Tyr Gly Ser Ser Pro Phe Thr

1 5

<210> 167

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 167

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 168

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 168

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 169

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 169

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 170

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 170

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 171

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 171

Ser Tyr Ala Met Ser

1 5

<210> 172

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 172

Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 173

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 173

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 174

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 174

Arg Ala Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala

1 5 10

<210> 175

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 175

Asp Ala Ser Ser Arg Ala Thr

1 5

<210> 176

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 176

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 177

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 177

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 178

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 178

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Thr

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 179

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 179

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 180

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 180

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 181

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 181

Thr Tyr Ala Met Ser

1 5

<210> 182

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 182

Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 183

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 183

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 184

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 184

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 185

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 185

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 186

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 186

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 187

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 187

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 188

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 188

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 189

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 189

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 190

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 190

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 191

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 191

Thr Tyr Ala Met Ser

1 5

<210> 192

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 192

Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 193

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 193

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 194

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 194

Arg Ala Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala

1 5 10

<210> 195

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 195

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 196

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 196

Gln Gln Tyr Gly Ser Thr Pro Pro Thr

1 5

<210> 197

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 197

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 198

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 198

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Ser Asp

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Leu Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr His Cys Gln Gln Tyr Gly Ser Thr Pro

85

90

95

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 199

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 199

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Leu Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
 180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

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

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 200

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 200

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Leu Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340	345	350	
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr			
355	360	365	
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
370	375	380	
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr			
385	390	395	400
Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly			
405	410	415	
Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly			
420	425	430	
Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly			
435	440	445	
Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu			
450	455	460	

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 201

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 201

Thr Tyr Ala Met Ser

1 5

<210> 202

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 202

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 203

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 203

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 204

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 204

Arg Ala Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala

1 5 10

<210> 205

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 205

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 206

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 206

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 207

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 207

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 208

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 208

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Thr

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 209

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 209

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 210

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 210

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 211

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 211

Ser Tyr Ala Met Ser

1 5

<210> 212

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 212

Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 213

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 213

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 214

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 214

Arg Ala Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 215

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 215

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 216

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 216

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 217

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 217

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 218

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 218

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 219

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 219

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 220

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 220

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275	280	285	
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr			
290	295	300	
Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr			
305	310	315	320
Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn			
	325	330	335
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn			
	340	345	350
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr			
	355	360	365
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
	370	375	380
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr			
385	390	395	400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 221

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 221

Val Tyr Ala Met Ser

1 5

<210> 222

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 222

Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 223

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 223

His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr

1 5 10

<210> 224

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 224

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 225

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 225

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 226

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 226

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 227

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 227

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 228

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 228

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100

105

<210> 229

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 229

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 230

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 230

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 231

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 231

Ser Tyr Ala Met Ser

1 5

<210> 232

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 232

Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 233

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 233

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 234

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 234

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 235

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 235

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 236

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 236

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 237

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 237

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 238

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 238

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 239

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 239

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 240

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 240

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 241

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 241

Ser Tyr Ala Met Ser

1 5

<210> 242

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 242

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 243

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 243

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 244

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 244

Arg Ala Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 245

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 245

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 246

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 246

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 247

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 247

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 248

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 248

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 249

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 249

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 250

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 250

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 251

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 251

Ser Tyr Ala Met Ser

1 5

<210> 252

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 252

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 253

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 253

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 254

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 254

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 255

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 255

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 256

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 256

Gln Gln Tyr Gly Ser Ser Pro Phe Thr

1 5

<210> 257

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 257

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 258

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 258

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 259

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 259

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 260

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 260

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 261

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 261

Thr Tyr Ala Met Ser

1 5

<210> 262

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 262

Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 263

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 263

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 264

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 264

Arg Ala Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 265

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 265

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 266

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 266

Gln Gln Tyr Gly Ser Ser Pro Phe Thr

1 5

<210> 267

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 267

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 268

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 268

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 269

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 269

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 270

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 270

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

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

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 271

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 271

Thr Tyr Ala Met Ser

1 5

<210> 272

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 272

Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 273

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 273

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 274

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 274

Arg Ala Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 275

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 275

Gly Ala Ser Asn Arg Ala Thr

1 5

<210> 276

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 276

Gln Gln Tyr Gly Ile Ser Pro Pro Thr

1 5

<210> 277

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 277

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 278

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 278

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Ile Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 279

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 279

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 280

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 280

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 281

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 281

Ser Tyr Ala Met Ser

1 5

<210> 282

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 282

Val Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Gly Lys

1 5 10 15

Gly

<210> 283

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 283

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 284

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 284

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 285

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 285

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 286

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 286

Glu Gln Tyr Gly Asn Ser Pro Pro Thr

1 5

<210> 287

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 287

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Ala Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Gly

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 288

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 288

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Glu Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Glu Gln Tyr Gly Asn Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 289

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 289

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Ala Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Gly

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Phe Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Glu Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Glu Gln Tyr Gly Asn Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 290

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 290

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Ala Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Gly

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Phe Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Glu Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Glu Gln Tyr Gly Asn Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
 355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 291

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 291

Thr Tyr Ala Met Ser

1 5

<210> 292

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 292

Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 293

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 293

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 294

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 294

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 295

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 295

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 296

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 296

Gln Gln Tyr Gly Ser Ser Pro Pro Pro

1 5

<210> 297

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 297

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 298

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 298

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Pro Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100

105

<210> 299

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 299

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 300

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 300

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 301

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 301

Ser Tyr Ala Met Ser

1 5

<210> 302

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 302

Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val Gln

1 5 10 15

Gly

<210> 303

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 303

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 304

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 304

Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala

1 5 10

<210> 305

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 305

Gly Ser Ser Ser Arg Ala Thr

1 5

<210> 306

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 306

Gln Gln Tyr Gly Ser Ser Pro Pro Pro

1 5

<210> 307

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 307

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 308

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 308

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn

20

25

30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile

35

40

45

Tyr Gly Ser Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro

65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Pro

85 90 95

Pro Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 309

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 309

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

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

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180

185

190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210

215

220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val Glu

225

230

235

240

Ile Lys

<210> 310

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 310

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130

135

140

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

145

150

155

160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180

185

190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210

215

220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val Glu

225

230

235

240

Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260

265

270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290

295

300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305

310

315

320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325

330

335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 311

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 311

Ser Tyr Ala Met Ser

1 5

<210> 312

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 312

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 313

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 313

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 314

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 314

Arg Ala Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala

1 5 10

<210> 315

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 315

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 316

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 316

Gln Gln Tyr Gly Ser Thr Pro Pro Thr

1 5

<210> 317

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 317

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 318

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 318

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Ser Asp

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr His Cys Gln Gln Tyr Gly Ser Thr Pro

85

90

95

Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100

105

<210> 319

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 319

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210

215

220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 320

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 320

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 321

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 321

Thr Tyr Ala Met Ser

1 5

<210> 322

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 322

Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Met

1 5 10 15

Gly

<210> 323

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 323

His Asp Tyr Ser Asn Tyr Ala Phe Phe Asp Tyr

1 5 10

<210> 324

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 324

Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala

1 5 10

<210> 325

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 325

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 326

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 326

Gln Gln Tyr Tyr Ser Thr Pro Phe Thr

1 5

<210> 327

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 327

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50

55

60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Phe Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 328

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 328

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile

35 40 45

Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala

65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe

85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 329

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 329

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

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

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu
225 230 235 240

Ile Lys

<210> 330

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 330

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

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

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
210 215 220

Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420	425	430	
Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr			
435	440	445	
Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr			
450	455	460	
Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu			
465	470	475	480
Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val			
485	490	495	

Leu

<210> 331

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 331

Thr Tyr Ala Met Ser

1 5

<210> 332

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 332

Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Met

1 5 10 15

Gly

<210> 333

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 333

His Asp Tyr Ser Asn Tyr Ala Phe Phe Asp Tyr

1 5 10

<210> 334

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 334

Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala

1 5 10

<210> 335

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 335

Gly Ala Ser Thr Arg Ala Thr

1 5

<210> 336

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 336

Gln Gln Tyr Tyr Ser Thr Pro Phe Thr

1 5

<210> 337

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 337

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val
50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Phe Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 338

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 338

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile

35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Ala Ile Ser Arg Leu Glu Pro

65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe

85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100

105

<210> 339

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 339

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50

55

60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

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

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly

180 185 190

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
195 200 205

Ala Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
210 215 220

Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys

<210> 340

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 340

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 165 170 175

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

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
 195 200 205

Ala Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
 210 215 220

Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
 260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 341

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 341

Thr Tyr Ala Met Ser

1 5

<210> 342

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 342

Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 343

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 343

His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro

1 5 10

<210> 344

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 344

Arg Ala Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala

1 5 10

<210> 345

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 345

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 346

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 346

Gln Gln Phe Gly Ser Ser Pro Phe Thr

1 5

<210> 347

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 347

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Ser His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 348

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 348

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ala

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 349

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 349

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Ser His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Phe Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 350

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 350

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Ser His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Phe Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 351

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 351

Ser Tyr Ala Met Ser

1

5

<210> 352

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 352

Ala Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 353

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 353

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 354

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 354

Arg Ala Ser Gln Ser Val Arg Gly Ser Tyr Leu Ala

1 5 10

<210> 355

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 355

Ser Ala Ser Ser Arg Ala Thr

1 5

<210> 356

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 356

Gln Gln Tyr Gly Asp Ser Pro Phe Thr

1 5

<210> 357

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 357

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 358

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 358

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

1

5

10

15

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

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Ser Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Ser Pro

85

90

95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100

105

<210> 359

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 359

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Gly Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 360

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 360

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 361

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 361

Ser Tyr Ala Met Ser

1

5

<210> 362

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 362

Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 363

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 363

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 364

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 364

Arg Ala Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala

1 5 10

<210> 365

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 365

Gly Ala Ser Thr Arg Ala Thr

1 5

<210> 366

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 366

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 367

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 367

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65

70

75

80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 368

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 368

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

1 5 10 15

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

20 25 30

Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

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

100 105

<210> 369

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 369

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 370

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 370

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65

70

75

80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 371

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 371

Ser Tyr Ala Met Ser

1 5

<210> 372

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 372

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 373

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 373

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 374

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 374

Arg Ala Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 375

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 375

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 376

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 376

Gln Gln Tyr Gly Ser Ser Pro Pro Ser

1 5

<210> 377

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 377

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 378

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 378

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100

105

<210> 379

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 379

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 380

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 380

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 381

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 381

Ser Tyr Ala Met Ser

1 5

<210> 382

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 382

Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 383

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 383

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 384

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 384

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 385

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 385

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 386

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 386

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 387

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 387

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 388

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 388

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 389

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 389

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 390

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 390

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 391

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 391

Ser Tyr Ala Met Ser

1 5

<210> 392

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 392

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 393

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 393

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 394

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 394

Arg Ala Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 395

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 395

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 396

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 396

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 397

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 397

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 398

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 398

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

100

105

<210> 399

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 399

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Asp Ile Lys

<210> 400

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 400

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 401

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 401

Ser Tyr Ala Met Ser

1 5

<210> 402

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 402

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 403

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 403

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 404

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 404

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 405

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 405

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 406

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 406

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 407

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 407

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 408

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 408

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

100 105

<210> 409

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 409

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Asp Ile Lys

<210> 410

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 410

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 411

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 411

Thr Tyr Ala Met Ser

1 5

<210> 412

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 412

Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 413

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 413

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 414

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 414

Arg Ala Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 415

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 415

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 416

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 416

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 417

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 417

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 418

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 418

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

1 5 10 15

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

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys

100 105

<210> 419

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 419

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180	185	190
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr		
195	200	205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys		
210	215	220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val			
225	230	235	240

Asp Ile Lys

<210> 420
 <211> 498
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 420

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 421

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 421

Ser Tyr Ala Met Ser

1 5

<210> 422

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 422

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 423

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 423

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 424

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 424

Arg Ala Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 425

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 425

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 426

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 426

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 427

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 427

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 428

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 428

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys

100 105

<210> 429

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 429

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Asp Ile Lys

<210> 430

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 430

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100	105	110	
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly			
115	120	125	
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly			
130	135	140	
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala			
145	150	155	160
Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro			
165	170	175	
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr			
180	185	190	
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr			
195	200	205	
Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys			
210	215	220	

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 431

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 431

Ser Tyr Ala Met Ser

1

5

<210> 432

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 432

Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 433

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 433

His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr

1 5 10

<210> 434

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 434

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn

1 5 10

<210> 435

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 435

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 436

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 436

Gln Gln Ser Tyr Ile Ser Pro Pro Thr

1 5

<210> 437

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 437

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 438

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 438

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Ser Gly Lys Ala Pro Glu Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Ser Pro Pro

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 439

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 439

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

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

Ile Lys

<210> 440

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 440

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Ser Gly

165 170 175

Lys Ala Pro Glu Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ile Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 441

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 441

Ser Tyr Ala Met Ser

1

5

<210> 442

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 442

Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 443

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 443

His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr

1 5 10

<210> 444

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 444

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 445

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 445

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 446

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 446

Gln Gln Ser Tyr Ile Ser Pro Pro Thr

1 5

<210> 447

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 447

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 448

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 448

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Ser Pro Pro

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 449

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 449

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ile Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu

225

230

235

240

Ile Lys

<210> 450

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 450

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ile Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu

225

230

235

240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260

265

270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 451

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 451

Ser Tyr Ala Met Ser

1 5

<210> 452

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 452

Val Ile Ser Gly Ser Gly Gly Arg Thr Asp Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 453

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 453

His Asp Tyr Ser Asn Arg Phe Tyr Phe Asp Tyr

1 5 10

<210> 454

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 454

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 455

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 455

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 456

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 456

Gln Gln Ser Tyr Ser Ala Pro Pro Thr

1 5

<210> 457

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 457

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Thr Asp Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Arg Phe Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 458

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 458

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Pro

85

90

95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100

105

<210> 459

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 459

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Val Ile Ser Gly Ser Gly Gly Arg Thr Asp Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Arg Phe Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ser Ala Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu

225

230

235

240

Ile Lys

<210> 460

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 460

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Thr Asp Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Arg Phe Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

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

145

150

155

160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ser Ala Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu

225

230

235

240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260

265

270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290

295

300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305

310

315

320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325

330

335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
 405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
 420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
 435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
 450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 485 490 495

Leu

<210> 461

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 461

Ser Tyr Ala Met Ser

1 5

<210> 462

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 462

Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 463

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 463

His Asp Tyr Ser Asn Arg Tyr Tyr Phe Asp Tyr

1 5 10

<210> 464

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 464

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 465

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 465

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 466

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 466

Gln Gln Ser Tyr Ser Thr Pro Leu Thr

1 5

<210> 467

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 467

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Arg Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 468

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 468

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20

25

30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu

85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 469

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 469

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Arg Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 470

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 470

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Arg Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
 260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
 275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
 290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
 325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
 340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 471

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 471

Ser Tyr Ala Met Ser

1 5

<210> 472

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 472

Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 473

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 473

His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr

1 5 10

<210> 474

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 474

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala

1 5 10

<210> 475

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 475

Ala Ala Ser Ile Leu Gln Ser

1 5

<210> 476

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 476

Gln Gln Tyr Phe Ala Tyr Pro Ile Thr

1 5

<210> 477

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 477

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 478

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 478

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Phe Ala Tyr Pro Ile

85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys

100 105

<210> 479

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 479

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

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

145

150

155

160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180

185

190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210

215

220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu

225

230

235

240

Ile Lys

<210> 480

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 480

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln
210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 481

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 481

Ser Tyr Ala Met Ser

1 5

<210> 482

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 482

Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 483

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 483

His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr

1 5 10

<210> 484

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 484

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 485

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 485

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 486

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 486

Gln Gln Ser Tyr Ser Thr Pro Ile Thr

1 5

<210> 487

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 487

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Ser Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 488

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 488

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Ile

85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys

100 105

<210> 489

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 489

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Ser Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145

150

155

160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu

225

230

235

240

Ile Lys

<210> 490

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 490

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Ser Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

600

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 491

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 491

Thr Tyr Ala Met Ser

1 5

<210> 492

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 492

Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 493

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 493

His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro

1 5 10

<210> 494

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 494

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 495

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 495

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 496

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 496

Gln Gln Ser Tyr Ser Thr Pro Phe Thr

1 5

<210> 497

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 497

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Ser His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 498

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 498

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe

85

90

95

Thr Phe Gly Pro Gly Thr Arg Leu Glu Ile Lys

100

105

<210> 499

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 499

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Ser His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu Glu

225

230

235

240

Ile Lys

<210> 500

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 500

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Ser His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

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

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 501

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 501

Thr Asp Gly Tyr Tyr Trp Ser

1 5

<210> 502

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 502

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

1 5 10 15

<210> 503

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 503

Gly Ile Gly Leu Gly Phe Glu Tyr

1 5

<210> 504

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 504

Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His

1 5 10

<210> 505

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 505

Asp Asp Ser Asp Arg Pro Ser

1 5

<210> 506

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 506

Gln Val Trp Asp Arg Ser Ser Asp Gln Asp Val Val

1 5 10

<210> 507

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 507

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Gly Ile Gly Leu Gly Phe Glu Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 508

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 508

Ser Tyr Val Leu Thr Gln Leu Thr Ser Val Ser Val Ala Pro Gly Gln

1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val

20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr

35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp Arg Ser Ser Asp Gln

85 90 95

Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 509

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 509

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35

40

45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser

50

55

60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65

70

75

80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85

90

95

Cys Ala Arg Gly Ile Gly Leu Gly Phe Glu Tyr Trp Gly Gln Gly Thr

100

105

110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115

120

125

Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Leu Thr Ser Val Ser

130

135

140

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

145

150

155

160

Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
165 170 175

Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu
180 185 190

Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
195 200 205

Arg Val Glu Ala Gly Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp
210 215 220

Arg Ser Ser Asp Gln Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr
225 230 235 240

Val Leu

<210> 510

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 510

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Gly Ile Gly Leu Gly Phe Glu Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Leu Thr Ser Val Ser
130 135 140

Val Ala Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile
145 150 155 160

Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
165 170 175

Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu
180 185 190

Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
195 200 205

Arg Val Glu Ala Gly Asp Glu Ala Asp Phe Tyr Cys Gln Val Trp Asp
210 215 220

Arg Ser Ser Asp Gln Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr
225 230 235 240

Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 511

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 511

Thr Asp Gly Tyr Tyr Trp Ser

1

5

<210> 512

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 512

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

1 5 10 15

<210> 513

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 513

Gly Ile Gly Leu Gly Phe Glu Tyr

1 5

<210> 514

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 514

Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His

1 5 10

<210> 515

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 515

Asp Asp Ser Asp Arg Pro Ser

1 5

<210> 516

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 516

Gln Val Trp Asp Arg Ser Ser Asp Gln Asp Val Val

1 5 10

<210> 517

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 517

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Gly Ile Gly Leu Gly Phe Glu Tyr Trp Gly Gln Gly Thr

100

105

110

Leu Val Thr Val Ser Ser

115

<210> 518

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 518

Ser Tyr Val Leu Thr Gln Leu Ser Ser Val Ser Val Ala Pro Gly Gln

1

5

10

15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val

20

25

30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr

35

40

45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50

55

60

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

65

70

75

80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg Ser Ser Asp Gln

85

90

95

Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

105

<210> 519

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 519

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1

5

10

15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Gly Ile Gly Leu Gly Phe Glu Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Leu Ser Ser Val Ser

130 135 140

Val Ala Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile
145 150 155 160

Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 165 170 175

Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu
 180 185 190

Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
 195 200 205

Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp
 210 215 220

Arg Ser Ser Asp Gln Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr
 225 230 235 240

Val Leu

<210> 520

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 520

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Gly Ile Gly Leu Gly Phe Glu Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Leu Ser Ser Val Ser
130 135 140

Val Ala Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile
145 150 155 160

Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
165 170 175

Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu
180 185 190

Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
195 200 205

Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp
210 215 220

Arg Ser Ser Asp Gln Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr

225 230 235 240

Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 521

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 521

Ser Tyr Ala Met Ser

1 5

<210> 522

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 522

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 523

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 523

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 524

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 524

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 525

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 525

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 526

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 526

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 527

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 527

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 528

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 528

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Pro Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 529

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 529

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Arg Leu
225 230 235 240

Glu Ile Lys

<210> 530

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 530

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 531

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 531

Ile Tyr Ala Met Ser

1 5

<210> 532

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 532

Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 533

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 533

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 534

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 534

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Val Ala

1 5 10

<210> 535

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 535

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 536

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 536

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 537

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 537

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 538

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 538

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

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

100 105

<210> 539

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 539

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys

<210> 540

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 540

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275	280	285			
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr					
290	295	300			
Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr					
305	310	315	320		
Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn					
	325	330	335		
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn					
	340	345	350		
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr					
	355	360	365		
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser					
	370	375	380		
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr					
385	390	395	400		

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 541

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 541

Ser Tyr Gly Met His

1 5

<210> 542

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 542

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 543

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 543

Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp Val

1 5 10 15

<210> 544

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 544

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 545

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 545

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 546

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 546

Gln Gln Ser Tyr Ser Thr Pro Phe Thr

1 5

<210> 547

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 547

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 548

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 548

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe

85

90

95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100

105

<210> 549

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 549

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130

135

140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145

150

155

160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165

170

175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly

225 230 235 240

Thr Lys Val Glu Ile Lys

245

<210> 550

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 550

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu

500

<210> 551

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 551

Ser Tyr Gly Met His

1 5

<210> 552

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 552

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 553

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 553

Gly Arg Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp Val

1 5 10 15

<210> 554

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 554

Arg Ala Ser Gln Ser Ile Phe Asp Tyr Leu Asn

1 5 10

<210> 555

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 555

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 556

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 556

Gln Gln Ser Tyr Ser Thr Pro Leu Thr

1 5

<210> 557

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 557

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 558

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 558

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Phe Asp Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu

85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 559

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 559

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Phe Asp Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Phe Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly

225 230 235 240

Thr Lys Leu Glu Ile Lys

245

<210> 560

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 560

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130

135

140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145

150

155

160

Thr Cys Arg Ala Ser Gln Ser Ile Phe Asp Tyr Leu Asn Trp Tyr Gln

165

170

175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180

185

190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Phe Gly Thr

195

200

205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly

225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340

345

350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385

390

395

400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405

410

415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420

425

430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu
 500

<210> 561

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 561

Ser Tyr Gly Met His

1 5

<210> 562

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 562

Val Ile Trp Tyr Asp Gly Ser Ser Glu Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 563

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 563

Asp Asn Ser Tyr Asn Tyr Tyr Gly Met Asp Val

1 5 10

<210> 564

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 564

Thr Gly Ser Ser Ser Asn Ile Gly Ala Ala Tyr Asp Val His

1 5 10

<210> 565

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 565

Val Asn Ser His Arg Pro Pro

1 5

<210> 566

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 566

Leu Ser Tyr Asp Asn Ser Leu Ser Gly Ser Val

1 5 10

<210> 567

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 567

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Ser Glu Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser Tyr Asn Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 568

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 568

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Ala

20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu

35 40 45

Leu Ile Tyr Val Asn Ser His Arg Pro Pro Gly Val Pro Asp Arg Phe

50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Leu Ser Tyr Asp Asn Ser

85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105 110

<210> 569

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 569

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Ser Glu Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser Tyr Asn Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Ala Tyr Asp Val His Trp Tyr Gln Gln Phe

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Ser His Arg Pro

180 185 190

Pro Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Leu Ser Tyr Asp Asn Ser Leu Ser Gly Ser Val Phe Gly Gly Gly

225 230 235 240

Thr Lys Leu Thr Val Leu

245

<210> 570

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 570

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Ser Glu Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser Tyr Asn Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Ala Tyr Asp Val His Trp Tyr Gln Gln Phe

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Ser His Arg Pro

180 185 190

Pro Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Leu Ser Tyr Asp Asn Ser Leu Ser Gly Ser Val Phe Gly Gly Gly

225 230 235 240

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465

470

475

480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu

500

<210> 571

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 571

Ser Ser Ser Tyr Tyr Trp Gly

1 5

<210> 572

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 572

Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 573

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 573

His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe Asp Ile

1 5 10 15

<210> 574

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 574

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 575

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 575

Ala Ala Ser Asn Leu Gln Ser

1 5

<210> 576

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 576

Gln Gln Ser Phe Ser Ser Pro Arg Thr

1 5

<210> 577

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 577

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

115 120 125

<210> 578

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 578

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 579

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 579

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Gln

225 230 235 240

Gly Thr Lys Val Glu Ile Lys

245

<210> 580

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 580

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Gln

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

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

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340 345 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu

385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly

405 410 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
420 425 430

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

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
450 455 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465 470 475 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
485 490 495

Thr Lys Leu Thr Val Leu
500

<210> 581

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 581

Gly Phe Tyr Trp Ser

1 5

<210> 582

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 582

Glu Ile Asp His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 583

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 583

Asn Gly Tyr Ser Gly Tyr Leu Phe Asp Tyr

1 5 10

<210> 584

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 584

Arg Ala Ser Gln Ile Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 585

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 585

Gly Ala Ser Ser Met Gln Ser

1 5

<210> 586

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 586

Gln Gln Ser Tyr Ser Ile Pro Arg Thr

1 5

<210> 587

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 587

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Asp Gly Ser Val Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Glu Ile Asp His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asn Gly Tyr Ser Gly Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 588

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 588

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ile Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile

35 40 45

Tyr Gly Ala Ser Ser Met Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Arg

85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 589

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 589

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Asp Gly Ser Val Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Glu Ile Asp His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asn Gly Tyr Ser Gly Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu

130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln

145 150 155 160

Ile Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala

165 170 175

Pro Lys Val Leu Ile Tyr Gly Ala Ser Ser Met Gln Ser Gly Val Pro

180 185 190

Ser Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile

195 200 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser

210 215 220

Tyr Ser Ile Pro Arg Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

225 230 235 240

<210> 590

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 590

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Asp Gly Ser Val Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Glu Ile Asp His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys

50

55

60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

65

70

75

80

Lys Leu Ser Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala

85

90

95

Arg Asn Gly Tyr Ser Gly Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr

100

105

110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115

120

125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu

130

135

140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln

145

150

155

160

Ile Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala

165 170 175

Pro Lys Val Leu Ile Tyr Gly Ala Ser Ser Met Gln Ser Gly Val Pro

180 185 190

Ser Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile

195 200 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser

210 215 220

Tyr Ser Ile Pro Arg Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

225 230 235 240

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly

245 250 255

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

260 265 270

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly

275 280 285

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr

290 295 300

Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg

305 310 315 320

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr

325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn

340 345 350

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr

355 360 365

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

370 375 380

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro

385 390 395 400

Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr

405 410 415

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
420 425 430

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala
435 440 445

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
450 455 460

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr
465 470 475 480

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

<210> 591

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 591

Thr Tyr Tyr Trp Ser

1 5

<210> 592

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 592

Arg Ile Tyr Pro Thr Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 593

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 593

Asp Arg Arg Phe Leu Glu Pro Ser Tyr Tyr Tyr Tyr Tyr Gly Met Asp

1 5 10 15

Val

<210> 594

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 594

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp

1 5 10 15

<210> 595

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 595

Leu Gly Ser Asn Arg Ala Ser

1 5

<210> 596

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 596

Met Gln Gly Leu Arg Thr Pro Phe Thr

1 5

<210> 597

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 597

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Thr Tyr

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Arg Ile Tyr Pro Thr Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asp Arg Arg Phe Leu Glu Pro Ser Tyr Tyr Tyr Tyr Tyr Gly Met

100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120 125

<210> 598

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 598

Asp Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser

20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly

85 90 95

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

100 105 110

<210> 599

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 599

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Thr Tyr

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Arg Ile Tyr Pro Thr Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asp Arg Arg Phe Leu Glu Pro Ser Tyr Tyr Tyr Tyr Tyr Gly Met

100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu

130 135 140

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

145 150 155 160

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn

165 170 175

Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu

180 185 190

Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser

195 200 205

Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu

210 215 220

Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Arg Thr Pro

225 230 235 240

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

245 250

<210> 600

<211> 507

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 600

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Thr Tyr

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Arg Ile Tyr Pro Thr Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asp Arg Arg Phe Leu Glu Pro Ser Tyr Tyr Tyr Tyr Tyr Gly Met

100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu

130 135 140

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

145 150 155 160

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn

165 170 175

Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu

180 185 190

Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser

195 200 205

Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu

210 215 220

Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Arg Thr Pro

225 230 235 240

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly

245 250 255

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro

260 265 270

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn

275

280

285

Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu

290

295

300

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr

305

310

315

320

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys

325

330

335

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala

340

345

350

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser

355

360

365

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly

370

375

380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr

385

390

395

400

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val

405

410

415

Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr

420

425

430

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile

435

440

445

Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly

450

455

460

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro

465

470

475

480

Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp

485

490

495

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

500

505

<210> 601

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 601

Ser Tyr Ala Met Ser

1 5

<210> 602

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 602

Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 603

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 603

His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr

1 5 10

<210> 604

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 604

Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Asn

1 5 10

<210> 605

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 605

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 606

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 606

Gln Gln Ser Tyr Ile Ile Pro Pro Thr

1 5

<210> 607

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 607

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 608

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 608

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr

20

25

30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Ser Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Ile Pro Pro

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys

100 105

<210> 609

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 609

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Leu Leu Ile Ser Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ile Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp

225 230 235 240

Ile Lys

<210> 610

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 610

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Leu Leu Ile Ser Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ile Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
485 490 495

Leu

<210> 611

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 611

Ser Tyr Ser Met Asn

1 5

<210> 612

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 612

Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 613

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 613

Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr

1 5 10

<210> 614

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 614

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala

1 5 10

<210> 615

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 615

Ala Ala Ser Thr Leu Gln Ser

1 5

<210> 616

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 616

Gln Gln Tyr Tyr Ser Thr Pro Leu Thr

1 5

<210> 617

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 617

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85

90

95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 618

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 618

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20

25

30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala

65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu

85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 619

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 619

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 620

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 620

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 621

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 621

Thr Tyr Thr Met Asn

1 5

<210> 622

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 622

Ser Ile Ser Ser Ser Ser Gly Tyr Ile Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 623

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 623

Gly Asp Tyr Ser Asn Tyr Leu Tyr Phe Asp Leu

1 5 10

<210> 624

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 624

Arg Ala Ser Gln Ser Phe Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 625

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 625

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 626

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 626

Gln Leu Tyr Gly Ser Leu Pro Ile Thr

1 5

<210> 627

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 627

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser Thr Tyr

20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ser Ser Ser Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Gly Asp Tyr Ser Asn Tyr Leu Tyr Phe Asp Leu Trp Gly Arg

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 628

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 628

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Phe Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile His Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Leu Tyr Gly Ser Leu Pro

85 90 95

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

100 105

<210> 629

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 629

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser Thr Tyr

20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ser Ser Ser Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Asp Tyr Ser Asn Tyr Leu Tyr Phe Asp Leu Trp Gly Arg

100	105	110	
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly			
115	120	125	
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly			
130	135	140	
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala			
145	150	155	160
Ser Gln Ser Phe Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro			
165	170	175	
Gly Gln Ala Pro Arg Leu Leu Ile His Gly Ala Ser Ser Arg Ala Thr			
180	185	190	
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr			
195	200	205	
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys			
210	215	220	

Gln Leu Tyr Gly Ser Leu Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys

<210> 630

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 630

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Phe Ser Thr Tyr

20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ser Ser Ser Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Asp Tyr Ser Asn Tyr Leu Tyr Phe Asp Leu Trp Gly Arg

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Phe Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile His Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Leu Tyr Gly Ser Leu Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
 355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 631

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 631

Val Tyr Ala Met Ser

1 5

<210> 632

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 632

Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 633

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 633

His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr

1 5 10

<210> 634

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 634

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 635

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 635

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 636

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 636

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 637

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 637

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 638

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 638

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 639

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 639

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 640

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 640

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 641

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 641

Thr Tyr Ala Met Ser

1 5

<210> 642

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 642

Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val Glu

1 5 10 15

Gly

<210> 643

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 643

His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro

1 5 10

<210> 644

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 644

Arg Ala Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala

1 5 10

<210> 645

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 645

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 646

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 646

Gln Gln Phe Gly Ser Ser Pro Phe Thr

1 5

<210> 647

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 647

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Asp Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Ser His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 648

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 648

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ala

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 649

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 649

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Asp Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Ser His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Phe Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 650

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 650

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Asp Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Ser His Asp Tyr Ser Asn Tyr Ala Trp Phe Asp Pro Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Phe Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 651

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 651

Ser Tyr Ala Met Ser

1 5

<210> 652

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 652

Ala Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 653

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 653

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 654

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 654

Arg Ala Ser Gln Ser Val Arg Gly Ser Tyr Leu Ala

1 5 10

<210> 655

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 655

Ser Ala Ser Ser Arg Ala Thr

1 5

<210> 656

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 656

Gln Gln Tyr Gly Asp Ser Pro Phe Thr

1 5

<210> 657

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 657

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 658

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 658

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

1

5

10

15

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

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Ser Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Ser Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 659

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 659

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Gly Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 660

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 660

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Gly Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ser Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 661

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 661

Ser Tyr Ala Met Ser

1 5

<210> 662

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 662

Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 663

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 663

His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr

1 5 10

<210> 664

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 664

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn

1 5 10

<210> 665

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 665

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 666

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 666

Gln Gln Ser Tyr Ile Ser Pro Pro Thr

1 5

<210> 667

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 667

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 668

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 668

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Ser Gly Lys Ala Pro Glu Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Ser Pro Pro

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 669

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 669

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Ser Gly

165 170 175

Lys Ala Pro Glu Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu
225 230 235 240

Ile Lys

<210> 670

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 670

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Ser Gly

165 170 175

Lys Ala Pro Ser Glu Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu

225

230

235

240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260

265

270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290

295

300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 671

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 671

Ser Tyr Ala Met Ser

1 5

<210> 672

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 672

Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 673

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 673

His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr

1 5 10

<210> 674

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 674

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala

1 5 10

<210> 675

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 675

Ala Ala Ser Ile Leu Gln Ser

1 5

<210> 676

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 676

Gln Gln Tyr Phe Ala Tyr Pro Ile Thr

1 5

<210> 677

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 677

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 678

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 678

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Phe Ala Tyr Pro Ile

85 90 95

Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys

100

105

<210> 679

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 679

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln
210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys

<210> 680

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 680

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly
 180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln
 210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
 260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 681

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 681

Thr Asp Gly Tyr Tyr Trp Ser

1 5

<210> 682

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 682

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

1 5 10 15

<210> 683

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 683

Gly Ile Gly Leu Gly Phe Glu Tyr

1 5

<210> 684

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 684

Gly Gly Asn Asn Ile Gly Ser Lys Ser Val His

1 5 10

<210> 685

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 685

Asp Asp Ser Asp Arg Pro Ser

1 5

<210> 686

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 686

Gln Val Trp Asp Arg Ser Ser Asp Gln Asp Val Val

1 5 10

<210> 687

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 687

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ile Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Gly Ile Gly Leu Gly Phe Glu Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 688

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 688

Ser Tyr Val Leu Thr Gln Leu Ser Ser Val Ser Val Ala Pro Gly Gln

1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val

20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr

35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser

50 55 60

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

65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg Ser Ser Asp Gln

85

90

95

Asp Val Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu

100

105

<210> 689

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 689

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1

5

10

15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp

20

25

30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35

40

45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser

50

55

60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65

70

75

80

Ser Leu Lys Leu Ile Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85

90

95

Cys Ala Arg Gly Ile Gly Leu Gly Phe Glu Tyr Trp Gly Gln Gly Thr

100

105

110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115

120

125

Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Leu Ser Ser Val Ser

130

135

140

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

145

150

155

160

Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro

165

170

175

Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu
180 185 190

Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
195 200 205

Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp
210 215 220

Arg Ser Ser Asp Gln Asp Val Val Phe Gly Cys Gly Thr Lys Leu Thr
225 230 235 240

Val Leu

<210> 690

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 690

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Thr Asp

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ile Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Gly Ile Gly Leu Gly Phe Glu Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Leu Ser Ser Val Ser
130 135 140

Val Ala Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile
145 150 155 160

Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
165 170 175

Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu
180 185 190

Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
195 200 205

Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp
210 215 220

Arg Ser Ser Asp Gln Asp Val Val Phe Gly Cys Gly Thr Lys Leu Thr
225 230 235 240

Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 691

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 691

Ser Tyr Gly Met His

1 5

<210> 692

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 692

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 693

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 693

Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp Val

1 5 10 15

<210> 694

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 694

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 695

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 695

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 696

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 696

Gln Gln Ser Tyr Ser Thr Pro Phe Thr

1 5

<210> 697

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 697

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 698

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 698

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20

25

30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe

85

90

95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 699

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 699

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr
 195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
 245

<210> 700

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 700

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130

135

140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145

150

155

160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165

170

175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180

185

190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195

200

205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210

215

220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu

500

<210> 701

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 701

Ser Tyr Gly Met His

1 5

<210> 702

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 702

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 703

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 703

Gly Arg Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp Val

1 5 10 15

<210> 704

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 704

Arg Ala Ser Gln Ser Ile Phe Asp Tyr Leu Asn

1 5 10

<210> 705

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 705

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 706

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 706

Gln Gln Ser Tyr Ser Thr Pro Leu Thr

1 5

<210> 707

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 707

Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 708

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 708

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Phe Asp Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu

85 90 95

Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 709

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 709

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Phe Asp Tyr Leu Asn Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Phe Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys

245

<210> 710

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 710

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Ser Tyr Asn Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
 130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Phe Asp Tyr Leu Asn Trp Tyr Gln
 165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
 180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Phe Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly

225 230 235 240

Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465

470

475

480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu

500

<210> 711

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 711

Thr Tyr Tyr Trp Ser

1 5

<210> 712

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 712

Arg Ile Tyr Pro Thr Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 713

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 713

Asp Arg Arg Phe Leu Glu Pro Ser Tyr Tyr Tyr Tyr Tyr Gly Met Asp

1 5 10 15

Val

<210> 714

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 714

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp

1 5 10 15

<210> 715

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 715

Leu Gly Ser Asn Arg Ala Ser

1 5

<210> 716

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 716

Met Gln Gly Leu Arg Thr Pro Phe Thr

1 5

<210> 717

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 717

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Thr Tyr

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Cys Leu Glu Trp Ile

35 40 45

Gly Arg Ile Tyr Pro Thr Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asp Arg Arg Phe Leu Glu Pro Ser Tyr Tyr Tyr Tyr Tyr Gly Met

100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120 125

<210> 718

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 718

Asp Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly

1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser

20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro

50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Lys Ile

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly

85 90 95

Leu Arg Thr Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 719

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 719

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Thr Tyr

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Cys Leu Glu Trp Ile

35 40 45

Gly Arg Ile Tyr Pro Thr Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asp Arg Arg Phe Leu Glu Pro Ser Tyr Tyr Tyr Tyr Tyr Gly Met

100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu

130 135 140

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

145 150 155 160

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn

165 170 175

Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu

180 185 190

Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser

195 200 205

Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu

210 215 220

Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Arg Thr Pro

225 230 235 240

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

245 250

<210> 720

<211> 507

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 720

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Thr Tyr

20 25 30

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

Gly Arg Ile Tyr Pro Thr Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Arg Arg Phe Leu Glu Pro Ser Tyr Tyr Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu
130 135 140

Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser
145 150 155 160

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn

165 170 175

Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu

180 185 190

Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser

195 200 205

Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu

210 215 220

Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Arg Thr Pro

225 230 235 240

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly

245 250 255

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro

260 265 270

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn

275	280	285
Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu		
290	295	300

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr			
305	310	315	320

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys			
325	330	335	

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala			
340	345	350	

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser			
355	360	365	

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly			
370	375	380	

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr			
385	390	395	400

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val

405

410

415

Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr

420

425

430

Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile

435

440

445

Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly

450

455

460

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro

465

470

475

480

Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp

485

490

495

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

500

505

<210> 721

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 721

Ser Tyr Ser Met Asn

1 5

<210> 722

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 722

Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 723

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 723

Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr

1 5 10

<210> 724

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 724

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala

1 5 10

<210> 725

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 725

Ala Ala Ser Thr Leu Gln Ser

1 5

<210> 726

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 726

Gln Gln Tyr Tyr Ser Thr Pro Leu Thr

1 5

<210> 727

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 727

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 728

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 728

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala

65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu

85

90

95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 729

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 729

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85

90

95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

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

145

150

155

160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210

215

220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225

230

235

240

Ile Lys

<210> 730

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 730

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 731

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 731

Ser Tyr Ala Met Ser

1 5

<210> 732

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 732

Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val Gln

1 5 10 15

Gly

<210> 733

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 733

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 734

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 734

Arg Ala Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala

1 5 10

<210> 735

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 735

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 736

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 736

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr

1 5

<210> 737

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 737

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 738

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 738

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Gly Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

100 105

<210> 739

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 739

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Asp Ile Lys

<210> 740

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 740

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 741

<211> 193

<212> PRT

<213> Homo sapiens

<400> 741

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
1 5 10 15

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

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Leu
 35 40 45

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

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala
65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu
85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu
100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu
115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg
130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro
145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu
165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg

180

185

190

Pro

<210> 742

<211> 151

<212> PRT

<213> Homo sapiens

<400> 742

Gln Ala Gln Gln Gln Leu Pro Leu Glu Ser Leu Gly Trp Asp Val Ala

1

5

10

15

Glu Leu Gln Leu Asn His Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr

20

25

30

Trp Gln Gly Gly Pro Ala Leu Gly Arg Ser Phe Leu His Gly Pro Glu

35

40

45

Leu Asp Lys Gly Gln Leu Arg Ile His Arg Asp Gly Ile Tyr Met Val

50

55

60

His Ile Gln Val Thr Leu Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg

65 70 75 80

His His Pro Thr Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ser Arg

85 90 95

Ser Ile Ser Leu Leu Arg Leu Ser Phe His Gln Gly Cys Thr Ile Ala

100 105 110

Ser Gln Arg Leu Thr Pro Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn

115 120 125

Leu Thr Gly Thr Leu Leu Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe

130 135 140

Gly Val Gln Trp Val Arg Pro

145 150

<210> 743

<211> 20

<212> PRT

<213> Homo sapiens

<400> 743

Gln Ala Gln Gln Gln Leu Pro Leu Glu Ser Leu Gly Trp Asp Val Ala

1 5 10 15

Glu Leu Gln Leu

20

<210> 744

<211> 22

<212> PRT

<213> Homo sapiens

<400> 744

Asn His Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly

1 5 10 15

Pro Ala Leu Gly Arg Ser

20

<210> 745

<211> 25

<212> PRT

<213> Homo sapiens

<400> 745

Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu Arg Ile His Arg

1 5 10 15

Asp Gly Ile Tyr Met Val His Ile Gln

20 25

<210> 746

<211> 25

<212> PRT

<213> Homo sapiens

<400> 746

Val Thr Leu Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro

1 5 10 15

Thr Thr Leu Ala Val Gly Ile Cys Ser

20 25

<210> 747

<211> 17

<212> PRT

<213> Homo sapiens

<400> 747

Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg Leu Ser Phe His Gln Gly

1 5 10 15

Cys

<210> 748

<211> 24

<212> PRT

<213> Homo sapiens

<400> 748

Thr Ile Ala Ser Gln Arg Leu Thr Pro Leu Ala Arg Gly Asp Thr Leu

1 5 10 15

Cys Thr Asn Leu Thr Gly Thr Leu

20

<210> 749

<211> 18

<212> PRT

<213> Homo sapiens

<400> 749

Leu Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val

1 5 10 15

Arg Pro

<210> 750

<211> 42

<212> PRT

<213> Homo sapiens

<400> 750

Gln Ala Gln Gln Gln Leu Pro Leu Glu Ser Leu Gly Trp Asp Val Ala

1 5 10 15

Glu Leu Gln Leu Asn His Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr

20 25 30

Trp Gln Gly Gly Pro Ala Leu Gly Arg Ser

35 40

<210> 751

<211> 50

<212> PRT

<213> Homo sapiens

<400> 751

Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu Arg Ile His Arg

1 5 10 15

Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu Ala Ile Cys Ser

20 25 30

Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu Ala Val Gly Ile

35 40 45

Cys Ser

50

<210> 752

<211> 42

<212> PRT

<213> Homo sapiens

<400> 752

Val Thr Leu Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro

1 5 10 15

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

20 25 30

Leu Leu Arg Leu Ser Phe His Gln Gly Cys

35 40

<210> 753

<211> 41

<212> PRT

<213> Homo sapiens

<400> 753

Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg Leu Ser Phe His Gln Gly

1 5 10 15

Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro Leu Ala Arg Gly Asp Thr

20 25 30

Leu Cys Thr Asn Leu Thr Gly Thr Leu

35 40

<210> 754

<211> 42

<212> PRT

<213> Homo sapiens

<400> 754

Thr Ile Ala Ser Gln Arg Leu Thr Pro Leu Ala Arg Gly Asp Thr Leu

1 5 10 15

Cys Thr Asn Leu Thr Gly Thr Leu Leu Pro Ser Arg Asn Thr Asp Glu

20 25 30

Thr Phe Phe Gly Val Gln Trp Val Arg Pro

35 40

<210> 755

<211> 194

<212> PRT

<213> *Macaca fascicularis*

<400> 755

Met Pro Glu Glu Gly Ser Gly Cys Ala Val Arg Arg Arg Pro Tyr Ala

1 5 10 15

Cys Val Leu Arg Ala Ala Val Val Pro Leu Val Ala Gly Leu Ala Ile

20 25 30

Cys Leu Val Val Cys Val Gln Arg Leu Ser Arg Ala Gln Gln Gln Leu

35 40 45

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

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala
65 70 75 80

Leu Gly Arg Ser Phe Leu Arg Gly Pro Glu Leu Asp Lys Gly Gln Leu
85 90 95

Arg Ile Arg Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu
100 105 110

Ala Ile Cys Ser Ser Thr Ser Thr Ser Arg His His His Pro Thr Thr
115 120 125

Leu Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu
130 135 140

Arg Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr
145 150 155 160

Pro Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu
165 170 175

Leu Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val

180

185

190

Arg Pro

<210> 756

<211> 152

<212> PRT

<213> Macaca fascicularis

<400> 756

Arg Ala Gln Gln Gln Leu Pro Leu Glu Ser Leu Gly Trp Asp Ile Ala

1

5

10

15

Glu Leu Gln Leu Asn His Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr

20

25

30

Trp Gln Gly Gly Pro Ala Leu Gly Arg Ser Phe Leu Arg Gly Pro Glu

35

40

45

Leu Asp Lys Gly Gln Leu Arg Ile Arg Arg Asp Gly Ile Tyr Met Val

50

55

60

His Ile Gln Val Thr Leu Ala Ile Cys Ser Ser Thr Ser Thr Ser Arg

65 70 75 80

His His His Pro Thr Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ser

85 90 95

Arg Ser Ile Ser Leu Leu Arg Leu Ser Phe His Gln Gly Cys Thr Ile

100 105 110

Ala Ser Gln Arg Leu Thr Pro Leu Ala Arg Gly Asp Thr Leu Cys Thr

115 120 125

Asn Leu Thr Gly Thr Leu Leu Pro Ser Arg Asn Thr Asp Glu Thr Phe

130 135 140

Phe Gly Val Gln Trp Val Arg Pro

145 150

<210> 757

<211> 195

<212> PRT

<213> Mus musculus

<400> 757

Met Pro Glu Glu Gly Arg Pro Cys Pro Trp Val Arg Trp Ser Gly Thr

1 5 10 15

Ala Phe Gln Arg Gln Trp Pro Trp Leu Leu Leu Val Val Phe Ile Thr

20 25 30

Val Phe Cys Cys Trp Phe His Cys Ser Gly Leu Leu Ser Lys Gln Gln

35 40 45

Gln Arg Leu Leu Glu His Pro Glu Pro His Thr Ala Glu Leu Gln Leu

50 55 60

Asn Leu Thr Val Pro Arg Lys Asp Pro Thr Leu Arg Trp Gly Ala Gly

65 70 75 80

Pro Ala Leu Gly Arg Ser Phe Thr His Gly Pro Glu Leu Glu Glu Gly

85 90 95

His Leu Arg Ile His Gln Asp Gly Leu Tyr Arg Leu His Ile Gln Val

100 105 110

Thr Leu Ala Asn Cys Ser Ser Pro Gly Ser Thr Leu Gln His Arg Ala

115 120 125

Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ala His Gly Ile Ser Leu

130 135 140

Leu Arg Gly Arg Phe Gly Gln Asp Cys Thr Val Ala Leu Gln Arg Leu

145 150 155 160

Thr Tyr Leu Val His Gly Asp Val Leu Cys Thr Asn Leu Thr Leu Pro

165 170 175

Leu Leu Pro Ser Arg Asn Ala Asp Glu Thr Phe Phe Gly Val Gln Trp

180 185 190

Ile Cys Pro

195

<210> 758

<211> 151

<212> PRT

<213> Mus musculus

<400> 758

Ser Lys Gln Gln Gln Arg Leu Leu Glu His Pro Glu Pro His Thr Ala

1 5 10 15

Glu Leu Gln Leu Asn Leu Thr Val Pro Arg Lys Asp Pro Thr Leu Arg

20 25 30

Trp Gly Ala Gly Pro Ala Leu Gly Arg Ser Phe Thr His Gly Pro Glu

35 40 45

Leu Glu Glu Gly His Leu Arg Ile His Gln Asp Gly Leu Tyr Arg Leu

50 55 60

His Ile Gln Val Thr Leu Ala Asn Cys Ser Ser Pro Gly Ser Thr Leu

65 70 75 80

Gln His Arg Ala Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ala His

85 90 95

Gly Ile Ser Leu Leu Arg Gly Arg Phe Gly Gln Asp Cys Thr Val Ala

100 105 110

Leu Gln Arg Leu Thr Tyr Leu Val His Gly Asp Val Leu Cys Thr Asn

115 120 125

Leu Thr Leu Pro Leu Leu Pro Ser Arg Asn Ala Asp Glu Thr Phe Phe

130

135

140

Gly Val Gln Trp Ile Cys Pro

145

150

<210> 759

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 759

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly

1

5

10

15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile

20

25

30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Ser Lys Gln Gln Gln Arg

35

40

45

Leu Leu Glu His Pro Glu Pro His Thr Ala Glu Leu Gln Leu Asn His

50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu

85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu

100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg

130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro

145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu

165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg

180

185

190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly

195

200

205

Leu Asp Ser Thr

210

<210> 760

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 760

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly

1

5

10

15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile

20

25

30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu

35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn Leu

50 55 60

Thr Val Pro Arg Lys Asp Pro Thr Leu Arg Trp Gly Ala Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu

85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu

100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg

130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro

145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu

165

170

175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg

180

185

190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly

195

200

205

Leu Asp Ser Thr

210

<210> 761

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 761

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly

1

5

10

15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile

20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu

35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His

50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Thr His Gly Pro Glu Leu Glu Glu Gly His Leu

85 90 95

Arg Ile His Gln Asp Gly Leu Tyr Arg Leu His Ile Gln Val Thr Leu

100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg

130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro

145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu

165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg

180 185 190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly

195 200 205

Leu Asp Ser Thr

210

<210> 762

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 762

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly

1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile

20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu

35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His

50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu

85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu

100 105 110

Ala Asn Cys Ser Ser Pro Gly Ser Thr Leu Gln His Arg Ala Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg

130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro

145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu

165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg

180 185 190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly

195 200 205

Leu Asp Ser Thr

210

<210> 763

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 763

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly

1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile

20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu

35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His

50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu

85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu

100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg

130 135 140

Leu Ser Phe His Gln Gly Cys Thr Val Ala Leu Gln Arg Leu Thr Tyr

145 150 155 160

Leu Val His Gly Asp Val Leu Cys Thr Asn Leu Thr Leu Pro Leu Leu

165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg

180 185 190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly

195 200 205

Leu Asp Ser Thr

210

<210> 764

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 764

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly

1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile

20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu

35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His

50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu

85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu

100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg

130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro

145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu

165 170 175

Pro Ser Arg Asn Ala Asp Glu Thr Phe Phe Gly Val Gln Trp Ile Cys

180 185 190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly

195 200 205

Leu Asp Ser Thr

210

<210> 765

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 765

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly

1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile

20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Ser Lys Gln Gln Gln Arg

35 40 45

Leu Leu Glu His Pro Glu Pro His Thr Ala Glu Leu Gln Leu Asn Leu

50 55 60

Thr Val Pro Arg Lys Asp Pro Thr Leu Arg Trp Gly Ala Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu

85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu

100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg

130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro

145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu

165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg

180 185 190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly

195 200 205

Leu Asp Ser Thr

210

<210> 766

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 766

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly

1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile

20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu

35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His

50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Thr His Gly Pro Glu Leu Glu Glu Gly His Leu

85 90 95

Arg Ile His Gln Asp Gly Leu Tyr Arg Leu His Ile Gln Val Thr Leu

100 105 110

Ala Asn Cys Ser Ser Pro Gly Ser Thr Leu Gln His Arg Ala Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg

130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro

145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu

165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg

180 185 190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
195 200 205

Leu Asp Ser Thr
210

<210> 767

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 767

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
1 5 10 15

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

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu
35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His

50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu

85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu

100 105 110

Ala Asn Cys Ser Ser Pro Gly Ser Thr Leu Gln His Arg Ala Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ala His Gly Ile Ser Leu Leu Arg

130 135 140

Gly Arg Phe Gly Gln Asp Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro

145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu

165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg
180 185 190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
195 200 205

Leu Asp Ser Thr
210

<210> 768

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 768

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
1 5 10 15

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

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu

35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His

50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala

65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu

85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu

100 105 110

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu

115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg

130 135 140

Leu Ser Phe His Gln Gly Cys Thr Val Ala Leu Gln Arg Leu Thr Tyr

145 150 155 160

Leu Val His Gly Asp Val Leu Cys Thr Asn Leu Thr Leu Pro Leu Leu
165 170 175

Pro Ser Arg Asn Ala Asp Glu Thr Phe Phe Gly Val Gln Trp Ile Cys
180 185 190

Pro Gly Gly Gly Gly Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
195 200 205

Leu Asp Ser Thr
210

<210> 769

<211> 261

<212> PRT

<213> Homo sapiens

<400> 769

Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
1 5 10 15

Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg

35 40 45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val

50 55 60

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser

65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys

85 90 95

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu

100 105 110

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser

115 120 125

Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly

130 135 140

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln

145 150 155 160

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr

165 170 175

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser

180 185 190

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala

195 200 205

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His

210 215 220

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn

225 230 235 240

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe

245 250 255

Gly Leu Leu Lys Leu

260

<210> 770

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 770

Gly Gly Gly Gly

1

<210> 771

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 771

Gly Gly Gly Gly Ser

1 5

<210> 772

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 772

Gly Gly Gly Gly Gln

1 5

<210> 773

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 773

Ser Gly Gly Gly Gly Ser

1 5

<210> 774

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 774

Pro Gly Gly Gly Gly Ser

1 5

<210> 775

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 775

Pro Gly Gly Asp Gly Ser

1 5

<210> 776

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 776

Gly Gly Gly Gly Ser Gly Gly Gly Ser

1 5

<210> 777

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 777

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10

<210> 778

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 778

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10 15

<210> 779

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 779

His His His His His His

1 5

<210> 780

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 780

Arg Asp Trp Asp Phe Asp Val Phe Gly Gly Gly Thr Pro Val Gly Gly

1 5 10 15

<210> 781

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> misc_feature

<222> (12)..(12)

<223> Xaa can be any naturally occurring amino acid

<400> 781

Gln Arg Phe Val Thr Gly His Phe Gly Gly Leu Xaa Pro Ala Asn Gly

1 5 10 15

<210> 782

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 782

Gln Arg Phe Val Thr Gly His Phe Gly Gly Leu Tyr Pro Ala Asn Gly

1 5 10 15

<210> 783

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 783

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

1 5 10 15

<210> 784

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 784

Thr Gly His Phe Gly Gly Leu His Pro

1 5

<210> 785

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 785

Gln Arg Phe Cys Thr Gly His Phe Gly Gly Leu His Pro Cys Asn Gly

1 5 10 15

<210> 786

<211> 585

<212> PRT

<213> Homo sapiens

<400> 786

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50

55

60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65

70

75

80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85

90

95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100

105

110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115

120

125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130

135

140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145

150

155

160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165

170

175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val

565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580 585

<210> 787

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 787

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165

170

175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180

185

190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195

200

205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210

215

220

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

225

230

235

240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245

250

255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260

265

270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275

280

285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

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

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Gly Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Ala Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val

565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580 585

<210> 788

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 788

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275

280

285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290

295

300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305

310

315

320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325

330

335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340

345

350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355

360

365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

375

380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545

550

555

560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565

570

575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580

585

<210> 789

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 789

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

1

5

10

15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

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

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Asp Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515

520

525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545

550

555

560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro His Leu Val

565

570

575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580

585

<210> 790

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 790

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130

135

140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145

150

155

160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165

170

175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180

185

190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195

200

205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210

215

220

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

225

230

235

240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245

250

255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Gly Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500

505

510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515

520

525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545

550

555

560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565

570

575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580

585

<210> 791

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 791

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115

120

125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130

135

140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145

150

155

160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165

170

175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180

185

190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195

200

205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210

215

220

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

225

230

235

240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

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

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Asp Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580 585

<210> 792

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 792

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355

360

365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

375

380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405

410

415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420

425

430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435

440

445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450

455

460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465

470

475

480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro His Leu Val

565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580 585

<210> 793

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 793

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340

345

350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355

360

365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

375

380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405

410

415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420

425

430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435

440

445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450

455

460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro His Leu Val
 565 570 575

Ala Ala Ser Lys Ala Ala Leu Gly Leu
 580 585

<210> 794

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 794

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565 570 575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580

585

<210> 795

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 795

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

1

5

10

15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20

25

30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35

40

45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50

55

60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Asp Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565

570

575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580

585

<210> 796

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 796

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

1

5

10

15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20

25

30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35

40

45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

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

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val

565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580 585

<210> 797

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 797

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290

295

300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305

310

315

320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325

330

335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340

345

350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355

360

365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

375

380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405

410

415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420

425

430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435

440

445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450

455

460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465

470

475

480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485

490

495

Tyr Val Pro Lys Glu Phe Asn Ala Gly Thr Phe Thr Phe His Ala Asp

500

505

510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515

520

525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Ala Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val

565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580 585

<210> 798

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 798

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275	280	285	
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser			
290	295	300	
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala			
305	310	315	320
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg			
	325	330	335
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr			
	340	345	350
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu			
	355	360	365
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro			
	370	375	380
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu			
385	390	395	400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545

550

555

560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565

570

575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580

585

<210> 799

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 799

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

1

5

10

15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Asp Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515

520

525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545

550

555

560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro His Leu Val

565

570

575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580

585

<210> 800

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 800

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Gly Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500	505	510	
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala			
515	520	525	
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu			
530	535	540	
Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys			
545	550	555	560
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val			
565	570	575	
Ala Ala Ser Gln Ala Ala Leu Gly Leu			
580	585		

<210> 801

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 801

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Asp Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580 585

<210> 802

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 802

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355

360

365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

375

380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405

410

415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420

425

430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435

440

445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450

455

460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465

470

475

480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro His Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 803

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 803

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

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

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro His Leu Val

565 570 575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580 585

<210> 804

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 804

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565 570 575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580

585

<210> 805

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 805

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

1

5

10

15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20

25

30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35

40

45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50

55

60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325

330

335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340

345

350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355

360

365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

375

380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405

410

415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420

425

430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435

440

445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Asp Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565 570 575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580 585

<210> 806

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 806

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val

565

570

575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580

585

<210> 807

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 807

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

1

5

10

15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20

25

30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35

40

45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50

55

60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65

70

75

80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85

90

95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100

105

110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115

120

125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130

135

140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145

150

155

160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165

170

175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420

425

430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435

440

445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450

455

460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465

470

475

480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485

490

495

Tyr Val Pro Lys Glu Phe Asn Ala Gly Thr Phe Thr Phe His Ala Asp

500

505

510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515

520

525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Ala Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
 580 585

<210> 808

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 808

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165

170

175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180

185

190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195

200

205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210

215

220

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

225

230

235

240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245

250

255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260

265

270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275

280

285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545

550

555

560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565

570

575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580

585

<210> 809

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 809

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

1

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10

15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275

280

285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290

295

300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305

310

315

320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325

330

335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340

345

350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355

360

365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

375

380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Asp Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro His Leu Val

565 570 575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580 585

<210> 810

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 810

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Gly Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515

520

525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545

550

555

560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565

570

575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580

585

<210> 811

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 811

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Asp Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500

505

510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515

520

525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545

550

555

560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565

570

575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580

585

<210> 812

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 812

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115

120

125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130

135

140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145

150

155

160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165

170

175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180

185

190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195

200

205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210

215

220

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

225

230

235

240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro His Leu Val

565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu

580 585

<210> 813

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 813

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

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

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355

360

365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

375

380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405

410

415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420

425

430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435

440

445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450

455

460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro His Leu Val

565 570 575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580 585

<210> 814

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 814

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro

210 215 220

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

225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp

245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser

260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340

345

350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355

360

365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

375

380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405

410

415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420

425

430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435

440

445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450

455

460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530 535 540

Lys Ala Val Met Asp Lys Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565 570 575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580

585

<210> 815

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 815

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

1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu

35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys

50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro

85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His

115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala

165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu

195	200	205	
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro			
210	215	220	
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys			
225	230	235	240
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp			
	245	250	255
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser			
	260	265	270
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His			
	275	280	285
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser			
	290	295	300
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala			
305	310	315	320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu

355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys

420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys

435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His

450

455

460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465

470

475

480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Asp Val Asp Glu Thr

485

490

495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500

505

510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515

520

525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

545

550

555

560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Pro Lys Leu Val

565

570

575

Ala Ala Ser Lys Ala Ala Leu Gly Leu

580

585

<210> 816

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 816

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

1

5

10

15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr

20

25

30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

35

40

45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

50

55

60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
 165 170 175

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
 180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

260 265 270

Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

275 280 285

Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

325 330

<210> 817

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 817

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser

1 5 10 15

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp

20 25 30

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro

35 40 45

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn

50 55 60

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys

65 70 75 80

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val

85 90 95

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr His Thr Cys

100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

165 170 175

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

180 185 190

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

225 230 235 240

Arg Lys Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly

275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

325 330

<210> 818

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 818

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg

1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr

20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr

65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys

85 90 95

Thr Val Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys

100 105 110

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu

165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu

180

185

190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

195

200

205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

210

215

220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

225

230

235

240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

245

250

255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

260

265

270

Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

275

280

285

Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

290

295

300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

325 330

<210> 819

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 819

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser

1 5 10 15

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp

20 25 30

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro

35 40 45

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn

50 55 60

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys

65 70 75 80

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val

85 90 95

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Glu Pro Lys Ser Ser Asp

100 105 110

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly

115 120 125

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

130 135 140

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu

145 150 155 160

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

165 170 175

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

180 185 190

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

195 200 205

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

210 215 220

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

225 230 235 240

Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys Asn Gln Val Ser Leu

245 250 255

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp

260 265 270

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

275 280 285

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

290 295 300

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

305 310 315 320

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

325 330 335

Gly Lys

<210> 820

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 820

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

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

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165

170

175

Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180

185

190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195

200

205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210

215

220

Pro Gly Lys

225

<210> 821

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 821

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

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

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro Gly Lys

225

<210> 822

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 822

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

65 70 75 80

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr

130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr

180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys

225 230

<210> 823

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 823

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

65 70 75 80

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

165 170 175

Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

180 185 190

Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys

225 230

<210> 824

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 824

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1 5 10 15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr

130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

165 170 175

Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr

180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys

225 230

<210> 825

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 825

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1 5 10 15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

165 170 175

Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

180 185 190

Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys

225 230

<210> 826

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 826

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

1 5 10 15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His

65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

100 105 110

Pro Arg Glu Pro Gln Val Thr Thr Leu Pro Pro Ser Arg Glu Glu Met

115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

145 150 155 160

Tyr Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

165 170 175

Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys

210

215

<210> 827

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 827

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

1

5

10

<210> 828

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 828

Gly Thr Lys Phe Leu Ala Pro

1

5

<210> 829

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 829

Ala Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 830

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 830

Ile Tyr Ala Met Asn

1 5

<210> 831

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 831

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Ser

<210> 832

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 832

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Phe Phe Ala Tyr

1 5 10

<210> 833

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 833

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ile Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Phe Phe

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120 125

<210> 834

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 834

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly

20 25 30

Tyr Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe

50

55

60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65

70

75

80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn

85

90

95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

105

<210> 835

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 835

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ile Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Phe Phe

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val

130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
145 150 155 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
 165 170 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 180 185 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 195 200 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 210 215 220

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Arg Trp Val Phe
 225 230 235 240

Gly Gly Gly Thr Lys Leu Thr Val Leu
 245

<210> 836

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 836

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

1 5 10

<210> 837

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 837

Gly Thr Lys Phe Leu Ala Pro

1 5

<210> 838

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 838

Ala Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 839

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 839

Lys Tyr Ala Met Asn

1 5

<210> 840

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 840

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Asp

<210> 841

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 841

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr

1 5 10

<210> 842

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 842

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

125

<210> 843

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 843

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1

5

10

15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly

20

25

30

Tyr Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35

40

45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe

50

55

60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn

85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 844

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 844

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val

130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu

145 150 155 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

165 170 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly

180 185 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu

195 200 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

210 215 220

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Arg Trp Val Phe

225 230 235 240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 845

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 845

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

1 5 10

<210> 846

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 846

Gly Thr Lys Phe Leu Ala Pro

1 5

<210> 847

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 847

Ala Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 848

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 848

Ser Tyr Ala Met Asn

1 5

<210> 849

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 849

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Gly

<210> 850

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 850

His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Phe Trp Ala Tyr

1 5 10

<210> 851

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 851

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Glu Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Phe Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120 125

<210> 852

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 852

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly

20 25 30

Tyr Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe

50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn

85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

105

<210> 853

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 853

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Glu Gln Pro Gly Gly

1

5

10

15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr

20

25

30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50

55

60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Phe Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val

130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu

145 150 155 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

165 170 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly

180 185 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu

195

200

205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

210

215

220

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Arg Trp Val Phe

225

230

235

240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 854

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 854

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

1

5

10

<210> 855

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 855

Gly Thr Lys Phe Leu Ala Pro

1 5

<210> 856

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 856

Ala Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 857

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 857

Arg Tyr Ala Met Asn

1 5

<210> 858

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 858

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Gly

<210> 859

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 859

His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Tyr Phe Ala Tyr

1 5 10

<210> 860

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 860

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Arg Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Tyr Phe

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120 125

<210> 861

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 861

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly

20 25 30

Tyr Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe

50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn

85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 862

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 862

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Arg Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Tyr Phe

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val

130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu

145 150 155 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

165 170 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly

180 185 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu

195 200 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

210 215 220

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Arg Trp Val Phe

225 230 235 240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 863

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 863

Arg Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

1 5 10

<210> 864

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 864

Ala Thr Asp Met Arg Pro Ser

1 5

<210> 865

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 865

Ala Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 866

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 866

Val Tyr Ala Met Asn

1 5

<210> 867

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 867

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Lys

<210> 868

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 868

His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Trp Trp Ala Tyr

1 5 10

<210> 869

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 869

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Val Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Lys Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Trp Trp
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 870

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 870

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

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

20 25 30

Tyr Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35 40 45

Leu Ile Gly Ala Thr Asp Met Arg Pro Ser Gly Thr Pro Ala Arg Phe

50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn

85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 871

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 871

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Val Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Lys Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Trp Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val

130

135

140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu

145

150

155

160

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

165

170

175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Ala

180

185

190

Thr Asp Met Arg Pro Ser Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu

195

200

205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

210

215

220

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Arg Trp Val Phe

225

230

235

240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 872

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 872

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

1 5 10

<210> 873

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 873

Gly Thr Lys Phe Leu Ala Pro

1 5

<210> 874

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 874

Ala Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 875

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 875

Lys Tyr Ala Met Asn

1 5

<210> 876

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 876

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Ser

<210> 877

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 877

His Gly Asn Phe Gly Asn Ser Tyr Thr Ser Tyr Tyr Ala Tyr

1 5 10

<210> 878

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 878

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Thr Ser Tyr Tyr

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120 125

<210> 879

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 879

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly

20 25 30

Tyr Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe

50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn

85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 880

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 880

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Ser Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Thr Ser Tyr Tyr

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val

130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu

145 150 155 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

165 170 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly

180 185 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu

195 200 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

210 215 220

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Arg Trp Val Phe

225 230 235 240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 881

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 881

Arg Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

1 5 10

<210> 882

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 882

Ala Thr Asp Met Arg Pro Ser

1 5

<210> 883

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 883

Ala Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 884

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 884

Gly Tyr Ala Met Asn

1 5

<210> 885

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 885

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Glu

<210> 886

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 886

His Arg Asn Phe Gly Asn Ser Tyr Leu Ser Trp Phe Ala Tyr

1 5 10

<210> 887

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 887

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Gly Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Glu Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Arg Asn Phe Gly Asn Ser Tyr Leu Ser Trp Phe

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

125

<210> 888

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 888

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1

5

10

15

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

20

25

30

Tyr Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35

40

45

Leu Ile Gly Ala Thr Asp Met Arg Pro Ser Gly Thr Pro Ala Arg Phe

50

55

60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn

85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 889

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 889

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Gly Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Glu Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Arg Asn Phe Gly Asn Ser Tyr Leu Ser Trp Phe

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val

130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu

145 150 155 160

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

165

170

175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Ala

180

185

190

Thr Asp Met Arg Pro Ser Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu

195

200

205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

210

215

220

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Arg Trp Val Phe

225

230

235

240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 890

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 890

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn

1 5 10

<210> 891

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 891

Gly Thr Lys Phe Leu Ala Pro

1 5

<210> 892

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 892

Ala Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 893

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 893

Val Tyr Ala Met Asn

1 5

<210> 894

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 894

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Lys

<210> 895

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 895

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Trp Trp Ala Tyr

1 5 10

<210> 896

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 896

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Val Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Lys Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Trp Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120 125

<210> 897

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 897

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly

20 25 30

Tyr Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe

50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn

85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

105

<210> 898

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 898

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Val Tyr

20

25

30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50

55

60

Ser Val Lys Lys Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Trp Trp
 100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
145 150 155 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
 165 170 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 180 185 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu

195 200 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

210 215 220

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Arg Trp Val Phe

225 230 235 240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 899

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 899

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn

1 5 10

<210> 900

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 900

Gly Thr Lys Phe Leu Ala Pro

1 5

<210> 901

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 901

Val Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 902

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 902

Ser Tyr Ala Met Asn

1 5

<210> 903

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 903

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Gly

<210> 904

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 904

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp Ala Tyr

1 5 10

<210> 905

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 905

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50

55

60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65

70

75

80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85

90

95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp

100

105

110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

125

<210> 906

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 906

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly

20 25 30

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe

50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn

85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 907

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 907

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val

130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu

145 150 155 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn

165 170 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly

180 185 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu

195 200 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

210

215

220

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe

225

230

235

240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 908

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 908

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn

1

5

10

<210> 909

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 909

Gly Thr Lys Phe Leu Ala Pro

1 5

<210> 910

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 910

Val Leu Trp Tyr Ser Asn Arg Trp Val

1 5

<210> 911

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 911

Lys Tyr Ala Met Asn

1 5

<210> 912

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 912

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Asp

<210> 913

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 913

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr

1 5 10

<210> 914

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 914

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120 125

<210> 915

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 915

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
20 25 30

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 916

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 916

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
145 150 155 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
165 170 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
180 185 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
195 200 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
210 215 220

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
225 230 235 240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 917

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 917

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp
 100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 918

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 918

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly

20 25 30

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly

35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe

50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val

65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn

85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105

<210> 919

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 919

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr

65 70 75 80

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

85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp

100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val

130

135

140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu

145

150

155

160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn

165

170

175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly

180

185

190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu

195

200

205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

210

215

220

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe

225

230

235

240

Gly Gly Gly Thr Lys Leu Thr Val Leu

245

<210> 920

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 920

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 921

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 921

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

1 5 10 15

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

20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 922

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 922

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 923

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 923

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 924

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 924

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 925

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 925

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 926

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 926

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 927

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 927

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 928

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 928

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 929

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 929

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 930

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 930

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 931

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 931

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 932

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 932

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 933

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 933

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 934

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 934

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 935

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 935

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 936

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 936

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 937

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 937

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 938

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 938

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 939

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 939

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 940

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 940

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 941

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 941

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Thr

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 942

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 942

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 943

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 943

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 944

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 944

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 945

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 945

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 946

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 946

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 947

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 947

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 948

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 948

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser

115

<210> 949

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 949

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Thr

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 950

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 950

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 951

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 951

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 952

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 952

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 953

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 953

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 954

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 954

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 955

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 955

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 956

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 956

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 957

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 957

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 958

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 958

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 959

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 959

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 960

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 960

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 961

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 961

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 962

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 962

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 963

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 963

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 964

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 964

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 965

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 965

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 966

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 966

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 967

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 967

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115	120	125			
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly					
130	135	140			
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala					
145	150	155	160		
Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro					
	165	170	175		
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr					
180	185	190			
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr					
195	200	205			
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys					
210	215	220			
Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val					
225	230	235	240		

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 968

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 968

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 969

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 969

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Gly Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 970

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 970

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 971

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 971

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 972

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 972

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 973

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 973

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Gly Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 974

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 974

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50

55

60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 975

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 975

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 976

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 976

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 977

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 977

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 978

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 978

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 979

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 979

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 980

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 980

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 981

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 981

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Ile Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 982

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 982

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

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

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 983

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 983

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210

215

220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 984

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 984

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 985

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 985

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile

35 40 45

Tyr Gly Ser Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro

65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Pro

85 90 95

Pro Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 986

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 986

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50

55

60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130

135

140

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

145

150

155

160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 987

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 987

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

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

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 988

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 988

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 989

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 989

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Ser Asp

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr His Cys Gln Gln Tyr Gly Ser Thr Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 990

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 990

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100	105	110	
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly			
115	120	125	
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly			
130	135	140	
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala			
145	150	155	160
Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro			
165	170	175	
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr			
180	185	190	
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr			
195	200	205	
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys			
210	215	220	

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 991

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 991

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
 355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 992

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 992

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 993

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 993

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

1 5 10 15

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

20 25 30

Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 994

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 994

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

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

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 995

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 995

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180

185

190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 996

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 996

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 997

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 997

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Ser Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 998

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 998

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 999

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 999

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1000

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1000

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1001

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1001

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 1002

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1002

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1003

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1003

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1004

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1004

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1005

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1005

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys

100

105

<210> 1006

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1006

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Asp Ile Lys

<210> 1007

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1007

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1008

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1008

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1009

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1009

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

1 5 10 15

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

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys

100 105

<210> 1010

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1010

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys

<210> 1011

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1011

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1012

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1012

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1013

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1013

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys

100 105

<210> 1014

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1014

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Asp Ile Lys

<210> 1015

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1015

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1016

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1016

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1017

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1017

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Phe Ala Tyr Pro Ile

85 90 95

Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys

100 105

<210> 1018

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1018

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

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

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly
180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln
210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys

<210> 1019

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1019

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 1020

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1020

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1021

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1021

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys

100 105

<210> 1022

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1022

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys

<210> 1023

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1023

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 1024

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1024

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1025

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1025

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20

25

30

Tyr Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys

100

105

<210> 1026

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1026

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Arg Leu

225

230

235

240

Glu Ile Lys

<210> 1027

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1027

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1028

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1028

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

115 120 125

<210> 1029

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1029

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1030

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1030

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Cys

225 230 235 240

Gly Thr Lys Val Glu Ile Lys

245

<210> 1031

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1031

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe
100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
130 135 140

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

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Cys

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

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

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340 345 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu

385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly

405

410

415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

420

425

430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe

435

440

445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly

450

455

460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu

465

470

475

480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly

485

490

495

Thr Lys Leu Thr Val Leu

500

<210> 1032

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1032

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1033

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1033

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20

25

30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35

40

45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala

65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1034

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1034

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 1035

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1035

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

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

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 1036

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1036

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1037

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1037

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1038

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1038

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 1039

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1039

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1040

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1040

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 1041

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1041

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe

85

90

95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 1042

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1042

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130

135

140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145

150

155

160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165

170

175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly

225 230 235 240

Thr Lys Val Glu Ile Lys

245

<210> 1043

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1043

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu

500

<210> 1044

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1044

Ser Tyr Ala Met Ser

1 5

<210> 1045

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1045

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

1 5 10 15

Gly

<210> 1046

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1046

Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr

1 5 10

<210> 1047

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1047

Arg Ala Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly

1 5 10

<210> 1048

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1048

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1049

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1049

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr

1 5

<210> 1050

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1050

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1051

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1051

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

1 5 10 15

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

20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1052

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1052

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 1053

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1053

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 1054

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1054

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

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

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1055

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1055

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

1 5 10 15

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

20 25 30

Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1056

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1056

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 1057

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1057

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1058

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1058

Ile Tyr Ala Met Ser

1 5

<210> 1059

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1059

Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1060

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1060

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1061

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1061

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1062

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1062

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1063

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1063

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1064

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1064

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1065

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1065

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 1066

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1066

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 1067

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1067

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 1068

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1068

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1069

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1069

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 1070

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1070

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 1071

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1071

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1072

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1072

Ser Tyr Ala Met Ser

1

5

<210> 1073

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1073

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1074

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1074

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1075

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1075

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1076

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1076

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1077

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1077

Gln Gln Tyr Gly Ser Ser Pro Phe Thr

1 5

<210> 1078

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1078

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1079

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1079

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1080

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1080

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 1081

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1081

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1082

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1082

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1083

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1083

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1084

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1084

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 1085

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1085

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115	120	125			
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly					
130	135	140			
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala					
145	150	155	160		
Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro					
	165	170	175		
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr					
180	185	190			
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr					
195	200	205			
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys					
210	215	220			
Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu					
225	230	235	240		

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1086

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1086

Ser Tyr Ala Met Ser

1 5

<210> 1087

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1087

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1088

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1088

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1089

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1089

Arg Ala Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1090

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1090

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1091

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1091

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1092

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1092

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1093

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1093

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1094

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1094

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 1095

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1095

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1096

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1096

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1097

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1097

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1098

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1098

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 1099

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1099

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1100

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1100

Ser Tyr Ala Met Ser

1 5

<210> 1101

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1101

Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1102

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1102

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1103

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1103

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1104

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1104

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1105

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1105

Gln Gln Tyr Gly Ser Ser Pro Phe Thr

1 5

<210> 1106

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1106

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1107

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1107

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 1108

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1108

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 1109

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1109

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1110

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1110

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1111

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1111

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1112

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1112

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 1113

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1113

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1114

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1114

Ser Tyr Ala Met Ser

1 5

<210> 1115

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1115

Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1116

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1116

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1117

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1117

Arg Ala Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala

1 5 10

<210> 1118

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1118

Asp Ala Ser Ser Arg Ala Thr

1 5

<210> 1119

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1119

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 1120

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1120

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1121

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1121

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Thr

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1122

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1122

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 1123

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1123

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1124

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1124

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1125

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1125

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Thr

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1126

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1126

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 1127

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1127

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1128

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1128

Thr Tyr Ala Met Ser

1 5

<210> 1129

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1129

Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1130

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1130

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1131

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1131

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1132

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1132

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1133

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1133

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1134

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1134

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1135

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1135

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 1136

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1136

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys

<210> 1137

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1137

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1138

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1138

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1139

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1139

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1140

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1140

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 1141

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1141

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275	280	285			
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr					
290	295	300			
Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr					
305	310	315	320		
Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn					
	325	330	335		
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn					
	340	345	350		
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr					
	355	360	365		
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser					
	370	375	380		
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr					
385	390	395	400		

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1142

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1142

Thr Tyr Ala Met Ser

1 5

<210> 1143

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1143

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1144

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1144

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1145

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1145

Arg Ala Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala

1 5 10

<210> 1146

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1146

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1147

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1147

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1148

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1148

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1149

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1149

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Thr

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 1150

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1150

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys

<210> 1151

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1151

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1152

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1152

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1153

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1153

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Thr

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 1154

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1154

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115	120	125	
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly			
130	135	140	
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala			
145	150	155	160
Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro			
165	170	175	
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr			
180	185	190	
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr			
195	200	205	
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys			
210	215	220	
Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu			
225	230	235	240

Glu Ile Lys

<210> 1155

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1155

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1156

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1156

Ser Tyr Ala Met Ser

1

5

<210> 1157

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1157

Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1158

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1158

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1159

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1159

Arg Ala Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 1160

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1160

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1161

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1161

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1162

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1162

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1163

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1163

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1164

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1164

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1165

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1165

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1166

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1166

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1167

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1167

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro
 85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 1168

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1168

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1169

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1169

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355	360	365			
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser					
370	375	380			
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr					
385	390	395	400		
Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly					
	405	410	415		
Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly					
	420	425	430		
Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly					
	435	440	445		
Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu					
	450	455	460		
Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val					
465	470	475	480		

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1170

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1170

Ser Tyr Ala Met Ser

1

5

<210> 1171

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1171

Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1172

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1172

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1173

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1173

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1174

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1174

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1175

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1175

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1176

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1176

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1177

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1177

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 1178

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1178

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1179

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1179

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1180

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1180

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1181

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1181

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1182

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1182

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1183

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1183

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1184

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1184

Ser Tyr Ala Met Ser

1 5

<210> 1185

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1185

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1186

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1186

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1187

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1187

Arg Ala Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 1188

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1188

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1189

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1189

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1190

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1190

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1191

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1191

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1192

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1192

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1193

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1193

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1194

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1194

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1195

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1195

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1196

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1196

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1197

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1197

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1198

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1198

Ser Tyr Ala Met Ser

1 5

<210> 1199

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1199

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1200

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1200

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1201

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1201

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1202

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1202

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1203

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1203

Gln Gln Tyr Gly Ser Ser Pro Phe Thr

1 5

<210> 1204

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1204

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1205

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1205

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 1206

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1206

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1207

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1207

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1208

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1208

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1209

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1209

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1210

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1210

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1211

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1211

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1212

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1212

Ser Tyr Ala Met Ser

1 5

<210> 1213

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1213

Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val Gln

1 5 10 15

Gly

<210> 1214

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1214

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1215

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1215

Arg Ala Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala

1 5 10

<210> 1216

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1216

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1217

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1217

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr

1 5

<210> 1218

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1218

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1219

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1219

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Gly Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 1220

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1220

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1221

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1221

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

1780

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1222

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1222

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1223

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1223

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Gly Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Tyr Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100

105

<210> 1224

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1224

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50

55

60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1225

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1225

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1226

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1226

Thr Tyr Ala Met Ser

1 5

<210> 1227

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1227

Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1228

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1228

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1229

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1229

Arg Ala Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 1230

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1230

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1231

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1231

Gln Gln Tyr Gly Ser Ser Pro Phe Thr

1 5

<210> 1232

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1232

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1233

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1233

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1234

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1234

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1235

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1235

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1236

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1236

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1237

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1237

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1238

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1238

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 1239

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1239

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1240

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1240

Thr Tyr Ala Met Ser

1 5

<210> 1241

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1241

Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1242

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1242

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1243

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1243

Arg Ala Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 1244

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1244

Gly Ala Ser Asn Arg Ala Thr

1 5

<210> 1245

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1245

Gln Gln Tyr Gly Ile Ser Pro Pro Thr

1 5

<210> 1246

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1246

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1247

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1247

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Ile Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1248

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1248

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1249

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1249

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275	280	285			
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr					
290	295	300			
Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr					
305	310	315	320		
Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn					
	325	330	335		
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn					
	340	345	350		
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr					
	355	360	365		
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser					
	370	375	380		
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr					
385	390	395	400		

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1250

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1250

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1251

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1251

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Ile Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1252

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1252

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1253

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1253

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100	105	110	
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly			
115	120	125	
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly			
130	135	140	
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala			
145	150	155	160
Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro			
165	170	175	
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr			
180	185	190	
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr			
195	200	205	
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys			
210	215	220	

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1254

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1254

Ser Tyr Ala Met Ser

1

5

<210> 1255

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1255

Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val Gln

1 5 10 15

Gly

<210> 1256

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1256

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1257

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1257

Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala

1 5 10

<210> 1258

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1258

Gly Ser Ser Ser Arg Ala Thr

1 5

<210> 1259

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1259

Gln Gln Tyr Gly Ser Ser Pro Pro Pro

1 5

<210> 1260

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1260

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1261

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1261

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn

20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ser Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Pro
85 90 95

Pro Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1262

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1262

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

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

Ile Lys

<210> 1263

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1263

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

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

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325

330

335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 1264

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1264

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1265

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1265

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile

35 40 45

Tyr Gly Ser Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro

65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Pro

85 90 95

Pro Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100

105

<210> 1266

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1266

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50

55

60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

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

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

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

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys

<210> 1267

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1267

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 165 170 175

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 195 200 205

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

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
 260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 1268

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1268

Ser Tyr Ala Met Ser

1 5

<210> 1269

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1269

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1270

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1270

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1271

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1271

Arg Ala Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala

1 5 10

<210> 1272

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1272

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1273

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1273

Gln Gln Tyr Gly Ser Thr Pro Pro Thr

1 5

<210> 1274

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1274

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1275

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1275

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Ser Asp

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr His Cys Gln Gln Tyr Gly Ser Thr Pro
 85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 1276

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1276

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 1277

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1277

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1278

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1278

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1279

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1279

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Ser Asp

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr His Cys Gln Gln Tyr Gly Ser Thr Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1280

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1280

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1281

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1281

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1282

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1282

Ser Tyr Ala Met Ser

1 5

<210> 1283

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1283

Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1284

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1284

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1285

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1285

Arg Ala Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala

1 5 10

<210> 1286

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1286

Gly Ala Ser Thr Arg Ala Thr

1 5

<210> 1287

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1287

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 1288

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1288

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser

115

<210> 1289

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1289

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

1 5 10 15

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

20 25 30

Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1290

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1290

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1291

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1291

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1292

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1292

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1293

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1293

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

1

5

10

15

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

20

25

30

Tyr Phe Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

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

100 105

<210> 1294

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1294

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1295

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1295

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180

185

190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1296

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1296

Ser Tyr Ala Met Ser

1 5

<210> 1297

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1297

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1298

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1298

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1299

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1299

Arg Ala Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 1300

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1300

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1301

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1301

Gln Gln Tyr Gly Ser Ser Pro Pro Ser

1 5

<210> 1302

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1302

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 1303

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1303

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Ser Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1304

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1304

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1305

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1305

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1306

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1306

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1307

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1307

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100

105

<210> 1308

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1308

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1309

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1309

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 1310

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1310

Ser Tyr Ala Met Ser

1 5

<210> 1311

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1311

Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1312

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1312

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1313

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1313

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1314

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1314

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1315

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1315

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1316

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1316

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1317

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1317

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1318

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1318

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1319

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1319

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1320

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1320

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1321

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1321

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Ser Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1322

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1322

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100	105	110	
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly			
115	120	125	
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly			
130	135	140	
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala			
145	150	155	160
Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro			
165	170	175	
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr			
180	185	190	
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr			
195	200	205	
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys			
210	215	220	

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1323

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1323

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
 355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1324

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1324

Ser Tyr Ala Met Ser

1 5

<210> 1325

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1325

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1326

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1326

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1327

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1327

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1328

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1328

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1329

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1329

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1330

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1330

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1331

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1331

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys

100

105

<210> 1332

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1332

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Asp Ile Lys

<210> 1333

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1333

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1334

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1334

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1335

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1335

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 1336

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1336

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Asp Ile Lys

<210> 1337

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1337

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1338

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1338

Thr Tyr Ala Met Ser

1 5

<210> 1339

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1339

Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1340

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1340

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1341

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1341

Arg Ala Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1342

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1342

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1343

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1343

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 1344

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1344

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1345

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1345

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys
100 105

<210> 1346

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1346

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
 35 40 45

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

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Asp Ile Lys

<210> 1347

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1347

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1348

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1348

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1349

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1349

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

1 5 10 15

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

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys

100 105

<210> 1350

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1350

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180	185	190
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr		
195	200	205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys		
210	215	220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val			
225	230	235	240

Asp Ile Lys

<210> 1351

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1351

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 1352

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1352

Ser Tyr Ala Met Ser

1 5

<210> 1353

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1353

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1354

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1354

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1355

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1355

Arg Ala Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala

1 5 10

<210> 1356

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1356

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1357

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1357

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 1358

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1358

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1359

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1359

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys

100 105

<210> 1360

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1360

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys

<210> 1361

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1361

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1362

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1362

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1363

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1363

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Asn

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys

100 105

<210> 1364

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1364

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Asp Ile Lys

<210> 1365

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1365

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1366

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1366

Ser Tyr Ala Met Ser

1 5

<210> 1367

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1367

Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1368

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1368

His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr

1 5 10

<210> 1369

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1369

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala

1 5 10

<210> 1370

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1370

Ala Ala Ser Ile Leu Gln Ser

1 5

<210> 1371

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1371

Gln Gln Tyr Phe Ala Tyr Pro Ile Thr

1 5

<210> 1372

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1372

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1373

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1373

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Phe Ala Tyr Pro Ile

85 90 95

Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys

100

105

<210> 1374

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1374

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln
210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys

<210> 1375

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1375

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly
 180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln
 210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
 260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 1376

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1376

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1377

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1377

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Phe Ala Tyr Pro Ile

85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys

100 105

<210> 1378

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1378

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu

225 230 235 240

Ile Lys

<210> 1379

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1379

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 485 490 495

Leu

<210> 1380

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1380

Ser Tyr Ala Met Ser

1 5

<210> 1381

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1381

Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val Glu

1 5 10 15

Gly

<210> 1382

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1382

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1383

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1383

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1384

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1384

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1385

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1385

Gln Gln Tyr Gly Ser Ser Pro Pro Thr

1 5

<210> 1386

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1386

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1387

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1387

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Pro Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys

100 105

<210> 1388

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1388

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys

<210> 1389

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1389

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu

<210> 1390

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1390

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1391

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1391

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Ser Ser Pro

85

90

95

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

100

105

<210> 1392

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1392

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Arg Leu

225

230

235

240

Glu Ile Lys

<210> 1393

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1393

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Arg Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu

<210> 1394

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1394

Ile Tyr Ala Met Ser

1 5

<210> 1395

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1395

Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1396

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1396

His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr

1 5 10

<210> 1397

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1397

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Val Ala

1 5 10

<210> 1398

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1398

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1399

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1399

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1400

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1400

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1401

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1401

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20 25 30

Tyr Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65

70

75

80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85

90

95

Phe Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys

100

105

<210> 1402

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1402

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys

<210> 1403

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1403

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Arg Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1404

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1404

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1405

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1405

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

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

100 105

<210> 1406

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1406

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys

<210> 1407

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1407

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1408

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1408

Ser Ser Ser Tyr Tyr Trp Gly

1 5

<210> 1409

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1409

Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 1410

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1410

His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe Asp Ile

1 5 10 15

<210> 1411

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1411

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 1412

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1412

Ala Ala Ser Asn Leu Gln Ser

1 5

<210> 1413

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1413

Gln Gln Ser Phe Ser Ser Pro Arg Thr

1 5

<210> 1414

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1414

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

115 120 125

<210> 1415

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1415

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1416

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1416

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Cys

225 230 235 240

Gly Thr Lys Val Glu Ile Lys

245

<210> 1417

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1417

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe
100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
130 135 140

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

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Cys

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

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

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340 345 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu

385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly

405

410

415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

420

425

430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe

435

440

445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly

450

455

460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu

465

470

475

480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly

485

490

495

Thr Lys Leu Thr Val Leu

500

<210> 1418

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1418

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100

105

110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

115

120

125

<210> 1419

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1419

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20

25

30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1420

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1420

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Gln

225 230 235 240

Gly Thr Lys Val Glu Ile Lys

245

<210> 1421

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1421

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

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

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Gln

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

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

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340 345 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
405 410 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
420 425 430

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

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
450 455 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465 470 475 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly

485

490

495

Thr Lys Leu Thr Val Leu

500

<210> 1422

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1422

Ser Tyr Ser Met Asn

1

5

<210> 1423

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1423

Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1424

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1424

Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr

1 5 10

<210> 1425

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1425

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala

1 5 10

<210> 1426

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1426

Ala Ala Ser Thr Leu Gln Ser

1 5

<210> 1427

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1427

Gln Gln Tyr Tyr Ser Thr Pro Leu Thr

1 5

<210> 1428

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1428

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1429

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1429

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala

65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1430

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1430

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 1431

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1431

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 1432

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1432

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1433

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1433

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala

65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu

85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100

105

<210> 1434

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1434

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys

<210> 1435

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1435

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 165 170 175

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
 210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
 260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 1436

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1436

Val Tyr Ala Met Ser

1 5

<210> 1437

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1437

Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1438

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1438

His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr

1 5 10

<210> 1439

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1439

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala

1 5 10

<210> 1440

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1440

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 1441

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1441

Gln Gln Tyr Gly Asp Leu Pro Phe Thr

1 5

<210> 1442

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1442

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1443

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1443

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

1

5

10

15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro
 85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 1444

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1444

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys

<210> 1445

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1445

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1446

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1446

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1447

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1447

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asp Leu Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1448

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1448

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys

<210> 1449

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1449

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu

<210> 1450

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1450

Ser Tyr Gly Met His

1 5

<210> 1451

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1451

Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 1452

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1452

Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp Val

1 5 10 15

<210> 1453

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1453

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn

1 5 10

<210> 1454

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1454

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 1455

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1455

Gln Gln Ser Tyr Ser Thr Pro Phe Thr

1 5

<210> 1456

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1456

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 1457

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1457

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1458

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1458

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly

225 230 235 240

Thr Lys Val Glu Ile Lys

245

<210> 1459

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1459

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275

280

285

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

290

295

300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305

310

315

320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325

330

335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340

345

350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385

390

395

400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405

410

415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420

425

430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465

470

475

480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu

500

<210> 1460

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1460

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1461

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1461

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe

85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1462

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1462

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly

225 230 235 240

Thr Lys Val Glu Ile Lys

245

<210> 1463

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1463

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
 245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
 260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
 275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu

500

<210> 1464

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1464

Ser Tyr Gly Met His

1 5

<210> 1465

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1465

Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val Lys

1 5 10 15

Gly

<210> 1466

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1466

Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val

1 5 10

<210> 1467

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1467

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala

1 5 10

<210> 1468

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1468

Asp Val Phe Asp Arg Ala Thr

1 5

<210> 1469

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1469

Gln Gln Tyr Ser Glu Ser Pro Phe Thr

1 5

<210> 1470

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1470

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 1471

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1471

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Arg Arg Ile

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Asp Val Phe Asp Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Glu Ser Pro

85 90 95

Phe Thr Phe Gly Cys Gly Thr Lys Val Asp Ile Lys

100 105

<210> 1472

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1472

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115

120

125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130

135

140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys

145

150

155

160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln

165

170

175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Val Phe Asp Arg

180

185

190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp

195

200

205

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr

210

215

220

Tyr Cys Gln Gln Tyr Ser Glu Ser Pro Phe Thr Phe Gly Cys Gly Thr

225

230

235

240

Lys Val Asp Ile Lys

245

<210> 1473

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1473

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys

145 150 155 160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln

165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Val Phe Asp Arg

180 185 190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp

195

200

205

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr

210

215

220

Tyr Cys Gln Gln Tyr Ser Glu Ser Pro Phe Thr Phe Gly Cys Gly Thr

225

230

235

240

Lys Val Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val

245

250

255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser

260

265

270

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val

275

280

285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser

290

295

300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg

305

310

315

320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met

325 330 335

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His

340 345 350

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln

355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

370 375 380

Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser

385 390 395 400

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser

405 410 415

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys

420 425 430

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala

435 440 445

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala

450 455 460

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr

465 470 475 480

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys

485 490 495

Leu Thr Val Leu

500

<210> 1474

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1474

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 1475

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1475

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Arg Arg Ile

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Asp Val Phe Asp Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Glu Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

100

105

<210> 1476

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1476

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys

145 150 155 160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln

165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Val Phe Asp Arg

180 185 190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp

195 200 205

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr

210 215 220

Tyr Cys Gln Gln Tyr Ser Glu Ser Pro Phe Thr Phe Gly Pro Gly Thr

225 230 235 240

Lys Val Asp Ile Lys

245

<210> 1477

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1477

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys

145 150 155 160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln

165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Val Phe Asp Arg

180 185 190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp

195 200 205

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr

210 215 220

Tyr Cys Gln Gln Tyr Ser Glu Ser Pro Phe Thr Phe Gly Pro Gly Thr

225 230 235 240

Lys Val Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val

245 250 255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser

260 265 270

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val

275 280 285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser

290 295 300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg

305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met

325 330 335

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His

340 345 350

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln

355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

370 375 380

Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
385 390 395 400

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
 405 410 415

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
 420 425 430

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

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
 450 455 460

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
465 470 475 480

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Thr Val Leu
 500

<210> 1478

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1478

Ser Tyr Gly Ile Ser

1 5

<210> 1479

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1479

Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu Gln

1 5 10 15

Gly

<210> 1480

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1480

Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val

1 5 10

<210> 1481

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1481

Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr

1 5 10

<210> 1482

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1482

Arg Ser Asp Gln Arg Pro Ser

1 5

<210> 1483

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1483

Ala Ala Phe Asp Glu Ser Leu Ser Gly Val Val

1 5 10

<210> 1484

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1484

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 1485

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1485

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn

20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

35 40 45

Ile Tyr Arg Ser Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Leu Ser Gly Leu Arg

65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Phe Asp Glu Ser Leu

85 90 95

Ser Gly Val Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu

100 105 110

<210> 1486

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1486

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Ala Ala Phe Asp Glu Ser Leu Ser Gly Val Val Phe Gly Cys Gly

225 230 235 240

Thr Lys Leu Thr Val Leu

245

<210> 1487

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1487

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Ala Ala Phe Asp Glu Ser Leu Ser Gly Val Val Phe Gly Cys Gly

225 230 235 240

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385

390

395

400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405

410

415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420

425

430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465

470

475

480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu

500

<210> 1488

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1488

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

1

5

10

15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20

25

30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 1489

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1489

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ile Asn

20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

35 40 45

Ile Tyr Arg Ser Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Leu Ser Gly Leu Arg

65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Phe Asp Glu Ser Leu

85 90 95

Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100 105 110

<210> 1490

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1490

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Ala Ala Phe Asp Glu Ser Leu Ser Gly Val Val Phe Gly Gly Gly

225 230 235 240

Thr Lys Leu Thr Val Leu

245

<210> 1491

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1491

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu

2200

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180

185

190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195

200

205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210

215

220

Cys Ala Ala Phe Asp Glu Ser Leu Ser Gly Val Val Phe Gly Gly Gly

225

230

235

240

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245

250

255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260

265

270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275

280

285

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

290

295

300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
 355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465

470

475

480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu

500

<210> 1492

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1492

Tyr Tyr Gly Met His

1 5

<210> 1493

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1493

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

1 5 10 15

Gly

<210> 1494

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1494

Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr

1 5 10

<210> 1495

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1495

Arg Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala

1 5 10

<210> 1496

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1496

Ala Val Ser Ile Leu Gln Ser

1 5

<210> 1497

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1497

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser

1 5

<210> 1498

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1498

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

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1499

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1499

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asn Asn Tyr

20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile

35 40 45

Tyr Ala Val Ser Ile Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Phe Tyr Pro Phe

85 90 95

Ser Phe Gly Cys Gly Thr Lys Val Asp Ile Lys

100

105

<210> 1500

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1500

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

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

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

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro

130 135 140

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

145 150 155 160

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro

165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser

180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys

210

215

220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Asp Ile Lys

<210> 1501

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1501

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

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro

130 135 140

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

145 150 155 160

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro

165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser

180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys

210 215 220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1502

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1502

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

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100

105

110

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1503

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1503

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Asn Asn Tyr

20

25

30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile

35

40

45

Tyr Ala Val Ser Ile Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Phe Tyr Pro Phe

85

90

95

Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys

100

105

<210> 1504

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1504

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

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro

130 135 140

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

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser
 180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Gln Gly Thr Lys Val
 225 230 235 240

Asp Ile Lys

<210> 1505

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1505

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

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

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

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser
180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu

<210> 1506

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1506

Gly Phe Tyr Trp Ser

1 5

<210> 1507

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1507

Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 1508

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1508

Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr

1 5 10

<210> 1509

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1509

Arg Thr Ser Gln Tyr Ile Gly Arg Tyr Leu Asn

1 5 10

<210> 1510

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1510

Gly Ala Ser Thr Leu Gln Gln

1 5

<210> 1511

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1511

Gln Gln Thr Tyr Ser Thr Pro Arg Thr

1 5

<210> 1512

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1512

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 1513

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1513

Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Tyr Ile Gly Arg Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile

35

40

45

Tyr Gly Ala Ser Thr Leu Gln Gln Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr Tyr Ser Thr Pro Arg

85

90

95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100

105

<210> 1514

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1514

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln
145 150 155 160

Tyr Ile Gly Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
195 200 205

Thr Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr
210 215 220

Tyr Ser Thr Pro Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
225 230 235 240

<210> 1515

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1515

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln
145 150 155 160

Tyr Ile Gly Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
195 200 205

Thr Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr
210 215 220

Tyr Ser Thr Pro Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

225 230 235 240

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly

245 250 255

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

260 265 270

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly

275 280 285

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr

290 295 300

Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg

305 310 315 320

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr

325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn

340 345 350

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr

355 360 365

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

370 375 380

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro

385 390 395 400

Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr

405 410 415

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro

420 425 430

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala

435 440 445

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser

450 455 460

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr

465 470 475 480

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

485 490 495

<210> 1516

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1516

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 1517

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1517

Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Tyr Ile Gly Arg Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile

35 40 45

Tyr Gly Ala Ser Thr Leu Gln Gln Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr Tyr Ser Thr Pro Arg

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1518

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1518

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu

130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln

145 150 155 160

Tyr Ile Gly Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala

165 170 175

Pro Lys Val Leu Ile Tyr Gly Ala Ser Thr Leu Gln Gln Gly Val Pro

180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile

195 200 205

Thr Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr

210 215 220

Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

225 230 235 240

<210> 1519

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1519

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu

130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln

145 150 155 160

Tyr Ile Gly Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala

165 170 175

Pro Lys Val Leu Ile Tyr Gly Ala Ser Thr Leu Gln Gln Gly Val Pro

180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile

195 200 205

Thr Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr

210 215 220

Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

225 230 235 240

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly

245 250 255

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

260 265 270

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly

275 280 285

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr

290 295 300

Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg

305 310 315 320

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr

325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn

340 345 350

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr

355 360 365

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

370 375 380

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro

385 390 395 400

Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr

405 410 415

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro

420 425 430

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala

435 440 445

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
450 455 460

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr
465 470 475 480

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

<210> 1520

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1520

Thr Tyr Gly Met His

1 5

<210> 1521

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1521

Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val Lys

1 5 10 15

Gly

<210> 1522

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1522

Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val

1 5 10

<210> 1523

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1523

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn

1 5 10

<210> 1524

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1524

Val Asn Asn Asn Arg Pro Ser

1 5

<210> 1525

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1525

Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val

1 5 10

<210> 1526

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1526

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 1527

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1527

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly

20 25 30

Tyr Asp Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu

35 40 45

Leu Ile Tyr Val Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe

50 55 60

Ser Gly Ser Thr Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser

85 90 95

Leu Ser Ala Ser Val Phe Gly Cys Gly Thr Arg Leu Thr Val Leu

100 105 110

<210> 1528

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1528

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130

135

140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145

150

155

160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165

170

175

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

180

185

190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195

200

205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210

215

220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly

225 230 235 240

Thr Arg Leu Thr Val Leu

245

<210> 1529

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1529

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165 170 175

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

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly

225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

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

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu
500

<210> 1530

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1530

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 1531

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1531

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly

20 25 30

Tyr Asp Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu

35 40 45

Leu Ile Tyr Val Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe

50 55 60

Ser Gly Ser Thr Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr Ser

85

90

95

Leu Ser Ala Ser Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu

100

105

110

<210> 1532

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1532

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165 170 175

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

180

185

190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195

200

205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210

215

220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly

225

230

235

240

Thr Arg Leu Thr Val Leu

245

<210> 1533

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1533

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165 170 175

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

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly

225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

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

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu

500

<210> 1534

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1534

Thr Tyr Gly Met His

1 5

<210> 1535

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1535

Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val Lys

1 5 10 15

Gly

<210> 1536

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1536

Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val

1 5 10

<210> 1537

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1537

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn

1 5 10

<210> 1538

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1538

Val Asn Asn Asn Arg Pro Ser

1 5

<210> 1539

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1539

Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val

1 5 10

<210> 1540

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1540

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1541

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1541

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

1

5

10

15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly

20

25

30

Tyr Asp Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu

35

40

45

Leu Ile Tyr Val Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe

50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Thr Ser

85 90 95

Leu Ser Ala Ser Val Phe Gly Cys Gly Thr Arg Leu Thr Val Leu

100 105 110

<210> 1542

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1542

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Leu

165 170 175

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

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly

225 230 235 240

Thr Arg Leu Thr Val Leu

245

<210> 1543

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1543

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Leu

165 170 175

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

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly
225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
 245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
 260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
 275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu

500

<210> 1544

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1544

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1545

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1545

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly

20 25 30

Tyr Asp Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu

35 40 45

Leu Ile Tyr Val Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe

50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Thr Ser

85 90 95

Leu Ser Ala Ser Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu

100 105 110

<210> 1546

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1546

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Leu

165 170 175

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

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly

225 230 235 240

Thr Arg Leu Thr Val Leu

245

<210> 1547

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1547

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130

135

140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145

150

155

160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Leu

165

170

175

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

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly

225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

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

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420

425

430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465

470

475

480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu

500

<210> 1548

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1548

Ser Gly Val Tyr Tyr Trp Ser

1 5

<210> 1549

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1549

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

1 5 10 15

<210> 1550

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1550

Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr

1 5 10

<210> 1551

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1551

Arg Ala Ser Gln Ser Val Asp Arg Tyr Phe Asn

1 5 10

<210> 1552

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1552

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 1553

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1553

Gln Gln Ser Tyr Ser Thr Pro Trp Thr

1 5

<210> 1554

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1554

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

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

20 25 30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 1555

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1555

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Asp Arg Tyr

20 25 30

Phe Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile

35 40 45

Phe Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Val Lys

100 105

<210> 1556

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1556

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

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

20 25 30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Val Asp Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Phe Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Val Lys

<210> 1557

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1557

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

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

20 25 30

Val Tyr Trp Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35

40

45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50

55

60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65

70

75

80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85

90

95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

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

145

150

155

160

Ser Gln Ser Val Asp Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Phe Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Val Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 1558

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1558

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

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

20 25 30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1559

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1559

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Asp Arg Tyr

20

25

30

Phe Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile

35

40

45

Phe Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

100 105

<210> 1560

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1560

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

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

20 25 30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Ser Val Asp Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Phe Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

225 230 235 240

Val Lys

<210> 1561

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1561

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

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

20 25 30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

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

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

225 230 235 240

Val Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu

<210> 1562

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1562

Ser Gly Gly Tyr Tyr Trp Ser

1

5

<210> 1563

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1563

Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser Leu Lys Ser

1 5 10 15

<210> 1564

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1564

Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala

1 5 10

<210> 1565

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1565

Arg Ala Ser Gln Phe Ile Gly Arg Tyr Phe Asn

1 5 10

<210> 1566

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1566

Ala Glu Ser Ser Leu Gln Ser

1 5

<210> 1567

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1567

Gln Gln Ser Tyr Ser Thr Pro Trp Thr

1 5

<210> 1568

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1568

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85

90

95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 1569

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1569

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Phe Ile Gly Arg Tyr

20

25

30

Phe Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile

35 40 45

Tyr Ala Glu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp

85 90 95

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1570

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1570

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 1571

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1571

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 1572

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1572

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

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

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1573

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1573

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Phe Ile Gly Arg Tyr

20 25 30

Phe Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile

35 40 45

Tyr Ala Glu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 1574

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1574

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

225

230

235

240

Ile Lys

<210> 1575

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1575

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1

5

10

15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20

25

30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

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

145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly
165 170 175

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

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu

<210> 1576

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1576

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1577

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1577

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1578

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1578

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1579

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1579

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1580

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1580

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1581

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1581

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
915 920 925

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 1582

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1582

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1583

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1583

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1584

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1584

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275	280	285			
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr					
290	295	300			
Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr					
305	310	315	320		
Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn					
	325	330	335		
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn					
	340	345	350		
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr					
	355	360	365		
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser					
	370	375	380		
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr					
385	390	395	400		

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1585

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1585

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

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<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1586

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 980 985

<210> 1587

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1587

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1588

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1588

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1589

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1589

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1590

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1590

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
 820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
 835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1591

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1591

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1592

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1592

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

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

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
 820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1593

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1593

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1594

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1594

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1595

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1595

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
915 920 925

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1596

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1596

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1597

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1597

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1598

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1598

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1599

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1599

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915	920	925
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe		
930	935	940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn			
945	950	955	960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr			
965	970	975	

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			
980	985		

<210> 1600

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1600

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1601

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1601

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340	345	350	
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr			
355	360	365	
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
370	375	380	
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr			
385	390	395	400
Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly			
405	410	415	
Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly			
420	425	430	
Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly			
435	440	445	
Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu			
450	455	460	

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1602

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1602

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
 355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1603

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1603

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

2560

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1604

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1604

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

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

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210

215

220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1605

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1605

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 1606

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1606

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly
 165 170 175

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 195 200 205

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

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
 260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515

520

525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530

535

540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545

550

555

560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565

570

575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580

585

590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595

600

605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610

615

620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625

630

635

640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645

650

655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660

665

670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675

680

685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690

695

700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705

710

715

720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725

730

735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740

745

750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755

760

765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770

775

780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785

790

795

800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805

810

815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820

825

830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835

840

845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850

855

860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865

870

875

880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1607

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1607

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

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

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725

730

735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740

745

750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755

760

765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770

775

780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785

790

795

800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805

810

815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820

825

830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835

840

845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1608

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1608

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1609

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1609

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1610

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1610

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1611

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1611

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1612

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1612

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

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

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

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

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

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

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
915 920 925

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 1613

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1613

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1614

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1614

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1615

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1615

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

2660

275	280	285			
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr					
290	295	300			
Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr					
305	310	315	320		
Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn					
	325	330	335		
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn					
	340	345	350		
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr					
	355	360	365		
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser					
	370	375	380		
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr					
385	390	395	400		

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1616

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1616

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1617

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1617

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 980 985

<210> 1618

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1618

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1619

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1619

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1620

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1620

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1621

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1621

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
 820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
 835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1622

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1622

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1623

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1623

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145

150

155

160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180

185

190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln
210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580

585

590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595

600

605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610

615

620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625

630

635

640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645

650

655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660

665

670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675

680

685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690

695

700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
 725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1624

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1624

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1625

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1625

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Arg Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1626

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1626

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1627

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1627

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

2760

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1628

<211> 990

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1628

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130

135

140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145

150

155

160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165

170

175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180

185

190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195

200

205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210

215

220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Gln

225

230

235

240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245

250

255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260

265

270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275

280

285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile

290

295

300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305

310

315

320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325

330

335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340

345

350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355

360

365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
 405 410 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
 420 425 430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
 435 440 445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
 450 455 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465 470 475 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
 485 490 495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys

500 505 510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

515 520 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

530 535 540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

545 550 555 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

565 570 575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

580 585 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

595 600 605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

610 615 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

625 630 635 640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

675 680 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

690 695 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr
755 760 765

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
770 775 780

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
785 790 795 800

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
805 810 815

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
820 825 830

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val
835 840 845

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
850 855 860

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
865 870 875 880

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

885 890 895

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val

900 905 910

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

915 920 925

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp

930 935 940

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp

945 950 955 960

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His

965 970 975

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985 990

<210> 1629

<211> 990

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1629

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Cys

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340

345

350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355

360

365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu

385

390

395

400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly

405

410

415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

420

425

430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe

435

440

445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly

450

455

460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465 470 475 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
 485 490 495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys
 500 505 510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 515 520 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 530 535 540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
545 550 555 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 565 570 575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
 580 585 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

595

600

605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

610

615

620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

625

630

635

640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

645

650

655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

660

665

670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

675

680

685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

690

695

700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr

755 760 765

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe

770 775 780

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro

785 790 795 800

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val

805 810 815

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr

820 825 830

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val

835

840

845

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys

850

855

860

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser

865

870

875

880

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

885

890

895

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val

900

905

910

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

915

920

925

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp

930

935

940

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp

945

950

955

960

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His

965

970

975

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

990

<210> 1630

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1630

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85

90

95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145

150

155

160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210

215

220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu

225

230

235

240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260

265

270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290

295

300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915	920	925
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu		
930	935	940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val			
945	950	955	960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln			
965	970	975	

Lys Ser Leu Ser Leu Ser Pro Gly Lys	
980	985

<210> 1631

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1631

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly			
1	5	10	15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
 405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
 420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
 435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
 450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755

760

765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770

775

780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785

790

795

800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805

810

815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820

825

830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835

840

845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850

855

860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865

870

875

880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885

890

895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900

905

910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915

920

925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930

935

940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945

950

955

960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965

970

975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1632

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1632

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1633

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1633

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
 355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1634

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1634

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys

755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1635

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1635

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130

135

140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145

150

155

160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165

170

175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180

185

190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195

200

205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210

215

220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
 245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
 260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
 275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595

600

605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610

615

620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625

630

635

640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645

650

655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660

665

670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675

680

685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690

695

700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705

710

715

720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1636

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1636

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 1637

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1637

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
 180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1638

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1638

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1639

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1639

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

2860

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1640

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1640

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1641

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1641

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1642

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1642

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1643

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1643

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 1644

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1644

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1645

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1645

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

2908

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1646

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1646

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275	280	285			
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr					
290	295	300			
Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr					
305	310	315	320		
Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn					
	325	330	335		
Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn					
	340	345	350		
Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr					
	355	360	365		
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser					
	370	375	380		
Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr					
385	390	395	400		

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1647

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1647

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1648

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1648

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
 980

<210> 1649

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1649

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1650

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1650

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

2950

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1651

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1651

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1652

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1652

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
 835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1653

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1653

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1654

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1654

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
 725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1655

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1655

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1656

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1656

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
 725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1657

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1657

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1658

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1658

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1659

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1659

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1660

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1660

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1661

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1661

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915	920	925
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr		
930	935	940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe			
945	950	955	960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys			
965	970	975	

Ser Leu Ser Leu Ser Pro Gly Lys			
980			

<210> 1662

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1662

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1663

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1663

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

3060

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1664

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1664

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
 355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1665

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1665

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1666

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1666

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130

135

140

Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180

185

190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210

215

220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
 260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
 275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
 290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
 325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
 340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595

600

605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610

615

620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625

630

635

640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645

650

655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660

665

670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675

680

685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690

695

700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705

710

715

720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915 920 925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930 935 940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945 950 955 960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965 970 975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1667

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1667

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Asp Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805

810

815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820

825

830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835

840

845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850

855

860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865

870

875

880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885

890

895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900

905

910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
930 935 940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
945 950 955 960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
965 970 975

Leu Ser Leu Ser Pro Gly Lys
980

<210> 1668

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1668

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
 180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys
 210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1669

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1669

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1670

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1670

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1671

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1671

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Gly Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1672

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1672

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1673

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1673

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1674

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1674

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 1675

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1675

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys
210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

3160

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1676

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1676

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1677

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1677

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1678

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1678

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225

230

235

240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1679

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1679

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
 980

<210> 1680

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1680

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225

230

235

240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1681

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1681

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1682

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1682

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145

150

155

160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180

185

190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915 920 925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930 935 940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945 950 955 960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965 970 975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1683

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1683

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Asp Ser Gly Gly Ile Thr Asp Phe Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
 820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
 835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945

950

955

960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1684

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1684

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1685

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1685

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Asp Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Arg Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
 725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1686

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1686

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1687

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1687

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Arg Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
 725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1688

<211> 988

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1688

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Gln

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340

345

350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355

360

365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu

385

390

395

400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly

405

410

415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

420

425

430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe

435

440

445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly

450

455

460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu

465 470 475 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly

485 490 495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys

500 505 510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

515 520 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

530 535 540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

545 550 555 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

565 570 575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

580 585 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

595 600 605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

610 615 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

625 630 635 640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

675 680 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

690 695 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro

755 760 765

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

770 775 780

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

785 790 795 800

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

805 810 815

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

820 825 830

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
835 840 845

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
850 855 860

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
865 870 875 880

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
885 890 895

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
900 905 910

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
915 920 925

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
930 935 940

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
945 950 955 960

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

965

970

975

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1689

<211> 988

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1689

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1

5

10

15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20

25

30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35

40

45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe
100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Cys

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340 345 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu

385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly

405 410 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

420

425

430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe

435

440

445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly

450

455

460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu

465

470

475

480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly

485

490

495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys

500

505

510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

515

520

525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

530

535

540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
545 550 555 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 565 570 575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
 580 585 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 595 600 605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 610 615 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
625 630 635 640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

675 680 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

690 695 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro

755 760 765

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

770 775 780

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

785 790 795 800

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

805 810 815

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

820 825 830

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

835 840 845

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

850 855 860

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

865 870 875 880

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

885 890 895

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

900 905 910

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

915

920

925

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

930

935

940

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

945

950

955

960

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

965

970

975

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1690

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1690

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145

150

155

160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210

215

220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu

225

230

235

240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
 405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
 420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
 435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
 450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915 920 925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930 935 940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945 950 955 960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965 970 975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1691

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1691

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
 580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835

840

845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850

855

860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865

870

875

880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885

890

895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900

905

910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945

950

955

960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1692

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1692

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

Ser Leu Ser Leu Ser Pro Gly Lys

<210> 1693

<211> 984

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic peptide

<400> 1693

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Asp Ser Gly Gly Ser Thr Phe Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 1694

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1694

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Ser Gly

725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly

740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro

755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

965

970

975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1695

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1695

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly
 355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675

680

685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690

695

700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705

710

715

720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly

725

730

735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

740

745

750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro

755

760

765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

770

775

780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

785

790

795

800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

805

810

815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

820

825

830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

835

840

845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

850

855

860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

865

870

875

880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

885

890

895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900

905

910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915

920

925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1696

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1696

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755	760	765	
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro			
770	775	780	
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys			
785	790	795	800
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp			
	805	810	815
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu			
	820	825	830
Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu			
	835	840	845
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn			
	850	855	860
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly			
865	870	875	880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1697

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1697

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1698

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1698

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 1699

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1699

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
 180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1700

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1700

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1701

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1701

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
 180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1702

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1702

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

3385

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1703

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1703

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1704

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1704

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1705

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1705

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 1706

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1706

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1707

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1707

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1708

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1708

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1709

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1709

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1710

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1710

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 980 985

<210> 1711

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1711

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1712

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1712

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115	120	125			
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly					
130	135	140			
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala					
145	150	155	160		
Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro					
	165	170	175		
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr					
180	185	190			
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr					
195	200	205			
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys					
210	215	220			
Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val					
225	230	235	240		

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1713

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1713

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1714

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1714

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
 820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
 835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1715

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1715

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1716

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1716

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
 820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1717

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1717

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
 820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
 835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1718

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1718

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1719

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1719

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1720

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1720

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50

55

60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1721

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1721

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1722

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1722

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1723

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1723

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1724

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1724

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1725

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1725

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys
210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1726

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1726

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675

680

685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690

695

700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705

710

715

720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725

730

735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740

745

750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755

760

765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770

775

780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785

790

795

800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1727

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1727

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885

890

895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900

905

910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915

920

925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930

935

940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945

950

955

960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965

970

975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1728

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1728

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210

215

220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1729

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1729

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 1730

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1730

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
 180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1731

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1731

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1732

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1732

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
 180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1733

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1733

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1734

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1734

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1735

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1735

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys
210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1736

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1736

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785

790

795

800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 1737

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1737

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1738

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1738

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1739

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1739

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1740

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1740

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1741

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1741

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 980 985

<210> 1742

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1742

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly
180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln
210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu
225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660

665

670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675

680

685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690

695

700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705

710

715

720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725

730

735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740

745

750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755

760

765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770

775

780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1743

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1743

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1744

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1744

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1745

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1745

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Arg Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755

760

765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770

775

780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
 820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
 835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1746

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1746

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1747

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1747

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
 820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1748

<211> 990

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1748

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Cys

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340 345 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu

385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly

405 410 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
420 425 430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
435 440 445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
450 455 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465 470 475 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly
485 490 495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys
500 505 510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
515 520 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
530 535 540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

545 550 555 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

565 570 575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

580 585 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

595 600 605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

610 615 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

625 630 635 640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

675 680 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

690 695 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr

755 760 765

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe

770 775 780

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro

785 790 795 800

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val

805 810 815

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr

820 825 830

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val

835 840 845

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys

850 855 860

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser

865 870 875 880

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

885 890 895

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val

900 905 910

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

915

920

925

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp

930

935

940

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp

945

950

955

960

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His

965

970

975

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

990

<210> 1749

<211> 990

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1749

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln
245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340 345 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu

385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly

405 410 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

420 425 430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe

435 440 445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly

450 455 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu

465 470 475 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly

485 490 495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys

500

505

510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

515

520

525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

530

535

540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

545

550

555

560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

565

570

575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

580

585

590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

595

600

605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

610

615

620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
625 630 635 640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 675 680 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 690 695 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly
 725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 740 745 750

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr

755

760

765

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe

770

775

780

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro

785

790

795

800

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val

805

810

815

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr

820

825

830

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val

835

840

845

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys

850

855

860

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser

865 870 875 880

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

885 890 895

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val

900 905 910

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

915 920 925

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp

930 935 940

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp

945 950 955 960

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His

965 970 975

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985 990

<210> 1750

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1750

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965

970

975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1751

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1751

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85

90

95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145

150

155

160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500

505

510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515

520

525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530

535

540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
 580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675

680

685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690

695

700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705

710

715

720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725

730

735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740

745

750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755

760

765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770

775

780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915

920

925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930

935

940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945

950

955

960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965

970

975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1752

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1752

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1753

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1753

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1754

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1754

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1755

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1755

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260

265

270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275

280

285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290

295

300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305

310

315

320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325

330

335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340

345

350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
 435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
 500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys

755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 1756

<211> 988

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1756

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys

145 150 155 160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln

165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Val Phe Asp Arg

180 185 190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp

195 200 205

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr

210 215 220

Tyr Cys Gln Gln Tyr Ser Glu Ser Pro Phe Thr Phe Gly Cys Gly Thr
225 230 235 240

Lys Val Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
 245 250 255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
 260 265 270

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val
 275 280 285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
290 295 300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg
305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
 325 330 335

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His

340 345 350

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln

355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

370 375 380

Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser

385 390 395 400

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser

405 410 415

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys

420 425 430

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala

435 440 445

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala

450 455 460

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr

465 470 475 480

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys

485 490 495

Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro

500 505 510

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

515 520 525

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

530 535 540

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

545 550 555 560

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

565 570 575

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

580 585 590

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
595 600 605

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
610 615 620

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
625 630 635 640

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
645 650 655

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
660 665 670

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
675 680 685

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
690 695 700

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
705 710 715 720

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro

755 760 765

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

770 775 780

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

785 790 795 800

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

805 810 815

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

820 825 830

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

835 840 845

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

850 855 860

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

865 870 875 880

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

885 890 895

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

900 905 910

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

915 920 925

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

930 935 940

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

945 950 955 960

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

965

970

975

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1757

<211> 988

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1757

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys

145 150 155 160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln

165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Val Phe Asp Arg

180

185

190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp

195

200

205

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr

210

215

220

Tyr Cys Gln Gln Tyr Ser Glu Ser Pro Phe Thr Phe Gly Pro Gly Thr

225

230

235

240

Lys Val Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val

245

250

255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser

260

265

270

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val

275

280

285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser

290

295

300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg
305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
 325 330 335

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
 340 345 350

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
 355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser
385 390 395 400

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser
 405 410 415

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
 420 425 430

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala

435 440 445

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala

450 455 460

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr

465 470 475 480

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys

485 490 495

Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro

500 505 510

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

515 520 525

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

530 535 540

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

545 550 555 560

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

565 570 575

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

580 585 590

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

595 600 605

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

610 615 620

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

625 630 635 640

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

645 650 655

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

660 665 670

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

675 680 685

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

690 695 700

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

705 710 715 720

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro

755 760 765

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

770 775 780

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

785 790 795 800

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

805

810

815

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

820

825

830

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

835

840

845

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

850

855

860

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

865

870

875

880

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

885

890

895

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

900

905

910

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

915

920

925

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

930 935 940

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

945 950 955 960

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

965 970 975

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1758

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1758

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro
130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Ala Ala Phe Asp Glu Ser Leu Ser Gly Val Val Phe Gly Cys Gly

225 230 235 240

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
 405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
 420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
 435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
 450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
 485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
 500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys

755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1759

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1759

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Ala Ala Phe Asp Glu Ser Leu Ser Gly Val Val Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Ser Glu Val Gln Leu
 245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
 260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
 275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
 290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
 325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595

600

605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610

615

620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625

630

635

640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645

650

655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660

665

670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675

680

685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690

695

700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705

710

715

720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1760

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1760

Gln Ala Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Ala Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro

130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg

145 150 155 160

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro

165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser

180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys

210 215 220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805

810

815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820

825

830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835

840

845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850

855

860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865

870

875

880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885

890

895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985

<210> 1761

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1761

Gln Ala Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Ala Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro

130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145 150 155 160

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro
 165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser
 180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Gln Gly Thr Lys Val
225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1762

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1762

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr

100	105	110	
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
115	120	125	
Gly Gly Gly Gly Ser Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu			
130	135	140	
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln			
145	150	155	160
Tyr Ile Gly Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala			
165	170	175	
Pro Lys Val Leu Ile Tyr Gly Ala Ser Thr Leu Gln Gln Gly Val Pro			
180	185	190	
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile			
195	200	205	
Thr Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr			
210	215	220	

Tyr Ser Thr Pro Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

225 230 235 240

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly

245 250 255

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

260 265 270

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly

275 280 285

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr

290 295 300

Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg

305 310 315 320

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr

325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn

340 345 350

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
355 360 365

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
370 375 380

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
385 390 395 400

Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr
405 410 415

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro
420 425 430

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala
435 440 445

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser
450 455 460

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr
465 470 475 480

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly

485 490 495

Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu

500 505 510

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

515 520 525

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

530 535 540

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly

545 550 555 560

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly

565 570 575

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp

580 585 590

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

595 600 605

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu

610 615 620

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn

625 630 635 640

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

645 650 655

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

660 665 670

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

675 680 685

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

690 695 700

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

705 710 715 720

Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725

730

735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740

745

750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755

760

765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770

775

780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785

790

795

800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805

810

815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820

825

830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835

840

845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850

855

860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865

870

875

880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885

890

895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900

905

910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945

950

955

960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1763

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1763

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu
 130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln
145 150 155 160

Tyr Ile Gly Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 165 170 175

Pro Lys Val Leu Ile Tyr Gly Ala Ser Thr Leu Gln Gln Gly Val Pro
 180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile

195 200 205

Thr Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr

210 215 220

Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

225 230 235 240

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly

245 250 255

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

260 265 270

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly

275 280 285

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr

290 295 300

Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg

305 310 315 320

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr

325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn

340 345 350

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr

355 360 365

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

370 375 380

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro

385 390 395 400

Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr

405 410 415

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro

420 425 430

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala

435

440

445

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser

450

455

460

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr

465

470

475

480

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly

485

490

495

Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu

500

505

510

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

515

520

525

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

530

535

540

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly

545

550

555

560

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly

565

570

575

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp

580

585

590

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

595

600

605

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu

610

615

620

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn

625

630

635

640

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

645

650

655

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

660

665

670

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

675

680

685

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

690 695 700

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

705 710 715 720

Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915 920 925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945

950

955

960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1764

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1764

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Asn Asn Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly

225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275

280

285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290

295

300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305

310

315

320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325

330

335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340

345

350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385

390

395

400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys

755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1765

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1765

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Asn Asn Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly

225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr
580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys

755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1766

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1766

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Asn Asn Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala
195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly
225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp
275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys
755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
770 775 780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
785 790 795 800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
805 810 815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

820 825 830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

835 840 845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

850 855 860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

865 870 875 880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

885 890 895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

900 905 910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

915 920 925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

930 935 940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

945 950 955 960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

965 970 975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1767

<211> 989

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1767

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Asn Asn Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly

225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275

280

285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290

295

300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305

310

315

320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325

330

335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340

345

350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385

390

395

400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser
405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys

755 760 765

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

770

775

780

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

785

790

795

800

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

805

810

815

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

820

825

830

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

835

840

845

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

850

855

860

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

865

870

875

880

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

885

890

895

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

900

905

910

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

915

920

925

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

930

935

940

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

945

950

955

960

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

965

970

975

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1768

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1768

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Glu Ser Gly

20 25 30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Asp Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Val Leu Ile Phe Ala Ala Ser Ser Leu Gln Ser Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu
225 230 235 240

Val Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740

745

750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755

760

765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770

775

780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785

790

795

800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805

810

815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820

825

830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835

840

845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1769

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1769

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1

5

10

15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Glu Ser Gly

20

25

30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35

40

45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50

55

60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Asp Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Phe Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

225 230 235 240

Val Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820

825

830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835

840

845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850

855

860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865

870

875

880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885

890

895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900

905

910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915

920

925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930

935

940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1770

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1770

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530

535

540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545

550

555

560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565

570

575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580

585

590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595

600

605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610

615

620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625

630

635

640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645

650

655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900

905

910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915

920

925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930

935

940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945

950

955

960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965

970

975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1771

<211> 985

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1771

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Ser Cys Arg Ala

145

150

155

160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

225

230

235

240

Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260

265

270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290

295

300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305

310

315

320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325

330

335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly

725 730 735

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
740 745 750

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
755 760 765

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
770 775 780

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
785 790 795 800

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
805 810 815

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
820 825 830

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
835 840 845

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
850 855 860

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

865 870 875 880

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

885 890 895

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

900 905 910

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

915 920 925

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

930 935 940

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

945 950 955 960

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

965 970 975

Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1772

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1772

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
 980

<210> 1773

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1773

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Val Ile Ser Gly Ser Gly Gly Arg Pro Asn Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Val Asp Tyr Ser Asn Tyr Leu Phe Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Gly Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Gly Gln Ser Val Arg Ser Ser Tyr Leu Gly Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1774

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1774

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1775

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1775

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1776

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1776

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
 835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1777

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1777

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1778

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1778

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
 725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1779

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1779

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1780

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1780

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
 725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1781

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1781

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1782

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1782

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1783

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1783

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr His Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1784

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1784

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1785

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1785

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1786

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1786

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1787

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1787

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1788

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1788

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

4098

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
 355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1789

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1789

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1790

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1790

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1791

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1791

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 1792

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1792

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
 180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1793

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1793

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1794

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1794

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
 180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1795

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1795

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1796

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1796

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1797

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1797

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Gly Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Tyr Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1798

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1798

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 1799

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1799

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1800

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1800

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr
355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1801

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1801

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Ile Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1802

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1802

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130

135

140

Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180

185

190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210

215

220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Cys Gly Thr Lys Val Glu

225

230

235

240

Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260

265

270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290

295

300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305

310

315

320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325

330

335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915 920 925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930 935 940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945 950 955 960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965 970 975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1803

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1803

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Ala Gln Tyr Ala Glu Ser Val

50 55 60

Gln Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala

130 135 140

Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ser Ser Ser Arg Ala Thr Gly

180 185 190

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Gly Ser Ser Pro Pro Pro Phe Gly Gly Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820

825

830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835

840

845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850

855

860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865

870

875

880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885

890

895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900

905

910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945 950 955 960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965 970 975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1804

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1804

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys
210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1805

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1805

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr His Cys

210 215 220

Gln Gln Tyr Gly Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1806

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1806

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180 185 190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1807

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1807

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Glu Gly Gly Gly Tyr Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Ser

65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Phe Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr

180

185

190

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
 835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1808

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1808

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465

470

475

480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485

490

495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1809

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1809

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Ile Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Ser Phe Gly Gln Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
 725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1810

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1810

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1811

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1811

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Leu

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Ser Cys

210

215

220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225

230

235

240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500

505

510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
 725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1812

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1812

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1813

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1813

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50

55

60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Thr Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725

730

735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1814

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1814

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val

225

230

235

240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245

250

255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260

265

270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275

280

285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290

295

300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305

310

315

320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325

330

335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1815

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1815

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Gly Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340

345

350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355

360

365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370

375

380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385

390

395

400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405

410

415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420

425

430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435

440

445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450

455

460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu
 565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
 580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1816

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1816

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1817

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1817

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1818

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1818

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180 185 190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210 215 220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Cys Gly Thr Arg Leu Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915 920 925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930 935 940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945 950 955 960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1819

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1819

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Val Ile Ser Gly Ser Gly Gly Ile Thr Asp Phe Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Phe Phe Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ile Leu Gln Ser Gly

180

185

190

Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln

210

215

220

Gln Tyr Phe Ala Tyr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu

225

230

235

240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260

265

270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290

295

300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675

680

685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690

695

700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705

710

715

720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725

730

735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740

745

750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755

760

765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770

775

780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785

790

795

800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805

810

815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820

825

830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835

840

845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850

855

860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865

870

875

880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885

890

895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900

905

910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945

950

955

960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1820

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1820

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210 215 220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
 405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
 420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
 435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
 450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
 485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965

970

975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1821

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1821

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Phe Tyr Ala Glu Ser Val

50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130

135

140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165

170

175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180

185

190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195

200

205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys

210

215

220

Gln Gln Tyr Gly Ser Ser Pro Pro Thr Phe Gly Gly Gly Thr Arg Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
 275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
 290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn
 325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn
 340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645

650

655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660

665

670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675

680

685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690

695

700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705

710

715

720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900

905

910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915

920

925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930

935

940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945

950

955

960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1822

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1822

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Arg Leu

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 1823

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1823

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys His Asp Tyr Ser Asn Tyr Pro Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Val Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr
 180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Arg Leu
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
 260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515

520

525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530

535

540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545

550

555

560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565

570

575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580

585

590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595

600

605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610

615

620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625

630

635

640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1824

<211> 988

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1824

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100	105	110	
Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly			
115	120	125	
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met			
130	135	140	
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr			
145	150	155	160
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr			
165	170	175	
Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser			
180	185	190	
Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly			
195	200	205	
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala			
210	215	220	

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Cys

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340 345 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp
355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu
385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly
405 410 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln
420 425 430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe
435 440 445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly
450 455 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu
465 470 475 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly

485

490

495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys

500

505

510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

515

520

525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

530

535

540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

545

550

555

560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys

565

570

575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu

580

585

590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

595 600 605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

610 615 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser

625 630 635 640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly

675 680 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

690 695 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser

725

730

735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

740

745

750

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro

755

760

765

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

770

775

780

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

785

790

795

800

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

805

810

815

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

820

825

830

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

835

840

845

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

850

855

860

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

865

870

875

880

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

885

890

895

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

900

905

910

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

915

920

925

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

930

935

940

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

945

950

955

960

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

965

970

975

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1825

<211> 988

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1825

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1

5

10

15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser

20

25

30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35

40

45

Trp Ile Gly Ser Ile Tyr His Ser Gly Gly Thr Tyr Phe Asn Pro Ser

50

55

60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg His Tyr Glu Ile Leu Thr Gly Tyr Tyr Pro Asp Val Phe

100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met

130 135 140

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr

165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser

180 185 190

Asn Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly

195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala

210 215 220

Thr Tyr Tyr Cys Gln Gln Ser Phe Ser Ser Pro Arg Thr Phe Gly Gln

225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln

245 250 255

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys

260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn

275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile

290 295 300

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys

305 310 315 320

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu

325 330 335

Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val

340 345 350

Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp

355 360 365

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu

385 390 395 400

Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly

405 410 415

Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln

420 425 430

Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe

435 440 445

Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly

450 455 460

Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu

465 470 475 480

Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly

485 490 495

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys

500 505 510

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

515 520 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

530 535 540

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

545 550 555 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
565 570 575

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu
580 585 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
595 600 605

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
610 615 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
625 630 635 640

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
645 650 655

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
660 665 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
675 680 685

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

690 695 700

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

705 710 715 720

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro

755 760 765

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

770 775 780

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

785 790 795 800

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

805 810 815

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

820 825 830

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

835 840 845

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

850 855 860

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

865 870 875 880

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

885 890 895

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

900 905 910

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

915 920 925

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

930

935

940

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

945

950

955

960

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

965

970

975

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1826

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1826

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290

295

300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305

310

315

320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325

330

335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645

650

655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660

665

670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675

680

685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690

695

700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705

710

715

720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725

730

735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740

745

750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755

760

765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900

905

910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945

950

955

960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1827

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1827

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Tyr Ile Ser Ser Ser Gly Gly Tyr Ile Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ser Arg Gly Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145 150 155 160

Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Val Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln

210 215 220

Gln Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850

855

860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865

870

875

880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885

890

895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900

905

910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945

950

955

960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1828

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1828

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Cys Gly Thr Lys Val
225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala
260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln
275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr
290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr
305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1829

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1829

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr

20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Asp Tyr Ser Asn Tyr Ala Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

145 150 155 160

Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

165 170 175

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr

180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

210 215 220

Gln Gln Tyr Gly Asp Leu Pro Phe Thr Phe Gly Pro Gly Thr Lys Val

225 230 235 240

Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865

870

875

880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885

890

895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys
980

<210> 1830

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1830

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr
195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Cys Gly
225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500

505

510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515

520

525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530

535

540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545

550

555

560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565

570

575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580

585

590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595

600

605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly

725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro

755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1831

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1831

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Met Phe Ser Ser Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ala Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Glu Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Arg Tyr Tyr Gly Ser Gly Asn Tyr Asn His Gly Met Asp

100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln

165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser

180 185 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr

195 200 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

210 215 220

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly

225 230 235 240

Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325

330

335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340

345

350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385

390

395

400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405

410

415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420

425

430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465

470

475

480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485

490

495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500

505

510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515

520

525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530

535

540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545

550

555

560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly

725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro

755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

820

825

830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

835

840

845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

850

855

860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

865

870

875

880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

885

890

895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900

905

910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915

920

925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930

935

940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1832

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1832

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130 135 140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys

145 150 155 160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln

165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Val Phe Asp Arg

180 185 190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp

195 200 205

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr

210 215 220

Tyr Cys Gln Gln Tyr Ser Glu Ser Pro Phe Thr Phe Gly Cys Gly Thr

225 230 235 240

Lys Val Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val

245 250 255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser

260 265 270

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val

275 280 285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser

290 295 300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg

305 310 315 320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met

325 330 335

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His

340 345 350

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln

355 360 365

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

370 375 380

Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser

385 390 395 400

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser

405

410

415

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys

420

425

430

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala

435

440

445

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala

450

455

460

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr

465

470

475

480

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys

485

490

495

Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro

500

505

510

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

515

520

525

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
530 535 540

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
545 550 555 560

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
565 570 575

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
580 585 590

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
595 600 605

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
610 615 620

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
625 630 635 640

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
645 650 655

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

660 665 670

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

675 680 685

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

690 695 700

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

705 710 715 720

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys

755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu

820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu

835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900

905

910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915

920

925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930

935

940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945

950

955

960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965

970

975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1833

<211> 986

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1833

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Thr Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Gly Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Leu Leu Arg Gly Val Lys Gly Tyr Ala Met Asp Val Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115

120

125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser

130

135

140

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys

145

150

155

160

Arg Ala Ser Gln Ser Leu Arg Arg Ile Tyr Leu Ala Trp Tyr Gln Gln

165

170

175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Val Phe Asp Arg

180

185

190

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp

195

200

205

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr

210

215

220

Tyr Cys Gln Gln Tyr Ser Glu Ser Pro Phe Thr Phe Gly Pro Gly Thr

225

230

235

240

Lys Val Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val

245

250

255

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser

260

265

270

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val

275

280

285

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser

290

295

300

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg

305

310

315

320

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met

325

330

335

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His

340

345

350

Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln

355

360

365

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

370

375

380

Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser

385

390

395

400

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser

405

410

415

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys

420

425

430

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala

435

440

445

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala

450

455

460

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr

465

470

475

480

Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys

485 490 495

Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro

500 505 510

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

515 520 525

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

530 535 540

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

545 550 555 560

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

565 570 575

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

580 585 590

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

595 600 605

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

610 615 620

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

625 630 635 640

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

645 650 655

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

660 665 670

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

675 680 685

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

690 695 700

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

705 710 715 720

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
740 745 750

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
755 760 765

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
770 775 780

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
785 790 795 800

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
805 810 815

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu
820 825 830

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu
835 840 845

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
850 855 860

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

865 870 875 880

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

885 890 895

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

900 905 910

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

915 920 925

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

930 935 940

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

945 950 955 960

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

965 970 975

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1834

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1834

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met

35 40 45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu

50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

130 135 140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145 150 155 160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Ala Ala Phe Asp Glu Ser Leu Ser Gly Val Val Phe Gly Cys Gly

225 230 235 240

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325

330

335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340

345

350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385

390

395

400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405

410

415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420

425

430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580

585

590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595

600

605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610

615

620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625

630

635

640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645

650

655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660

665

670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675

680

685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly

725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro

755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

820

825

830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

835

840

845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

850

855

860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

865

870

875

880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

885

890

895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900

905

910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915

920

925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930

935

940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 980 985

<210> 1835

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1835

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Trp Ile Ser Ala Tyr Gln Gly Tyr Thr His Tyr Ala Gln Lys Leu

50

55

60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr

65

70

75

80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp Tyr Gly Gly Asn Asp Tyr Tyr Gly Met Asp Val Trp Gly

100

105

110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115

120

125

Gly Gly Ser Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

130

135

140

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly

145

150

155

160

Ser Ser Ser Asn Ile Gly Ile Asn Tyr Val Tyr Trp Tyr Gln Gln Leu

165

170

175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Ser Asp Gln Arg Pro

180

185

190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195

200

205

Ser Leu Ala Leu Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr

210

215

220

Cys Ala Ala Phe Asp Glu Ser Leu Ser Gly Val Val Phe Gly Gly Gly

225

230

235

240

Thr Lys Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245

250

255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260

265

270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275

280

285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530

535

540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545

550

555

560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565

570

575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580

585

590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595

600

605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610

615

620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625

630

635

640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645

650

655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660

665

670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675

680

685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690

695

700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705

710

715

720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly

725

730

735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

740

745

750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro

755

760

765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

770

775

780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
 820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val
 835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1836

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1836

Gln Ala Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Ala Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro

130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg

145 150 155 160

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro

165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser

180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys

210 215 220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Cys Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr
385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly
405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly
420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly
435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu
450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val
465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr
485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His

580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740

745

750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755

760

765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770

775

780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785

790

795

800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805

810

815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820

825

830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835

840

845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850

855

860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1837

<211> 984

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1837

Gln Ala Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Asp Ala Ser Asn Lys Tyr Tyr Ala Asp Ala Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Arg Glu Met Gly Ser Arg Gly Asp Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro

130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg

145 150 155 160

Ala Ser Gln Gly Ile Asn Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro

165 170 175

Gly Lys Ala Pro Lys Ser Leu Ile Tyr Ala Val Ser Ile Leu Gln Ser

180 185 190

Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys

210 215 220

Gln Gln Tyr Asn Phe Tyr Pro Phe Ser Phe Gly Gln Gly Thr Lys Val

225 230 235 240

Asp Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser

245 250 255

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala

260 265 270

Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln

275 280 285

Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr

290 295 300

Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr

305 310 315 320

Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn

325 330 335

Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn

340 345 350

Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr

355 360 365

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

370 375 380

Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr

385 390 395 400

Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly

405 410 415

Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly

420 425 430

Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly

435 440 445

Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu

450 455 460

Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val

465 470 475 480

Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr

485 490 495

Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro

500 505 510

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

515 520 525

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

530 535 540

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

545 550 555 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu

565 570 575

Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His
580 585 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
595 600 605

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
610 615 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
625 630 635 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
645 650 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
660 665 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
675 680 685

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

705 710 715 720

Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly

725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

740 745 750

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

755 760 765

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

770 775 780

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

785 790 795 800

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

805 810 815

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

820 825 830

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

835 840 845

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

850 855 860

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

865 870 875 880

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

885 890 895

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

900 905 910

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

915 920 925

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

930 935 940

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

945 950 955 960

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

965 970 975

Ser Leu Ser Leu Ser Pro Gly Lys

980

<210> 1838

<211> 981

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1838

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu

130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln

145 150 155 160

Tyr Ile Gly Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala

165 170 175

Pro Lys Val Leu Ile Tyr Gly Ala Ser Thr Leu Gln Gln Gly Val Pro

180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile

195 200 205

Thr Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr

210 215 220

Tyr Ser Thr Pro Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys

225 230 235 240

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly

245 250 255

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

260 265 270

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly

275 280 285

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr
290 295 300

Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg
305 310 315 320

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr
325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn
340 345 350

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
355 360 365

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
370 375 380

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro
385 390 395 400

Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr
405 410 415

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro

420 425 430

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala

435 440 445

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser

450 455 460

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr

465 470 475 480

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly

485 490 495

Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu

500 505 510

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

515 520 525

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

530 535 540

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly

545 550 555 560

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly

565 570 575

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp

580 585 590

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

595 600 605

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu

610 615 620

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn

625 630 635 640

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

645 650 655

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

660

665

670

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

675

680

685

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

690

695

700

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

705

710

715

720

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

725

730

735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740

745

750

Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu

755

760

765

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

770

775

780

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
785 790 795 800

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 805 810 815

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser
 820 825 830

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 835 840 845

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 850 855 860

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
865 870 875 880

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 885 890 895

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 900 905 910

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

915 920 925

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

930 935 940

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

945 950 955 960

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

965 970 975

Leu Ser Pro Gly Lys

980

<210> 1839

<211> 981

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1839

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Phe

20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Glu Ile Tyr His Ser Gly His Ala Thr Asn Asn Pro Ser Leu Lys

50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu

65 70 75 80

Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Gly Asn Ser Gly Tyr Ile Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Gly Gly Gly Gly Ser Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu

130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln

145 150 155 160

Tyr Ile Gly Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala

165 170 175

Pro Lys Val Leu Ile Tyr Gly Ala Ser Thr Leu Gln Gln Gly Val Pro

180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile

195 200 205

Thr Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Thr

210 215 220

Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

225 230 235 240

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly

245 250 255

Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

260 265 270

Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly

275 280 285

Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr

290 295 300

Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg

305 310 315 320

Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr

325 330 335

Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn

340 345 350

Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr

355 360 365

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

370

375

380

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro

385

390

395

400

Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr

405

410

415

Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro

420

425

430

Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala

435

440

445

Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser

450

455

460

Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr

465

470

475

480

Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly

485

490

495

Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
500 505 510

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
515 520 525

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
530 535 540

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
545 550 555 560

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
565 570 575

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
580 585 590

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
595 600 605

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
610 615 620

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn

625 630 635 640

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

645 650 655

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr

660 665 670

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

675 680 685

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys

690 695 700

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

705 710 715 720

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

725 730 735

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

740 745 750

Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu

755 760 765

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

770 775 780

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

785 790 795 800

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

805 810 815

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser

820 825 830

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

835 840 845

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

850 855 860

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

865 870 875 880

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

885 890 895

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

900 905 910

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

915 920 925

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

930 935 940

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

945 950 955 960

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

965 970 975

Leu Ser Pro Gly Lys

980

<210> 1840

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1840

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130

135

140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145

150

155

160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165

170

175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Asn Asn Arg Pro

180

185

190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195

200

205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210

215

220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly

225

230

235

240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245

250

255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260

265

270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275

280

285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290

295

300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305

310

315

320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325

330

335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580

585

590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595

600

605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610

615

620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625

630

635

640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645

650

655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660

665

670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675

680

685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690

695

700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
 725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro
 755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys
 820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1841

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1841

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Phe

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Asn Asn Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Thr Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Asp Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly

225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln
420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu
435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr
485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro
500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly

725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro

755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915

920

925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930

935

940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

945

950

955

960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

965

970

975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1842

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1842

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser
130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser
145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Leu
165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Asn Asn Arg Pro
180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala
195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Cys Gly
225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340 345 350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355 360 365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

370 375 380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385 390 395 400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405 410 415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420 425 430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435 440 445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450 455 460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500

505

510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515

520

525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530

535

540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545

550

555

560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565

570

575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580

585

590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595

600

605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610

615

620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly
 725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro

755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

835 840 845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

850 855 860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

865 870 875 880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

885 890 895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900 905 910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915 920 925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930 935 940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

945 950 955 960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

965 970 975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980 985

<210> 1843

<211> 987

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1843

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ala Val Ile Trp Tyr Glu Gly Ser Asn Lys Tyr Tyr Gly Glu Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Asn Ser His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser

130 135 140

Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser

145 150 155 160

Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn Trp Tyr Gln Gln Leu

165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Val Asn Asn Asn Arg Pro

180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala

195 200 205

Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

210 215 220

Cys Gln Ser Tyr Glu Thr Ser Leu Ser Ala Ser Val Phe Gly Gly Gly

225 230 235 240

Thr Arg Leu Thr Val Leu Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

245 250 255

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu

260 265 270

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp

275 280 285

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg

290 295 300

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp

305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln

325 330 335

Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg

340

345

350

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly

355

360

365

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly

370

375

380

Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro

385

390

395

400

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser

405

410

415

Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln

420

425

430

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu

435

440

445

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys

450

455

460

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr

465 470 475 480

Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr

485 490 495

Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro

500 505 510

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe

515 520 525

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

530 535 540

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe

545 550 555 560

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

565 570 575

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr

580 585 590

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

595 600 605

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

610 615 620

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg

625 630 635 640

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

645 650 655

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

660 665 670

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

675 680 685

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

690 695 700

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

705 710 715 720

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly

725 730 735

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

740 745 750

Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro

755 760 765

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro

770 775 780

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

785 790 795 800

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

805 810 815

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys

820 825 830

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val

835

840

845

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser

850

855

860

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

865

870

875

880

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu

885

890

895

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

900

905

910

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

915

920

925

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

930

935

940

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

945

950

955

960

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

965

970

975

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

980

985

<210> 1844

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1844

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1

5

10

15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Glu Ser Gly

20

25

30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35

40

45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50

55

60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65

70

75

80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85

90

95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Asp Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Ala Pro Lys Val Leu Ile Phe Ala Ala Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Val Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465

470

475

480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485

490

495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500

505

510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515

520

525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530

535

540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
 580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945

950

955

960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1845

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1845

Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Glu Ser Gly

20 25 30

Val Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130

135

140

Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

145

150

155

160

Ser Gln Ser Val Asp Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165

170

175

Lys Ala Pro Lys Val Leu Ile Phe Ala Ala Ser Ser Leu Gln Ser Gly

180

185

190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210

215

220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

225

230

235

240

Val Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245

250

255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260

265

270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275

280

285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290

295

300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305

310

315

320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325

330

335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
 405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
 420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
 435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
 450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915 920 925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930 935 940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945 950 955 960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965 970 975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1846

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1846

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Ser Cys Arg Ala

145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Cys Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340

345

350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355

360

365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly

370

375

380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385

390

395

400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405

410

415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420

425

430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435

440

445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450

455

460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln
 565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln
 580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys

770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835

840

845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850

855

860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865

870

875

880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885

890

895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900

905

910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915

920

925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930

935

940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945

950

955

960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965

970

975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1847

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1847

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1

5

10

15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ile Ser Gly

20

25

30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

35

40

45

Trp Ile Gly Tyr Ile Phe Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe

65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85 90 95

Cys Ala Arg Ser Gly Tyr Ser Tyr Ala Leu Phe Asp Ala Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Ser Cys Arg Ala

145 150 155 160

Ser Gln Phe Ile Gly Arg Tyr Phe Asn Trp Tyr Gln Gln Lys Pro Gly

165 170 175

Lys Ala Pro Lys Val Leu Ile Tyr Ala Glu Ser Ser Leu Gln Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu

225 230 235 240

Ile Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly

245 250 255

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala

260 265 270

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala

275 280 285

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn

290 295 300

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile

305 310 315 320

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu

325 330 335

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe

340 345 350

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu

355 360 365

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly

370 375 380

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val

385 390 395 400

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala

405 410 415

Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln

420 425 430

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr

435 440 445

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr

450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu

465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val

485 490 495

Leu Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

500 505 510

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

515 520 525

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val

530 535 540

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

545 550 555 560

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln

565 570 575

Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln

580 585 590

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

595 600 605

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

610 615 620

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr

625 630 635 640

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

645 650 655

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

660 665 670

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
675 680 685

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
690 695 700

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
705 710 715 720

Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
725 730 735

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
740 745 750

Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
755 760 765

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
770 775 780

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
785 790 795 800

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp

805 810 815

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr

820 825 830

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

835 840 845

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

850 855 860

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

865 870 875 880

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys

885 890 895

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp

900 905 910

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

915 920 925

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser

930 935 940

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser

945 950 955 960

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

965 970 975

Leu Ser Leu Ser Pro Gly Lys

980

<210> 1848

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1848

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro Gly Lys

225

<210> 1849

<211> 225

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1849

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro

225

<210> 1850

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1850

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195

200

205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210

215

220

Pro Gly Lys

225

<210> 1851

<211> 225

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1851

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1

5

10

15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20

25

30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165

170

175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180

185

190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195

200

205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210

215

220

Pro

225

<210> 1852

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1852

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro Gly Lys

225

<210> 1853

<211> 225

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1853

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro

225

<210> 1854

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1854

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Asn Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 1855

<211> 225

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1855

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Asn Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165

170

175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180

185

190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195

200

205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210

215

220

Pro

225

<210> 1856

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1856

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
225 230 235 240

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
245 250 255

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

260 265 270

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu

275 280 285

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

290 295 300

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

305 310 315 320

Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr

325 330 335

Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

340 345 350

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

355 360 365

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

370 375 380

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val

385 390 395 400

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

405 410 415

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

420 425 430

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr

435 440 445

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

450 455 460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu

465 470 475 480

Ser Pro Gly Lys

<210> 1857

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1857

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp

245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly

260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu

290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

305 310 315 320

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg

325 330 335

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

340

345

350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

355

360

365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

370

375

380

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu

385

390

395

400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp

405

410

415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

420

425

430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

435

440

445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

450

455

460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

465 470 475 480

<210> 1858

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1858

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

225 230 235 240

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

245 250 255

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

260 265 270

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu

275 280 285

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

290 295 300

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

305 310 315 320

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr

325 330 335

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

340 345 350

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

355 360 365

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

370 375 380

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val

385 390 395 400

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

405 410 415

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

420 425 430

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr

435

440

445

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

450

455

460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu

465

470

475

480

Ser Pro Gly Lys

<210> 1859

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1859

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1

5

10

15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp

245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly

260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

275

280

285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu

290

295

300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

305

310

315

320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

325

330

335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

340

345

350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

355

360

365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

370

375

380

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu

385

390

395

400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp

405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

465 470 475 480

<210> 1860

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1860

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

225 230 235 240

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

245 250 255

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

260 265 270

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu

275 280 285

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

290 295 300

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

305 310 315 320

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr

325 330 335

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

340 345 350

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

355 360 365

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

370

375

380

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val

385

390

395

400

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

405

410

415

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

420

425

430

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr

435

440

445

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

450

455

460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu

465

470

475

480

Ser Pro Gly Lys

<210> 1861

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1861

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr

65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85

90

95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100

105

110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115

120

125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130

135

140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145

150

155

160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165

170

175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180

185

190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195

200

205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305 310 315 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
325 330 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

370 375 380

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu

385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp

405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

465 470 475 480

<210> 1862

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1862

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Asn Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180	185	190	
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met			
195	200	205	
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser			
210	215	220	
Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly			
225	230	235	240
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly			
245	250	255	
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu			
260	265	270	
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu			
275	280	285	
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser			
290	295	300	

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

305 310 315 320

Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Asn Ser Thr

325 330 335

Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

340 345 350

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

355 360 365

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

370 375 380

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val

385 390 395 400

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

405 410 415

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

420 425 430

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
435 440 445

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
450 455 460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465 470 475 480

Ser Pro Gly Lys

<210> 1863

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1863

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

50 55 60

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Asn Ser Thr Tyr

65 70 75 80

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser

130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp

245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly

260 265 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

275 280 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu

290 295 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

305 310 315 320

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

325 330 335

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

340 345 350

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

355 360 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

370 375 380

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu

385 390 395 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp

405 410 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

420 425 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

435 440 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

450 455 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

465 470 475 480

<210> 1864

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1864

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

1 5 10 15

Gly Gly Gly Ser

20

<210> 1865

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1865

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser

20 25

<210> 1866

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1866

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

20 25 30

<210> 1867

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1867

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

20 25 30

Gly Gly Ser

35

<210> 1868

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 1868

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser

35 40

<210> 1869

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa is S, T or V

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa is A or S

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is S or N

<400> 1869

Xaa Tyr Xaa Met Xaa

1 5

<210> 1870

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> misc_feature

<222> (1)..(1)

<223> Xaa is A, Y, V, L, or T

<220>

<221> misc_feature

<222> (4)..(4)

<223> Xaa is G or S

<220>

<221> misc_feature

<222> (8)..(8)

<223> Xaa is R, Y, S, G or I

<220>

<221> misc_feature

<222> (9)..(9)

<223> Xaa is T, I, P, or A

<220>

<221> misc_feature

<222> (10)..(10)

<223> Xaa is F, Y, N, Q or D

<220>

<221> misc_feature

<222> (11)..(11)

<223> Xaa is Y or F

<220>

<221> misc_feature

<222> (16)..(16)

<223> Xaa is E, K or Q

<400> 1870

Xaa Ile Ser Xaa Ser Gly Gly Xaa Xaa Xaa Xaa Ala Glu Ser Val Xaa

1 5 10 15

Gly

<210> 1871

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa is H, G or V

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is P, A, L or F

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa is Y or F

<400> 1871

Xaa Asp Tyr Ser Asn Tyr Xaa Xaa Phe Asp Tyr

1 5 10

<210> 1872

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa is S or G

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is S or G

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa is I or V

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is R, S or no amino acid

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa is S or G

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa is S, N, T or D

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa is Y or no amino acid

<220>

<221> MISC_FEATURE

<222> (12)..(12)

<223> Xaa is A or G

<400> 1872

Arg Ala Xaa Gln Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa

1 5 10

<210> 1873

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa is G or A

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa is A or S

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa is S, T, N or I

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is R or L

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa is A or Q

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is T or S

<400> 1873

Xaa Xaa Ser Xaa Xaa Xaa Xaa

1 5

<210> 1874

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa is G, Y or F

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is D, S, Y, I or A

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa is L, T, S or Y

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa is F, L, P or I

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa is T or P

<400> 1874

Gln Gln Tyr Xaa Xaa Xaa Pro Xaa Xaa

1 5

<210> 1875

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa is S, T or V

<400> 1875

Xaa Tyr Ala Met Ser

1 5

<210> 1876

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa is A, V, L or T

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa is R, S, or G

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa is T, P or A

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa is F, N, Y or Q

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Xaa is E, K, or Q

<400> 1876

Xaa Ile Ser Gly Ser Gly Gly Xaa Xaa Xaa Tyr Ala Glu Ser Val Xaa

1

5

10

15

Gly

<210> 1877

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa is H or V

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is P, L or A

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa is Y or F

<400> 1877

Xaa Asp Tyr Ser Asn Tyr Xaa Xaa Phe Asp Tyr

1 5 10

<210> 1878

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa is S or G

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is S or G

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa is I or V

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is R or S

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa is S or G

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa is S, T, N or D

<220>

<221> MISC_FEATURE

<222> (12)..(12)

<223> Xaa is A or G

<400> 1878

Arg Ala Xaa Gln Xaa Xaa Xaa Xaa Xaa Tyr Leu Xaa

1 5 10

<210> 1879

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa is T or I

<400> 1879

Ala Ala Ser Xaa Leu Gln Ser

1 5

<210> 1880

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa is A or S

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa is S or N

<400> 1880

Gly Xaa Ser Xaa Arg Ala Thr

1 5

<210> 1881

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is D, Y, S or I

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa is L, S or T

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa is F or P

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa is T or P

<400> 1881

Gln Gln Tyr Gly Xaa Xaa Pro Xaa Xaa

1 5

Claims

1. A bispecific antibody construct comprising a first binding domain which binds to human CD70 on the surface of a target cell and a second binding domain which binds to human CD3 on the surface of a T cell and at least macaque CD3.
2. The antibody construct according to claim 1, wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3, wherein
 - said CDR-H1 has the amino acid sequence $X_1YX_2MX_3$ (SEQ ID NO: 1869), wherein X_1 is S, T or V, X_2 is A or S, and X_3 is S or N;
 - said CDR-H2 has the amino acid sequence $X_1ISX_2SGGX_3X_4X_5X_6AESVX_7G$ (SEQ ID NO: 1870), wherein X_1 is A, Y, V, L, or T, X_2 is G or S, X_3 is R, Y, S, G or I, X_4 is T, I, P, or A, X_5 is F, Y, N, Q or D, X_6 is Y or F, and X_7 is E, K or Q;
 - said CDR-H3 has the amino acid sequence $X_1DYSNYX_2X_3FDY$ (SEQ ID NO: 1871), wherein X_1 is H, G or V, X_2 is P, A, L or F, and X_3 is Y or F;
 - said CDR-L1 has the amino acid sequence $RAX_1QX_2X_3X_4X_5X_6X_7LX_8$ (SEQ ID NO: 1872), wherein X_1 is S or G, X_2 is S or G, X_3 is I or V, X_4 is R, S or no amino acid, X_5 is S or G, X_6 is S, N, T or D, X_7 is Y or no amino acid, and X_8 is A or G;
 - said CDR-L2 has the amino acid sequence $X_1X_2SX_3X_4X_5X_6$ (SEQ ID NO: 1873), wherein X_1 is G or A, X_2 is A or S, X_3 is S, T, N or I, X_4 is R or L, X_5 is A or Q, and X_6 is T or S; and
 - said CDR-L3 has the amino acid sequence $QQYX_1X_2X_3PX_4X_5$ (SEQ ID NO: 1874), wherein X_1 is G, Y or F, X_2 is D, S, Y, I or A, X_3 is L, T, S or Y, X_4 is F, L, P or I, and X_5 is T or P.
3. The antibody construct according to claim 1 or 2, wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3, wherein
 - said CDR-H1 has the amino acid sequence SYSMN (SEQ ID NO: 1422) or X_1YAMS (SEQ ID NO: 1875), wherein X_1 is S, T or V;
 - said CDR-H2 has an amino acid sequence selected from the group consisting of YISSSGGYIYYAESVKG (SEQ ID NO: 1423), VISGSGGITDFAESVKG (SEQ ID

- NO: 1367) and X_1 ISGSGGX $_2$ X $_3$ X $_4$ YAESVX $_5$ G (SEQ ID NO: 1876), wherein X $_1$ is A, V, L or T, X $_2$ is R, S, or G, X $_3$ is T, P or A, X $_4$ is F, N, Y or Q, and X $_5$ is E, K, or Q;
- said CDR-H3 has an amino acid sequence selected from the group consisting of GDYSNYAYFDY (SEQ ID NO: 1424), HDYSNYFFFDY (SEQ ID NO: 1368), and X_1 DYSNYX $_2$ X $_3$ FDY (SEQ ID NO: 1877), wherein X $_1$ is H or V, X $_2$ is P, L or A, and X $_3$ is Y or F;
 - said CDR-L1 has the amino acid sequence RASQGISNYLA (SEQ ID NO: 1425) or RAX $_1$ QX $_2$ X $_3$ X $_4$ X $_5$ X $_6$ YLX $_7$ (SEQ ID NO: 1878), wherein X $_1$ is S or G, X $_2$ is S or G, X $_3$ is I or V, X $_4$ is R or S, X $_5$ is S or G, X $_6$ is S, T, N or D, and X $_7$ is A or G;
 - said CDR-L2 has the amino acid sequence AASXLQS (SEQ ID NO: 1879), wherein X is T or I, or GX $_1$ SX $_2$ RAT (SEQ ID NO: 1880), wherein X $_1$ is A or S, and X $_2$ is S or N; and
 - said CDR-L3 has an amino acid sequence selected from the group consisting of QQYYSTPLT (SEQ ID NO: 1427), QQYFAYPIT (SEQ ID NO: 1371), and QQYGX $_1$ X $_2$ PX $_3$ X $_4$ (SEQ ID NO: 1881), wherein X $_1$ is D, Y, S or I, X $_2$ is L, S or T, X $_3$ is F or P, and X $_4$ is T or P.
4. The antibody construct according any one of the preceding claims, wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3, wherein
- said CDR-H1 has the amino acid sequence X_1 YAMS (SEQ ID NO: 1875), wherein X $_1$ is S, T or V;
 - said CDR-H2 has the amino acid sequence X_1 ISGSGGX $_2$ X $_3$ X $_4$ YAESVX $_5$ G (SEQ ID NO: 1876), wherein X $_1$ is A, V, L or T, X $_2$ is R, S, or G, X $_3$ is T, P or A, X $_4$ is F, N, Y or Q, and X $_5$ is E, K, or Q;
 - said CDR-H3 has the amino acid sequence X_1 DYSNYX $_2$ X $_3$ FDY (SEQ ID NO: 1877), wherein X $_1$ is H or V, X $_2$ is P, L or A, and X $_3$ is Y or F;
 - said CDR-L1 has the amino acid sequence RAX $_1$ QX $_2$ X $_3$ X $_4$ X $_5$ X $_6$ YLX $_7$ (SEQ ID NO: 1878), wherein X $_1$ is S or G, X $_2$ is S or G, X $_3$ is I or V, X $_4$ is R or S, X $_5$ is S or G, X $_6$ is S, T, N or D, and X $_7$ is A or G;
 - said CDR-L2 has the amino acid sequence GX $_1$ SX $_2$ RAT (SEQ ID NO: 1880), wherein X $_1$ is A or S, and X $_2$ is S or N; and
 - said CDR-L3 has the amino acid sequence QQYGX $_1$ X $_2$ PX $_3$ X $_4$ (SEQ ID NO: 1881), wherein X $_1$ is D, Y, S or I, X $_2$ is L, S or T, X $_3$ is F or P, and X $_4$ is T or P.

5. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3, wherein
- said CDR-H1 has an amino acid sequence selected from the group consisting of SYAMS (SEQ ID NO: 1044), TYAMS (SEQ ID NO: 1142), VYAMS (SEQ ID NO: 1436), and SYSMN (SEQ ID NO: 1422);
 - said CDR-H2 has an amino acid sequence selected from the group consisting of AISGSGGRTFYAESVEG (SEQ ID NO: 1087), VISGSGGRPNYAESVKG (SEQ ID NO: 1045), AISGSGGSTFYAESVKG (SEQ ID NO: 1171), AISGSGGSTFYAESVQG (SEQ ID NO: 1213), AISGSGGGTFYAESVKG (SEQ ID NO: 1227), LISGSGGRTYYAESVKG (SEQ ID NO: 1241), AISGSGGRAQYAESVQG (SEQ ID NO: 1255), TISGSGGSTFYAESVKG (SEQ ID NO: 1437), YISSSGGYIYYAESVKG (SEQ ID NO: 1423), and VISGSGGITDFAESVKG (SEQ ID NO: 1367);
 - said CDR-H3 has an amino acid sequence selected from the group consisting of HDYSNYPYFDY (SEQ ID NO: 1088), VDYSNYLFFDY (SEQ ID NO: 1046), HDYSNYAYFDY (SEQ ID NO: 1438), GDYSNYAYFDY (SEQ ID NO: 1424), and HDYSNYFFFDY (SEQ ID NO: 1368);
 - said CDR-L1 has an amino acid sequence selected from the group consisting of RASQSIRSSYLA (SEQ ID NO: 1089), RASQSVRSTYLA (SEQ ID NO: 1145), RAGQSVRSSYLG (SEQ ID NO: 1047), RASQSVRSSYLA (SEQ ID NO: 1173), RASQSVRSNYLA (SEQ ID NO: 1187), RASQSVRGNYLA (SEQ ID NO: 1215), RASQSIRSNYLA (SEQ ID NO: 1229), RASQSVSSNLA (SEQ ID NO: 1257), RASQGVRSDYLA (SEQ ID NO: 1271), RASQGVRSSYLA (SEQ ID NO: 1341), and RASQGISNYLA (SEQ ID NO: 1369);
 - said CDR-L2 has an amino acid sequence selected from the group consisting of GASSRAT (SEQ ID NO: 1048), GASNRAT (SEQ ID NO: 1244), GSSSRAT (SEQ ID NO: 1258), AASTLQS (SEQ ID NO: 1426), and AASILQS (SEQ ID NO: 1370); and
 - said CDR-L3 has an amino acid sequence selected from the group consisting of QQYGDLPFT (SEQ ID NO: 1091); QQYGYSPPT (SEQ ID NO: 1049), QQYGYSPFT (SEQ ID NO: 1217), QQYGSSPFT (SEQ ID NO: 1231), QQYGISPPT (SEQ ID NO: 1245), QQYGSSPPP (SEQ ID NO: 1259), QQYGSTPPT (SEQ ID NO: 1273), QQYGSSPPT (SEQ ID NO: 1343), QQYYSTPLT (SEQ ID NO: 1427), and QQYFAYPIT (SEQ ID NO: 1371).

6. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3, wherein said CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 are selected from the group consisting of those depicted in:
- 16) SEQ: ID NOs: 1044-1049;
 - 17) SEQ: ID NOs: 1086-1091;
 - 18) SEQ: ID NOs: 1142-1147;
 - 19) SEQ: ID NOs: 1170-1175;
 - 20) SEQ: ID NOs: 1184-1189;
 - 21) SEQ: ID NOs: 1212-1217;
 - 22) SEQ: ID NOs: 1226-1231;
 - 23) SEQ: ID NOs: 1240-1245;
 - 24) SEQ: ID NOs: 1254-1259;
 - 25) SEQ: ID NOs: 1268-1273;
 - 26) SEQ: ID NOs: 1338-1343;
 - 27) SEQ: ID NOs: 1352-1357;
 - 28) SEQ: ID NOs: 1366-1371;
 - 29) SEQ: ID NOs: 1422-1427; and
 - 30) SEQ: ID NOs: 1436-1441;
- .
7. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a VH region selected from the group consisting of those depicted in SEQ ID NO: 1050, SEQ ID NO: 1092, SEQ ID NO: 1148, SEQ ID NO: 1176, SEQ ID NO: 1190, SEQ ID NO: 1218, SEQ ID NO: 1232, SEQ ID NO: 1246, SEQ ID NO: 1260, SEQ ID NO: 1274, SEQ ID NO: 1344, SEQ ID NO: 1358, SEQ ID NO: 1372, SEQ ID NO: 1428, and SEQ ID NO: 1442.
8. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a VL region selected from the group consisting of those depicted in SEQ ID NO: 1051, SEQ ID NO: 1093, SEQ ID NO: 1149, SEQ ID NO: 1177, SEQ ID NO: 1191, SEQ ID NO: 1219, SEQ ID NO: 1233, SEQ ID NO: 1247, SEQ ID NO: 1261, SEQ ID NO: 1275, SEQ ID NO: 1345, SEQ ID NO: 1359, SEQ ID NO: 1373, SEQ ID NO: 1429, and SEQ ID NO: 1443.

9. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a VH region and a VL region selected from the group consisting of pairs of a VH region and a VL region as depicted in SEQ ID NOs: 1050+1051, SEQ ID NOs: 1092+1093, SEQ ID NOs: 1148+1149, SEQ ID NOs: 1176+1177, SEQ ID NOs: 1190+1191, SEQ ID NOs: 1218+1219, SEQ ID NOs: 1232+1233, SEQ ID NOs: 1246+1247, SEQ ID NOs: 1260+1261, SEQ ID NOs: 1274+1275, SEQ ID NOs: 1344+1345, SEQ ID NOs: 1358+1359, NOs: 1372+1373, SEQ ID NOs: 1428+1429, and SEQ ID NOs: 1442+1443.
10. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 1052, SEQ ID NO: 1094, SEQ ID NO: 1150, SEQ ID NO: 1178, SEQ ID NO: 1192, SEQ ID NO: 1220, SEQ ID NO: 1234, SEQ ID NO: 1248, SEQ ID NO: 1262, SEQ ID NO: 1276, SEQ ID NO: 1346, SEQ ID NO: 1360, SEQ ID NO: 1374, SEQ ID NO: 1430, and SEQ ID NO: 1444.
11. The antibody construct according to any one of the preceding claims, comprising a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 1053, SEQ ID NO: 1095, SEQ ID NO: 1151, SEQ ID NO: 1179, SEQ ID NO: 1193, SEQ ID NO: 1221, SEQ ID NO: 1235, SEQ ID NO: 1249, SEQ ID NO: 1263, SEQ ID NO: 1277, SEQ ID NO: 1347, SEQ ID NO: 1361, SEQ ID NO: 1375, SEQ ID NO: 1431, and SEQ ID NO: 1445.
12. The antibody construct according to any one of the preceding claims, comprising or consisting of a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 1696, SEQ ID NO: 1702, SEQ ID NO: 1710, SEQ ID NO: 1714, SEQ ID NO: 1716, SEQ ID NO: 1720, SEQ ID NO: 1722, SEQ ID NO: 1724, SEQ ID NO: 1726, SEQ ID NO: 1728, SEQ ID NO: 1738, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1750, and SEQ ID NO: 1752.
13. The antibody construct according to any one of the preceding claims, wherein the first binding domain further binds to macaque CD70, preferably to *Macaca fascicularis* CD70.

14. The antibody construct according to any one of the preceding claims, wherein the second binding domain binds to human CD3 epsilon and to *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus* CD3 epsilon.
15. The antibody construct according to any one of the preceding claims, wherein the antibody construct is in a format selected from the group consisting of (scFv)₂, scFv-single domain mAb, diabodies and oligomers of the foregoing formats.
16. A polynucleotide encoding an antibody construct as defined in any one of the preceding claims.
17. A vector comprising the polynucleotide as defined in claim 16.
18. A host cell transformed or transfected with the polynucleotide as defined in claim 16 or with the vector as defined in claim 17.
19. A process for the production of an antibody construct according to any one of claims 1 to 15, said process comprising culturing a host cell as defined in claim 18 under conditions allowing the expression of said antibody construct and recovering the produced antibody construct from the culture.
20. A pharmaceutical composition comprising an antibody construct according to any one of claims 1 to 15 or produced according to the process of claim 19.
21. The antibody construct according to any one of claims 1 to 15, or produced according to the process of claim 19, for use in the prevention, treatment or amelioration of a tumor or cancer disease or of a metastatic cancer disease.
22. A method for the treatment or amelioration of a tumor or cancer disease or of a metastatic cancer disease, comprising the step of administering to a subject in need thereof the antibody construct according to any one of claims 1 to 15, or produced according to the process of claim 19.
23. The method according to claim 22 or the antibody construct according to claim 21, wherein the tumor or cancer disease is selected from the group consisting of renal, lung,

pancreatic, ovarian, breast, colon, head and neck, stomach, rectal, thymic, and brain tumor or cancer, leukemia, lymphoma, melanoma, Kaposi's Sarcoma, embryonal carcinoma, and a metastatic cancer disease derived from any of the foregoing.

24. A kit comprising an antibody construct according to any one of claims 1 to 15, an antibody construct produced according to the process of claim 19, a polynucleotide as defined in claim 16, a vector as defined in claim 17, and/or a host cell as defined in claim 18.