
BISPECIFIC ANTIBODY CONSTRUCTS BINDING DLL3 AND CD3

The present invention relates to a bispecific antibody construct comprising a first binding domain which binds to human DLL3 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.

Small cell lung cancer (SCLC) is an aggressive form of lung cancer with a poor prognosis and limited therapeutic options, representing about 15% of all newly diagnosed lung cancers and equal to about 25,000 new cases in the US and 180,000 new cases worldwide per year. Survival rates have remained low for several decades, with only 5% of SCLC patients surviving five years, in a large part due to the lack of new therapies to combat this form of lung cancer. Most patients present with extensive-stage disease, while about a third of patients present with limited stage disease, defined by the presence of tumors in only one side of the chest and that fit in a single radiation field. These stages impact available therapeutic regimens, with limited stage disease treated with chemotherapy and radiation and extensive stage disease treated with chemotherapy alone. Disseminated, metastatic tumors with lymphoma-like characteristics are a hallmark of SCLC. The first known diagnosis of SCLC patients described it as a disease of the lymphatic system, not being recognized as lung cancer until 1926, which highlights some of the unique nature of SCLC tumors as compared to other solid tumors.

Patients typically respond well to the current front-line therapy, which includes etoposide and cisplatin, but invariably quickly relapse with chemoresistant disease, for which no therapeutic options are currently available. Prognosis in the relapsed refractory setting is extremely poor, with rapid disease progression and short median survival of less than six months. Furthermore, SCLC patients have high rates of comorbidities, including hypertension, cardiac disease, diabetes and paraneoplastic syndromes. These, coupled with the typically advanced age of SCLC patients, impact the ability of patients to endure harsh chemo regimens, further limiting treatment options.

A bispecific antibody modality, comprising an scFv that recognizes CD3 expressed on T cells and another scFv that recognizes a tumor-associated antigen, has shown promising efficacy in the clinic, with high response rates in hematological malignancies such as refractory B-ALL (Topp, M.S. *et al.* Blood, 2012. 120(26):p.5185-5187), resulting in the approval of Blincyto. While efficacy with T cell-engaging therapies has yet to be demonstrated in a solid tumor indication, SCLC may represent a promising solid tumor indication for the CD3 x tumor target bispecific antibody modality, given the disseminated nature of the disease. Therefore, a bispecific T cell engager that directs T cells against a specific tumor antigen presents a new opportunity as a new therapeutic option in the treatment of SCLC.

DLL3 was presently identified as an SCLC-specific tumor antigen by next-generation sequencing, comparing the prevalence of DLL3 mRNA in a panel of primary patient tumors and a large collection of normal tissues. The level of DLL3 expression in SCLC tumors was moderate, but highly prevalent, with approximately 90% of the tumors analyzed showing evidence of DLL3 expression by RNA-seq. In contrast to SCLC tumors, normal tissues showed very low expression of DLL3 transcript, with small levels detected in testis, optic nerve and cerebellum. Comparison of SCLC cell lines and tumors by RNA-seq showed similar expression levels, while cell surface quantitation of DLL3 expression on SCLC cell lines indicated expression levels below 5000 DLL3 per cell, with typical expression levels below 2000 DLL3/cell. Expression of DLL3 protein was confirmed by IHC, where 86% of SCLC tumors showed positive staining for DLL3, with a homogeneous and membranous staining pattern. Aside from very faint staining in cerebellum, all other normal tissues were negative for DLL3 staining.

DLL3 is a non-canonical Notch ligand, functioning in a cell autonomous manner to inhibit Notch signaling, binding to Notch in cis, thus blocking cell to cell interactions and internalization of Notch in the target cell, a hallmark of canonical Notch signaling. The primary role for DLL3 is in somitogenesis during embryonic development. Mice with DLL3 knockouts show segmental defects in the axial skeleton and cranial and neuronal development. Somitic patterning defects are also seen in humans with certain germline DLL3 mutations, resulting in a condition called spondylocostal dysostosis.

DLL3 has been proposed previously in methods to diagnose and treat glioma, in addition to SCLC, using an antibody-drug conjugate (ADC) (WO 2013/126746). Using an ADC-based approach for DLL3 may have limitations, given the low expression levels of the protein on the

cell surface and the reduced performance of ADCs against targets with low expression. Furthermore, ADC molecules often demonstrate toxicity related to free warhead, likely a result of linker degradation, resulting in maximum tolerated dose limitations and potential impacts on efficacy unrelated to the target chosen for the antibody. This is less likely to be an issue for a T cell-engaging bispecific molecule, engineered to engage DLL3 and CD3 simultaneously, given the required sensitivity of T cells for their targets, and highly potent in vitro cytotoxicity has been demonstrated on cell lines expressing several hundred target proteins per cell. Additionally, the usually smaller size of a bispecific T cell engaging antibody construct relative to a normal antibody (full-length IgG) may improve tissue penetration and increase potency due to more efficient engagement of the DLL3 and CD3 targets, resulting in improved synapse formation between the T cell and target tumor cell.

SCLC remains a significant unmet medical need, and new therapeutic options are required to improve the outlook for this sizable patient population. The above discussed bispecific antibody modality is clinically validated, and as such an antibody construct targeting DLL3 and CD3 represents a promising new possibility for the treatment of SCLC and an opportunity to improve the survival of patients suffering with this indication. As there is still a need for having available further options for the treatment of tumor or cancer diseases related to the overexpression of DLL3, there are provided herewith means and methods for the solution of this problem in the form of a bispecific antibody construct with one binding domain directed to DLL3 and a second binding domain directed to CD3 on T cells.

Thus, in a first aspect, the present invention provides a bispecific antibody construct comprising a first binding domain which binds to human DLL3 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 an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 260.

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 DLL3 or CD3 epsilon (Schier, *Human Antibodies Hybridomas* 7 (1996), 97-105; Malmborg, 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 DLL3. 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: DLL3 and CD3, respectively. The structure and function of the first binding domain (recognizing DLL3), 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 DLL3 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), Tuaillon *et al.* (1993), Choi *et al.* (1993), Lonberg *et al.* (1994), Taylor *et al.* (1994), and Tuaillon *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 DLL3 and/or a human binding domain against CD3 in order to vitiate concerns and/or effects of HAMA or HACA response.

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: DLL3 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 DLL3 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 DLL3 protein is exchanged / replaced with its corresponding region of a non-human and non-primate DLL3 antigen (e.g., mouse DLL3, 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 DLL3 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 DLL3 protein, whereby binding to the respective region in the human DLL3 protein is set to be 100%. It is envisaged that the aforementioned human DLL3 / non-human DLL3 chimeras are expressed in CHO cells. It is also envisaged that the human DLL3 / non-human DLL3 chimeras are fused with a transmembrane domain and/or cytoplasmic domain of a different membrane-bound protein such as EpCAM.

In an alternative or additional method for epitope mapping, several truncated versions of the human DLL3 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 DLL3 domains / sub-domains or regions are stepwise deleted, starting from the N-terminus. The truncated DLL3 versions that were generated and used in the context of the present invention

are depicted in Figure 1. It is envisaged that the truncated DLL3 versions are expressed in CHO cells. It is also envisaged that the truncated DLL3 versions are fused with a transmembrane domain and/or cytoplasmic domain of a different membrane-bound protein such as EpCAM. It is also envisaged that the truncated DLL3 versions encompass a signal peptide domain at their N-terminus, for example a signal peptide derived from mouse IgG heavy chain signal peptide. It is furthermore envisaged that the truncated DLL3 versions encompass a v5 domain at their N-terminus (following the signal peptide) which allows verifying their correct expression on the cell surface. A decrease or a loss of binding is expected to occur with those truncated DLL3 versions which do not encompass any more the DLL3 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 DLL3 protein (or its extracellular region or domain) is set to be 100%. A method to test this loss of binding is described in Example 2.

A further method to determine the contribution of a specific residue of a target antigen to the recognition by a 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: DLL3 and CD3, respectively) and, generally, does not exhibit significant reactivity with proteins or antigens other than DLL3 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 DLL3 or CD3. Preferably, a binding domain of the invention does not essentially or substantially bind to proteins or antigens other than

DLL3 or CD3 (*i.e.*, the first binding domain is not capable of binding to proteins other than DLL3 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 DLL3 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 DLL3 or CD3, whereby binding to DLL3 or CD3, respectively, is set to be 100%.

It is also envisaged that the antibody constructs of the present invention bind to a human DLL3 isoform having one or both of the following DLL3 point mutations: F172C and L218P. See Example 5.

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.

The antibody constructs according to the invention bind to an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 260, corresponding to an amino acid stretch encompassing the regions EGF-3 and EGF-4. Other groups of anti-DLL3 binders were also generated and their DLL3 binding specificities were identified during epitope mapping (see Example 2).

The largest group of generated binders recognized an epitope within the DSL domain. However, none of those antibody constructs fulfilled the criteria for sufficient cytotoxic activity in an initial 18-hour ⁵¹Cr-based cytotoxicity assay with stimulated human CD8⁺ T cells as effector cells and hu DLL3 transfected CHO cells as target cells.

In a further initial 48 hour FACS-based cytotoxicity assay (using unstimulated human PBMC as effector cells and hu DLL3 transfected CHO cells as target cells), those binders that recognized a DLL3 epitope within the N-terminus of the protein had EC50 values between 1455 and 1580 pM. In the present context, these values are not considered adequate for bispecific antibodies that are provided for a therapeutic use in directing a patient's immune system, more specifically the T cells' cytotoxic activity, against cancer cells.

Finally, another group of binders was generated and characterized for its cytotoxic activity in a variety of assays. The epitope mapping of these binders revealed a specificity for a DLL3 epitope comprised within the EGF-5 region, and to some extent also within the EGF-6 region (for details, see Example 2). An overall view of the data generated in the different cytotoxicity assays (see Examples 8.3, 8.5, 8.6 and 8.7) for these binders denominated DLL3-18, DLL3-19, DLL3-20 and DLL3-21 revealed the following: While not all of the binders fail in all of the assays in terms of favorable EC50 values, the entire group clearly underperforms if compared with the antibody constructs according to the invention. This observation is highlighted with a darker shadowing of the results shown in Tables 6-9.

In summary, it can clearly be stated that the antibody constructs according to the invention (which bind to an epitope of DLL3 comprised within the region as depicted in SEQ ID NO: 260) show by far the best activity performance compared to a variety of other groups of DLL3 binders having different epitope specificities. In other words, the antibody constructs according to the invention present with a favorable epitope-activity relationship, hence supporting potent bispecific antibody construct mediated cytotoxic activity.

In another aspect, the present invention provides a bispecific antibody construct comprising a first binding domain which binds to human DLL3 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 an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 258.

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 selected from the group consisting of:

- a) CDR-H1 as depicted in SEQ ID NO: 31, CDR-H2 as depicted in SEQ ID NO: 32, CDR-H3 as depicted in SEQ ID NO: 33, CDR-L1 as depicted in SEQ ID NO: 34, CDR-L2 as depicted in SEQ ID NO: 35 and CDR-L3 as depicted in SEQ ID NO: 36;
- b) CDR-H1 as depicted in SEQ ID NO: 41, CDR-H2 as depicted in SEQ ID NO: 42, CDR-H3 as depicted in SEQ ID NO: 43, CDR-L1 as depicted in SEQ ID NO: 44, CDR-L2 as depicted in SEQ ID NO: 45 and CDR-L3 as depicted in SEQ ID NO: 46;
- c) CDR-H1 as depicted in SEQ ID NO: 51, CDR-H2 as depicted in SEQ ID NO: 52, CDR-H3 as depicted in SEQ ID NO: 53, CDR-L1 as depicted in SEQ ID NO: 54, CDR-L2 as depicted in SEQ ID NO: 55 and CDR-L3 as depicted in SEQ ID NO: 56;
- d) CDR-H1 as depicted in SEQ ID NO: 61, CDR-H2 as depicted in SEQ ID NO: 62, CDR-H3 as depicted in SEQ ID NO: 63, CDR-L1 as depicted in SEQ ID NO: 64, CDR-L2 as depicted in SEQ ID NO: 65 and CDR-L3 as depicted in SEQ ID NO: 66;
- e) CDR-H1 as depicted in SEQ ID NO: 71, CDR-H2 as depicted in SEQ ID NO: 72, CDR-H3 as depicted in SEQ ID NO: 73, CDR-L1 as depicted in SEQ ID NO: 74, CDR-L2 as depicted in SEQ ID NO: 75 and CDR-L3 as depicted in SEQ ID NO: 76;
- f) CDR-H1 as depicted in SEQ ID NO: 81, CDR-H2 as depicted in SEQ ID NO: 82, CDR-H3 as depicted in SEQ ID NO: 83, CDR-L1 as depicted in SEQ ID NO: 84, CDR-L2 as depicted in SEQ ID NO: 85 and CDR-L3 as depicted in SEQ ID NO: 86;
- g) CDR-H1 as depicted in SEQ ID NO: 91, CDR-H2 as depicted in SEQ ID NO: 92, CDR-H3 as depicted in SEQ ID NO: 93, CDR-L1 as depicted in SEQ ID NO: 94, CDR-L2 as depicted in SEQ ID NO: 95 and CDR-L3 as depicted in SEQ ID NO: 96;
- h) CDR-H1 as depicted in SEQ ID NO: 101, CDR-H2 as depicted in SEQ ID NO: 102, CDR-H3 as depicted in SEQ ID NO: 103, CDR-L1 as depicted in SEQ ID NO: 104, CDR-L2 as depicted in SEQ ID NO: 105 and CDR-L3 as depicted in SEQ ID NO: 106; and
- i) CDR-H1 as depicted in SEQ ID NO: 111, CDR-H2 as depicted in SEQ ID NO: 112, CDR-H3 as depicted in SEQ ID NO: 113, CDR-L1 as depicted in SEQ ID NO: 114, CDR-L2 as depicted in SEQ ID NO: 115 and CDR-L3 as depicted in SEQ ID NO: 116.

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 DLL3 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 of DLL3 as an antibody selected from the group consisting of DLL3-4, DLL3-5, DLL3-6, DLL3-7, DLL3-8, DLL3-9, and DLL3-10, *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:

- a) CDR-H1 as depicted in SEQ ID NO: 31, CDR-H2 as depicted in SEQ ID NO: 32, CDR-H3 as depicted in SEQ ID NO: 33, CDR-L1 as depicted in SEQ ID NO: 34, CDR-L2 as depicted in SEQ ID NO: 35 and CDR-L3 as depicted in SEQ ID NO: 36;
- b) CDR-H1 as depicted in SEQ ID NO: 41, CDR-H2 as depicted in SEQ ID NO: 42, CDR-H3 as depicted in SEQ ID NO: 43, CDR-L1 as depicted in SEQ ID NO: 44, CDR-L2 as depicted in SEQ ID NO: 45 and CDR-L3 as depicted in SEQ ID NO: 46;
- c) CDR-H1 as depicted in SEQ ID NO: 51, CDR-H2 as depicted in SEQ ID NO: 52, CDR-H3 as depicted in SEQ ID NO: 53, CDR-L1 as depicted in SEQ ID NO: 54, CDR-L2 as depicted in SEQ ID NO: 55 and CDR-L3 as depicted in SEQ ID NO: 56;
- d) CDR-H1 as depicted in SEQ ID NO: 61, CDR-H2 as depicted in SEQ ID NO: 62, CDR-H3 as depicted in SEQ ID NO: 63, CDR-L1 as depicted in SEQ ID NO: 64, CDR-L2 as depicted in SEQ ID NO: 65 and CDR-L3 as depicted in SEQ ID NO: 66;
- e) CDR-H1 as depicted in SEQ ID NO: 71, CDR-H2 as depicted in SEQ ID NO: 72, CDR-H3 as depicted in SEQ ID NO: 73, CDR-L1 as depicted in SEQ ID NO: 74, CDR-L2 as depicted in SEQ ID NO: 75 and CDR-L3 as depicted in SEQ ID NO: 76;
- f) CDR-H1 as depicted in SEQ ID NO: 81, CDR-H2 as depicted in SEQ ID NO: 82, CDR-H3 as depicted in SEQ ID NO: 83, CDR-L1 as depicted in SEQ ID NO: 84, CDR-L2 as depicted in SEQ ID NO: 85 and CDR-L3 as depicted in SEQ ID NO: 86; and
- g) CDR-H1 as depicted in SEQ ID NO: 91, CDR-H2 as depicted in SEQ ID NO: 92, CDR-H3 as depicted in SEQ ID NO: 93, CDR-L1 as depicted in SEQ ID NO: 94, CDR-L2 as depicted in SEQ ID NO: 95 and CDR-L3 as depicted in SEQ ID NO: 96.

Whether or not an antibody construct binds to the same epitope of DLL3 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 DLL3 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 DLL3-4, DLL3-5, DLL3-6, DLL3-7, DLL3-8, DLL3-9, and DLL3-10, *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 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.

In one embodiment of the invention, 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: 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: 435 and SEQ ID NO: 529.

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: 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: 436 and SEQ ID NO: 530.

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: 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: 435+436; and SEQ ID NOs: 529+530.

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: 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: 437 and SEQ ID NO: 531.

The above first binding domains (which are specified by their CDRs, VH region and VL region and combinations thereof) characterize as binding domains which bind to a DLL3 epitope comprised within the region as depicted in SEQ ID NO: 258.

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: DLL3), 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: 286), 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: 285-293. 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, *e.g.* 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 DLL3 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 DLL3 binding domain via a peptide linker, and the VH of the DLL3 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 furthermore envisaged that the present invention provides a bispecific antibody construct comprising a first binding domain which binds to human DLL3 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 an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 259.

Accordingly, in a further aspect of the invention, the first binding domain of the bispecific antibody construct comprises 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:

- a) CDR-H1 as depicted in SEQ ID NO: 121, CDR-H2 as depicted in SEQ ID NO: 122, CDR-H3 as depicted in SEQ ID NO: 123, CDR-L1 as depicted in SEQ ID NO: 124, CDR-L2 as depicted in SEQ ID NO: 125 and CDR-L3 as depicted in SEQ ID NO: 126;
- b) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 134, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;

- c) CDR-H1 as depicted in SEQ ID NO: 141, CDR-H2 as depicted in SEQ ID NO: 142, CDR-H3 as depicted in SEQ ID NO: 143, CDR-L1 as depicted in SEQ ID NO: 144, CDR-L2 as depicted in SEQ ID NO: 145 and CDR-L3 as depicted in SEQ ID NO: 146;
- d) CDR-H1 as depicted in SEQ ID NO: 151, CDR-H2 as depicted in SEQ ID NO: 152, CDR-H3 as depicted in SEQ ID NO: 153, CDR-L1 as depicted in SEQ ID NO: 154, CDR-L2 as depicted in SEQ ID NO: 155 and CDR-L3 as depicted in SEQ ID NO: 156; and
- e) CDR-H1 as depicted in SEQ ID NO: 161, CDR-H2 as depicted in SEQ ID NO: 162, CDR-H3 as depicted in SEQ ID NO: 163, CDR-L1 as depicted in SEQ ID NO: 164, CDR-L2 as depicted in SEQ ID NO: 165 and CDR-L3 as depicted in SEQ ID NO: 166;
- f) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 439, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 134, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;
- g) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 440, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 134, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;
- h) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 441, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;
- i) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 442, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;
- j) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 443, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;
- k) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 444, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;
- l) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 439, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 441, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136; and
- m) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 440, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 442, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136.

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: 127, SEQ ID NO: 137, SEQ ID NO: 147, SEQ ID NO: 157, SEQ ID NO: 167, SEQ ID NO: 445, SEQ ID NO: 446, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 454, and SEQ ID NO: 455.

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: 128, SEQ ID NO: 138, SEQ ID NO: 148, SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 456, SEQ ID NO: 457, SEQ ID NO: 458, SEQ ID NO: 459, SEQ ID NO: 460, SEQ ID NO: 461, SEQ ID NO: 462, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, and SEQ ID NO: 470.

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: 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 137+456; SEQ ID NOs 137+457; SEQ ID NOs 137+458; SEQ ID NOs 137+459; SEQ ID NOs 137+460; SEQ ID NOs 445+138; SEQ ID NOs 446+138; SEQ ID NOs 447+138; SEQ ID NOs 445+460; SEQ ID NOs 448+461; SEQ ID NOs 449+462; SEQ ID NOs 450+463; SEQ ID NOs 450+464; SEQ ID NOs 450+465; SEQ ID NOs 450+466; SEQ ID NOs 450+467; SEQ ID NOs 450+468; SEQ ID NOs 451+463; SEQ ID NOs 452+463; SEQ ID NOs 453+463; SEQ ID NOs 451+468; SEQ ID NOs 454+469; and SEQ ID NOs 455+470.

In 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: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, and SEQ ID NO: 493.

The above first binding domains (which are specified by their CDRs, VH region and VL region and combinations thereof) characterize as binding domains which bind to a DLL3 epitope comprised within the region as depicted in SEQ ID NO: 259.

Another 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 DLL3 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 of DLL3 as an antibody selected from the group consisting of DLL3-13, DLL3-14, and DLL3-15, *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:

- a) CDR-H1 as depicted in SEQ ID NO: 121, CDR-H2 as depicted in SEQ ID NO: 122, CDR-H3 as depicted in SEQ ID NO: 123, CDR-L1 as depicted in SEQ ID NO: 124, CDR-L2 as depicted in SEQ ID NO: 125 and CDR-L3 as depicted in SEQ ID NO: 126;
- b) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 134, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136; and
- c) CDR-H1 as depicted in SEQ ID NO: 141, CDR-H2 as depicted in SEQ ID NO: 142, CDR-H3 as depicted in SEQ ID NO: 143, CDR-L1 as depicted in SEQ ID NO: 144, CDR-L2 as depicted in SEQ ID NO: 145 and CDR-L3 as depicted in SEQ ID NO: 146.

Another 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 DLL3 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 DLL3-13, DLL3-14, and DLL3-15, *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 above.

It is also envisaged that the antibody construct of the invention has, in addition to its function to bind to the target molecules DLL3 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 DLL3, 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: 295-341. 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: 285-293.

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: 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: 437, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, and SEQ ID NO: 531;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 285-293; and
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 350, SEQ ID NO: 359, SEQ ID NO: 368, SEQ ID NO: 377, SEQ ID NO: 386, SEQ ID NO: 395, SEQ ID NO: 404, SEQ ID NO: 413, SEQ ID NO: 422, SEQ ID NO: 431, and SEQ ID NO: 434; and
 - optionally a His-tag, such as the one depicted in SEQ ID NO: 294;
- (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: 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: 437, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, and SEQ ID NO: 531;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 285-293;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 350, SEQ ID NO: 359, SEQ ID NO: 368, SEQ ID NO: 377, SEQ ID NO: 386, SEQ ID NO: 395, SEQ ID NO: 404, SEQ ID NO: 413, SEQ ID NO: 422, SEQ ID NO: 431, and SEQ ID NO: 434;

- optionally a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 285-293;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOs: 295 and 301-330; and
 - optionally a His-tag, such as the one depicted in SEQ ID NO: 294;
- (c) a polypeptide comprising in the following order starting from the N-terminus:
- a polypeptide having the amino acid sequence QRFVTGHFGGLX₁PANG (SEQ ID NO: 296) wherein X₁ is Y or H; and
 - a polypeptide having an amino acid sequence selected from the group consisting of 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: 437, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, and SEQ ID NO: 531;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 285-293;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 350, SEQ ID NO: 359, SEQ ID NO: 368, SEQ ID NO: 377, SEQ ID NO: 386, SEQ ID NO: 395, SEQ ID NO: 404, SEQ ID NO: 413, SEQ ID NO: 422, SEQ ID NO: 431, and SEQ ID NO: 434;
 - a polypeptide having the amino acid sequence QRFVTGHFGGLHPANG (SEQ ID NO: 298) or QRFCTGHFGGLHPCNG (SEQ ID NO: 300); and
 - optionally a His-tag, such as the one depicted in SEQ ID NO: 294;
- (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: 348, SEQ ID NO: 357, SEQ ID NO: 366, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 393, SEQ ID NO: 402, SEQ ID NO: 411, SEQ ID NO: 420, SEQ ID NO: 429, and SEQ ID NO: 432;
 - a peptide linker having the amino acid sequence depicted in SEQ ID NO: 292;

- a polypeptide having an amino acid sequence selected from the group consisting of 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: 436, SEQ ID NO: 456, SEQ ID NO: 457, SEQ ID NO: 458, SEQ ID NO: 459, SEQ ID NO: 460, SEQ ID NO: 461, SEQ ID NO: 462, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, and SEQ ID NO: 530, followed by a serine residue at the C-terminus;
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 331; 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: 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: 435, SEQ ID NO: 445, SEQ ID NO: 446, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 454, and SEQ ID NO: 455, and SEQ ID NO: 529;
 - a peptide linker having the amino acid sequence depicted in SEQ ID NO: 292;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 349, SEQ ID NO: 358, SEQ ID NO: 367, SEQ ID NO: 376, SEQ ID NO: 385, SEQ ID NO: 394, SEQ ID NO: 403, SEQ ID NO: 412, SEQ ID NO: 421, SEQ ID NO: 430, and SEQ ID NO: 433 followed by a serine residue at the C-terminus; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 332;
- (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: 348, SEQ ID NO: 357, SEQ ID NO: 366, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 393, SEQ ID NO: 402, SEQ ID NO: 411, SEQ ID NO: 420, SEQ ID NO: 429, and SEQ ID NO: 432;
 - a peptide linker having the amino acid sequence depicted in SEQ ID NO: 292;
 - a polypeptide having an amino acid sequence selected from the group consisting of 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: 436, SEQ ID NO: 456, SEQ ID NO: 457, SEQ ID NO: 458, SEQ ID NO: 459, SEQ ID NO: 460, SEQ ID NO: 461, SEQ ID NO: 462, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, and SEQ ID NO: 530; and

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 333; 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: 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, and SEQ ID NO: 167, SEQ ID NO: 435, SEQ ID NO: 445, SEQ ID NO: 446, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 454, SEQ ID NO: 455, and SEQ ID NO: 529;
 - a peptide linker having the amino acid sequence depicted in SEQ ID NO: 292;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 349, SEQ ID NO: 358, SEQ ID NO: 367, SEQ ID NO: 376, SEQ ID NO: 385, SEQ ID NO: 394, SEQ ID NO: 403, SEQ ID NO: 412, SEQ ID NO: 421, SEQ ID NO: 430, and SEQ ID NO: 433 followed by a serine residue at the C-terminus; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 334;
- (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: 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: 437, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, and SEQ ID NO: 531;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 285-293;

- a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 350, SEQ ID NO: 359, SEQ ID NO: 368, SEQ ID NO: 377, SEQ ID NO: 386, SEQ ID NO: 395, SEQ ID NO: 404, SEQ ID NO: 413, SEQ ID NO: 422, SEQ ID NO: 431, and SEQ ID NO: 434;
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 335; and
a polypeptide having the amino acid sequence depicted in SEQ ID NO: 336;
- (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: 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: 437, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, and SEQ ID NO: 531; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 337; 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: 350, SEQ ID NO: 359, SEQ ID NO: 368, SEQ ID NO: 377, SEQ ID NO: 386, SEQ ID NO: 395, SEQ ID NO: 404, SEQ ID NO: 413, SEQ ID NO: 422, SEQ ID NO: 431, and SEQ ID NO: 434; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 338;
- (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: 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: 437, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID

NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, and SEQ ID NO: 531; and

- a polypeptide having the amino acid sequence depicted in SEQ ID NO: 339; 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: 350, SEQ ID NO: 359, SEQ ID NO: 368, SEQ ID NO: 377, SEQ ID NO: 386, SEQ ID NO: 395, SEQ ID NO: 404, SEQ ID NO: 413, SEQ ID NO: 422, SEQ ID NO: 431, and SEQ ID NO: 434; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 340; 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: 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: 437, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, and SEQ ID NO: 531;
 - a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 285-293;
 - a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO: 350, SEQ ID NO: 359, SEQ ID NO: 368, SEQ ID NO: 377, SEQ ID NO: 386, SEQ ID NO: 395, SEQ ID NO: 404, SEQ ID NO: 413, SEQ ID NO: 422, SEQ ID NO: 431, and SEQ ID NO: 434; and
 - a polypeptide having the amino acid sequence depicted in SEQ ID NO: 341.

For example, a preferred bispecific antibody construct of the present invention comprises or consists of a polypeptide selected from the group consisting of those depicted in:

SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 231, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 235, SEQ ID NO: 236, SEQ ID NO: 237; SEQ ID NO: 242,

SEQ ID NO: 243, SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 247, SEQ ID NO: 248, SEQ ID NO: 249, SEQ ID NO: 250, and SEQ ID NO: 251.

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: 541-548. Each of said polypeptide monomers preferably has an amino acid sequence that is selected from the group consisting of SEQ ID NOs: 533-540, 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: 285, 286, 288, 289, 290, 292 and 293.

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: 286, 292 and 293;
- (c) the second binding domain;
- (d) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 285, 286, 288, 289, 290, 292 and 293;
- (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: 550, 551, 552 and 553; 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: 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: 437, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID

NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, SEQ ID NO: 493, and SEQ ID NO: 531;

- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 286, 292 and 293;
- the second binding domain having an amino acid sequence selected from the group consisting of SEQ ID NO: 350, SEQ ID NO: 359, SEQ ID NO: 368, SEQ ID NO: 377, SEQ ID NO: 386, SEQ ID NO: 395, SEQ ID NO: 404, SEQ ID NO: 413, SEQ ID NO: 422, SEQ ID NO: 431, and SEQ ID NO: 434;
- a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 285, 286, 288, 289, 290, 292 and 293; and
- the third domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 541-548.

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 NO: 517, SEQ ID NO: 518, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, and SEQ ID NO: 528.

The sequence table (Table 18) also provides sequence variations of the binders denominated DLL3-4 and DLL3-14. The point mutations that were inserted into these sequence variants are identified according to the position of this mutation within the respective scFv molecule. It is understood that an alternative way of identifying these positions is also possible, depending on the polypeptide of reference, which could as well be the CDR region or the VH / VL region. For example, the variant denominated DLL3-4-001 has a G44C-G243C double mutation in its scFv molecule (SEQ ID NO: 437). This translates into a G44C mutation in the corresponding VH chain (SEQ ID NO: 435) and a G101C mutation in the corresponding VL chain (SEQ ID NO: 436).

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.

Cysteiny residues most commonly are reacted with α -haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteiny 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.

Arginy 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 ($\text{R}'\text{—N}=\text{C}=\text{N—R}'$), 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 asparaginy and glutaminy 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.

Glutamyl and asparagyl 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 DLL3 antibody fragment or derivative fused to a leucine zipper peptide are expressed in suitable host cells, and the soluble oligomeric DLL3 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) 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 DLL3 on the surface of a target cell. The preferred amino acid sequence of human DLL3 is represented by SEQ ID NO: 252. 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 DLL3 extracellular domain (DLL3 ECD). The first binding domain according to the invention hence preferably binds to DLL3 when it is expressed by naturally expressing cells or cell lines, and/or by cells or cell lines transformed or (stably / transiently) transfected with DLL3. In a preferred embodiment the first binding domain also binds to DLL3 when DLL3 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 DLL3 on its surface; preferably the target cell is a cell that is part of the human or animal body, such as a specific DLL3 expressing cancer or tumor cell.

The term "DLL3 ECD" refers to a form of DLL3 which is essentially free of transmembrane and cytoplasmic domains of DLL3. It will be understood by the skilled artisan that the transmembrane domain identified for the DLL3 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 DLL3 ECD is shown in SEQ ID NO: 253.

The affinity of the first binding domain for human DLL3 is preferably ≤ 20 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 DLL3xCD3 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 DLL3, 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) DLL3, e.g. human or macaque DLL3. Target cells can be a cell line (such as CHO) which is stably or transiently transfected with DLL3, e.g. human or macaque DLL3. Alternatively, the target cells can be a DLL3 positive natural expresser cell line, such as the human lung carcinoma cell line SHP-77. Usually EC₅₀ values are expected to be lower with target cell lines expressing higher levels of DLL3 on the cell surface. The effector to target cell (E:T) ratio is usually about 10:1, but can also vary. Cytotoxic activity of DLL3xCD3 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 DLL3xCD3 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 EC₅₀ 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 EC₅₀ value of the DLL3xCD3 bispecific antibody constructs is ≤ 5000 pM or ≤ 4000 pM, more preferably ≤ 3000 pM or ≤ 2000 pM, even more preferably ≤ 1000 pM or ≤ 500 pM, even more preferably ≤ 400 pM or ≤ 300 pM, even more preferably ≤ 200 pM, even more preferably ≤ 100 pM, even more preferably ≤ 50 pM, even more preferably ≤ 20 pM or ≤ 10 pM, and most preferably ≤ 5 pM.

The above given EC₅₀ values can be measured in different assays. The skilled person is aware that an EC₅₀ 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 EC₅₀ 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 DLL3 transfected cells such as CHO cells or a DLL3 positive human lung carcinoma cell line SHP-77 are used as target cells), the EC₅₀ value of the DLL3 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. When human PBMCs are used as effector cells, the EC₅₀ value of the DLL3xCD3 bispecific antibody construct is preferably ≤ 5000 pM or ≤ 4000 pM (in particular when the target cells are a DLL3 positive human lung carcinoma cell line SHP-77), more preferably ≤ 2000 pM (in particular when the target cells are DLL3 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 lower. When a macaque T cell line such as LnPx4119 is used as effector cells, and a macaque DLL3 transfected cell line such as CHO cells is used as target cell line, the EC₅₀ value of the DLL3 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.

Preferably, the DLL3xCD3 bispecific antibody constructs of the present invention do not induce / mediate lysis or do not essentially induce / mediate lysis of DLL3 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 DLL3 negative cells, whereby lysis of a DLL3 positive human lung carcinoma cell line SHP-77 (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 DLL3xCD3 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 DLL3xCD3 bispecific antibody constructs of the present invention are preferably ≤ 5 , more preferably ≤ 4 , even more preferably ≤ 3 , even more preferably ≤ 2 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 DLL3 and human CD3, respectively, will also bind to DLL3 / 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 DLL3 on the surface of a target cell also binds at least to macaque DLL3, 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 DLL3 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 this embodiment, the first binding domain binds to an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 260.

In one aspect of the invention, the first binding domain binds to human DLL3 and further binds to macaque DLL3, such as DLL3 of *Macaca fascicularis*, and more preferably, to macaque DLL3 ECD. A preferred *Macaca fascicularis* DLL3 is depicted in SEQ ID NO: 271. A preferred macaque DLL3 ECD is depicted in SEQ ID NO: 272. The affinity of the first binding domain for macaque DLL3 is preferably ≤ 15 nM, more preferably ≤ 10 nM, even more preferably ≤ 5 nM, even more preferably ≤ 1 nM, even more preferably ≤ 0.5 nM, even more preferably ≤ 0.1 nM, and most preferably ≤ 0.05 nM or even ≤ 0.01 nM.

Preferably the affinity gap of the antibody constructs according to the invention for binding macaque DLL3 versus human DLL3 [ma DLL3:hu DLL3] (as determined e.g. by BiaCore or by Scatchard analysis) is between 0.1 and 10, more preferably between 0.2 and 5, 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: 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: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 438 and SEQ ID NO: 532. These antibody constructs have a first binding domain which binds to an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 258.

In an alternative embodiment, the antibody construct of the invention comprises a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 130, SEQ ID NO: 140, SEQ ID NO: 150, SEQ ID NO: 160, SEQ ID NO: 170; SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 505, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 513, SEQ ID NO: 514, SEQ ID NO: 515, and SEQ ID NO: 516. These antibody constructs have a first binding domain which binds to an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 259.

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 DLL3 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);

pro line (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 sidechain (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 DLL3 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 1, below) is envisaged as long as the antibody construct retains its capability to bind to DLL3 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 1 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 1, or as further described below in reference to amino acid classes, may be introduced and the products screened for a desired characteristic.

Table 1: 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 $\geq 96\%$. 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 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 ≥ 3 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 ≤ 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 DLL3. 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 $\leq 1\%$ or $\leq 0.5\%$ 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 $\leq 0.5\%$, 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 $\geq 59^\circ\text{C}$. The thermostability parameter can be determined in terms of antibody aggregation temperature as follows: Antibody solution at a concentration $250\text{ }\mu\text{g/ml}$ 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°C/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 $250\text{ }\mu\text{g/ml}$ 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/ $^\circ\text{C}$) 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 DLL3xCD3 bispecific antibody constructs of the invention do not cross-react with (*i.e.*, do not essentially bind to) the human DLL3 paralogues DLL1 and/or DLL4. Furthermore, it is envisaged that the DLL3xCD3 bispecific antibody constructs of the invention do not cross-react with (*i.e.*, do not essentially bind to) the macaque / cyno DLL3 paralogues DLL1 and/or DLL4. See Example 6.

The DLL3 xCD3 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 . See Example 12.

The DLL3xCD3 bispecific antibody constructs of the invention are also envisaged to not be internalized or to not undergo significant internalization by the target cell. The rate of internalization can be assayed *e.g.* as described in Example 16. Preferably, the internalization rate (*e.g.* measured as a decrease in cytotoxicity) 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 $\leq 5\%$.

It is furthermore envisaged that shed or soluble DLL3 does not significantly impair the efficacy or biologic activity of the DLL3xCD3 bispecific antibody constructs of the invention. This can be measured *e.g.* in a cytotoxicity assay where soluble DLL3 is added at increasing concentrations to the assay, *e.g.* at 0 nM – 0.3 nM – 0.7 nM – 1 nM – 3 nM – 7 nM – 12 nM. The EC₅₀ value of the tested antibody construct should not be significantly increased in the presence of soluble DLL3. See Example 17.

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 $\geq 30\%$, more preferably $\geq 40\%$, more preferably $\geq 50\%$, even more preferably $\geq 60\%$, even more preferably $\geq 70\%$, 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 DLL3 positive cancer cell line (*e.g.* SHP-77) 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 mm³. 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 DLL3xCD3 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. drosophilarum* (ATCC 36906), *K. thermotolerans*, and *K. marxianus*; yarrowia (EP 402 226); *Pichia pastoris* (EP 183 070); *Candida*; *Trichoderma reesia* (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 SEPHAROSETM, chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromato-focusing, 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.

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 including, but not limited to, (or consisting of) lung cancer, preferably SCLC, breast, cervical, colon, colorectal, endometrial, head and neck, liver, ovarian, pancreatic, prostate, skin, gastric, testis, thyroid, adrenal, renal, bladder, uterine, esophageal, urothelial and brain tumor or cancer, lymphoma, carcinoma, and sarcoma, 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 small cell lung cancer (SCLC), non-small cell lung cancer (NSCLC), glioma, glioblastoma,

melanoma, neuroendocrine prostate cancer, neuroendocrine pancreatic cancer, hepatoblastoma, and hepatocellular carcinoma. 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.

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 DLL3-expressing tumors, a therapeutically effective amount of the antibody construct of the invention, e.g. an anti-DLL3 /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 polypeptide 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**

Schematic representation of the DLL3 ECD / truncated DLL3 constructs expressed on CHO cells for epitope mapping. The transmembrane and the intracellular domain are derived from EpCAM. See Example 1.

Figure 2

Epitope mapping of the anti-DLL3 antibody constructs. Examples of bispecific antibody constructs recognizing the EGF-3 domain and the EGF-4 domain, respectively, as detected by epitope mapping. The x-axis depicts PE-A (PE = phycoerythrin, A = signal area), and the y-axis depicts counts. See Example 2.

Figure 3

Cross-Reactivity of anti-DLL3 antibody constructs as detected by flow cytometry: binding to human and macaque DLL3 and CD3. The x-axis depicts FL2-H, and the y-axis depicts counts. See Example 5.

Figure 4

Analysis of anti-DLL3 antibody constructs by flow cytometry: non-binding to human paralogues DLL1 and DLL4. The x-axis depicts FL1-H, and the y-axis depicts counts. See Example 6.

Figure 5

Stability of anti-DLL3 antibody constructs after incubation for 96 hours in human plasma. See Example 11.

Figure 6

Potency gap between the monomeric and the dimeric isoform of the anti-DLL3 antibody constructs. See Example 15.

Figure 7

In vitro internalization assay, carried out as described in Example 16. Antibody construct was pre-incubated on target cells (SHP-77) in the absence of T cells in order to measure loss of antibody construct due to internalization. Results suggest that no significant internalization

occurs. The results achieved with a control target which is well known for its internalization are shown for comparison at the right.

Figure 8

Results of the mouse xenograft efficacy study of the SHP-77 model (Fig. 8A) and the WM266-4 model (Figure 8B). The tumor volume is plotted against the time. See Example 18.

Figure 9

Pharmacokinetics of different HLE antibody constructs (albumin fusion in Fig. 9A and Fc fusions in Fig. 9B) as determined in Example 20.

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 DLL3**

The extracellular domain of the DLL3 antigen can be subdivided into different sub-domains or regions that are defined, for the purposes of Examples 1 and 2, by the following amino acid positions:

Signal peptide: 1-26

N-terminus: 27-175

DSL: 176-215

EGF-1: 216-249

EGF-2: 274-310

EGF-3: 312-351

EGF-4: 353-389

EGF-5: 391-427

EGF-6: 429-465

For the construction of the truncated DLL3 molecules used for epitope mapping, the sequences of the respective eight extracellular domains (Signal peptide plus N-terminus, DSL, EGF1, EGF2, EGF3, EGF4, EGF5 and EGF6) of human DLL3 were stepwise deleted from the antigen, starting from the N-terminus. The following molecules were generated; see also Figure 1:

- | | |
|------------------------------|----------------|
| • Hu DLL3 ECD / complete ECD | SEQ ID NO: 263 |
| • Hu DLL3 ECD / up to DSL | SEQ ID NO: 264 |
| • Hu DLL3 ECD / up to EGF-1 | SEQ ID NO: 265 |
| • Hu DLL3 ECD / up to EGF-2 | SEQ ID NO: 266 |
| • Hu DLL3 ECD / up to EGF-3 | SEQ ID NO: 267 |
| • Hu DLL3 ECD / up to EGF-4 | SEQ ID NO: 268 |
| • Hu DLL3 ECD / up to EGF-5 | SEQ ID NO: 269 |
| • Hu DLL3 ECD / only EGF-6 | SEQ ID NO: 270 |

For the generation of CHO cells expressing human, cynomolgus macaque ("cyno") and truncated human N-terminal V5 tagged DLL3, the respective coding sequences for human DLL3-ECD (SEQ ID NO: 253; see also GeneBank accession number NM_016941), cyno DLL3-ECD (SEQ ID NO: 272) and the seven truncated human N-terminal V5 tagged DLL3-ECD versions (see above) were cloned into a plasmid designated pEF-DHFR (pEF-DHFR is described in Raum *et al.* Cancer Immunol Immunother 50 (2001) 141-150). For cell surface expression of human and cyno DLL3 the original signal peptide was used, and for cell surface expression of the truncated human N-terminal DLL3 a mouse IgG heavy chain signal peptide was used, followed by a V5 tag. All mentioned DLL3-ECD sequences were followed in frame by the coding sequence of an artificial Ser/Gly-linker followed by a domain derived from the transmembrane / intracellular domain of human EpCAM (amino acids 266-314 of the sequence as published in GenBank accession number NM_002354). 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 human and cyno DLL3 on CHO cells was verified in a FACS assay using a monoclonal mouse IgG2b anti-human DLL3 antibody. The expression of the seven truncated versions of human DLL3-ECD was verified using a monoclonal mouse IgG2a anti-v5 tag antibody. 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.

Example 2

Epitope mapping of anti-DLL3 antibody constructs

Cells transfected with human DLL3 and with the truncated human DLL3 molecules (see Example 1) were stained with crude, undiluted periplasmic extract containing bispecific DLL3xCD3 antibody constructs (with the CD3 binding domain being denominated I2C) fused to a human albumin (variant 1), in PBS/1,5%FCS. Bound molecules were detected with an in-house mouse monoclonal anti-CD3 binding domain antibody (50 µl) followed by an anti-mouse IgG Fc-gamma-PE (1:100, 50 µl; 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.

The regions that were recognized by the respective DLL3 binding domains are indicated in the sequence table (Table 18). Binders were mapped that were specific for an epitope located within the N-terminus of DLL3, within the DSL domain, and within the different EGF domains.

Figure 2 shows two exemplary binders which bind to a DLL3 epitope comprised within the EGF-3 region (loss of the FACS signal in the respective truncated DLL3 constructs not comprising EGF-3). Figure 2 also shows an exemplary binder which binds to a DLL3 epitope comprised within the EGF-3 region (loss of the FACS signal in the respective truncated DLL3 constructs not comprising EGF-4).

Some of the binders are described to be specific for an epitope located with the region denominated EGF-5/[6]. The squared brackets are meant to indicate that the FACS signal of the binder is decreased (*i.e.*, neither fully present nor fully lost) for the truncated DLL3 construct having only the EGF-6 domain left (last construct in Figure 1).

The bispecific DLL3xCD3 constructs used in the following examples are chosen from those constructs having "I2C" as the CD3 binding domain and having a C-terminal fusion to a wild-type human serum albumin, see e.g. SEQ ID NOs: 224-230, 233-235, 238-241.

Example 3

Biacore-based determination of antibody affinity to human and cynomolgus DLL3

Biacore analysis experiments were performed using recombinant human / cyno DLL3-ECD fusion proteins with chicken 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 DLL3xCD3 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 μ l/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.

The DLL3xCD3 bispecific antibody constructs according to the invention showed very high affinities to human DLL3 in the subnanomolar range (with the exception of DLL3-13 having a KD value in the very low one-digit nanomolar range). Binding to macaque DLL3 was balanced, also showing affinities in similar ranges. The affinity values as well as the calculated affinity gap are shown in Table 2.

Table 2: Affinities of DLL3xCD3 bispecific antibody constructs to human and macaque DLL3 as determined by Biacore analysis, as well as the calculated interspecies affinity gaps.

DLL3xCD3 bispecific antibody construct	KD hu DLL3 [nM]	KD cyno DLL3 [nM]	Affinity gap KD mac/KD hu
DLL3-4	0.41	0.55	1.34
DLL3-5	0.82	1.03	1.26
DLL3-6	0.55	0.75	1.36
DLL3-7	0.19	0.29	1.52
DLL3-8	0.69	0.96	1.39
DLL3-9	0.35	0.54	1.54
DLL3-10	0.24	0.33	1.38
DLL3-13	1.74	5.55	3.19
DLL3-14	0.47	0.86	1.83
DLL3-15	0.45	0.69	1.53

Furthermore, the binding of the bispecific antibody constructs to both human CD3 and macaque CD3 was confirmed in a Biacore assay to be in a low 2-digit nanomolar range (data not shown).

Example 4

Scatchard-based analysis of DLL3xCD3 bispecific antibody construct affinity to human and macaque DLL3 on target antigen positive cells and determination of the interspecies affinity gap

The affinities of DLL3xCD3 bispecific antibody constructs to CHO cells transfected with human or macaque DLL3 were also determined by Scatchard analysis as the most reliable method for measuring potential affinity gaps between human and macaque DLL3. For the Scatchard analysis, saturation binding experiments are performed using a monovalent detection system to precisely determine monovalent binding of the DLL3xCD3 bispecific antibody constructs to the respective cell line.

2×10^4 cells of the respective cell line (recombinantly human DLL3-expressing CHO cell line, recombinantly macaque DLL3-expressing CHO cell line) were incubated each with 50 μ l of a triplet dilution series (twelve dilutions at 1:2) of the respective DLL3xCD3 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 DLL3xCD3 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.

Values depicted in Table 3 were derived from two independent experiments per DLL3xCD3 bispecific antibody construct. Cell based Scatchard analysis confirmed that the DLL3xCD3 bispecific antibody constructs of the invention are subnanomolar in affinity to human DLL3 and to mac DLL3 and present with a small cyno/human interspecies affinity gap of around 1.

Table 3: Affinities (KD) of DLL3xCD3 bispecific antibody constructs as determined in cell based Scatchard analysis with the calculated affinity gap KD macaque DLL3 / KD human DLL3. Antibody constructs were measured in two independent experiments, each using triplicates.

DLL3xCD3 bispecific antibody construct	Cell based affinity hu DLL3 [nM]	Cell based affinity mac DLL3 [nM]	Affinity gap KD mac/KD hu
DLL3-4	0.39	0.24	0.6
DLL3-5	0.33	0.22	0.7

DLL3-6	0.33	0.23	0.7
DLL3-7	0.21	0.33	1.6
DLL3-8	0.18	0.34	1.9
DLL3-9	0.30	0.49	1.6
DLL3-10	0.37	0.32	0.8
DLL3-13	0.24	0.29	1.2
DLL3-14	0.53	0.51	1.0
DLL3-15	0.25	0.50	2.0

Example 5

Bispecific binding and interspecies cross-reactivity

For confirmation of binding to human DLL3 and CD3 and to cyno DLL3 and CD3, bispecific antibody constructs of the invention were tested by flow cytometry using

- CHO cells transfected with human DLL3, with an artificial human DLL3 isoform (characterized by the point mutations F172C and L218P), and with macaque DLL3, respectively,
- the human DLL3 positive human lung carcinoma cell line SHP-77,
- 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 3. The DLL3xCD3 bispecific antibody constructs of the invention stained CHO cells transfected with human DLL3, the artificial DLL3 isoform and with cyno DLL3, and they also stained the human DLL3 positive human lung carcinoma cell line SHP-77 (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 (non-transfected CHO, data shown in Example 6).

Example 6

Confirmation of the absence of binding to human paralogues

Human DLL3 paralogues DLL1 and DLL4 were stably transfected into CHO cells. The sequences of the paralogues as used in the present Example are identified in the sequence listing (SEQ ID NOs: 283 and 284). Protein expression was confirmed in FACS analyses with antibodies specific for the respective paralogues: Antibodies were anti-human DLL1 MAB1818 (R&D; 5 µg/ml), and anti-human DLL4 MAB1506 (R&D; 5 µg/ml) for DLL4.

The flow cytometry assay was carried out as described in Example 5, with the exception that bound mouse antibodies were detected with a goat anti-mouse FITC (1:100). The results are shown in Figure 4. The analysis confirmed that none of the DLL3xCD3 bispecific antibody constructs of the invention cross-reacts with the human DLL3 paralogues DLL1 and DLL4.

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 DLL3 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 4 below:

Table 4: Identity of VH and VL to human germline

DLL3xCD3 bispecific antibody construct	% identity to human germline [VH / VL]
DLL3-4	96.9 / 93.3
DLL3-5	96.9 / 96.6
DLL3-6	96.9 / 96.6

DLL3-7	93.9 / 96.6
DLL3-8	94.8 / 96.6
DLL3-9	96.9 / 95.5
DLL3-10	91.9 / 95.5
DLL3-13	95.9 / 95.7
DLL3-14	94.9 / 94.6
DLL3-15	93.9 / 94.6

Example 8

Cytotoxic activity

The potency of DLL3xCD3 bispecific antibody constructs of the invention in redirecting effector T cells against DLL3-expressing target cells was analyzed in five *in vitro* cytotoxicity assays:

- The potency of DLL3xCD3 bispecific antibody constructs in redirecting stimulated human CD8⁺ effector T cells against human DLL3-transfected CHO cells was measured in an 18 hour 51-chromium release assay.
- The potency of DLL3xCD3 bispecific antibody constructs in redirecting stimulated human CD8⁺ effector T cells against the DLL3 positive human lung carcinoma cell line SHP-77 was measured in an 18 hour 51-chromium release assay.
- The potency of DLL3xCD3 bispecific antibody constructs in redirecting the T cells in unstimulated human PBMC against human DLL3-transfected CHO cells was measured in a 48 hour FACS-based cytotoxicity assay.
- The potency of DLL3xCD3 bispecific antibody constructs in redirecting the T cells in unstimulated human PBMC against the DLL3-positive human cell line SHP-77 was measured in a 48 hour FACS-based cytotoxicity assay.
- For confirmation that the cross-reactive DLL3xCD3 bispecific antibody constructs are capable of redirecting macaque T cells against macaque DLL3-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 DLL3- or human DLL3-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 DLL3-transfected CHO cells

The cytotoxic activity of DLL3xCD3 bispecific antibody constructs according to the invention was analyzed in a 51-chromium (⁵¹Cr) release cytotoxicity assay using CHO cells transfected with human DLL3 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 5. The DLL3xCD3 bispecific antibody constructs showed very potent cytotoxic activity against human DLL3 transfected CHO cells in the 1-digit picomolar range.

Table 5: EC₅₀ values [pM] of DLL3xCD3 bispecific antibody constructs analyzed in a 51-chromium (⁵¹Cr) release cytotoxicity assay using CHO cells transfected with human DLL3 as target cells, and stimulated human CD8 T cells as effector cells.

DLL3xCD3 bispecific antibody construct	EC ₅₀ [pM]
DLL3-4	3.8
DLL3-5	4.2
DLL3-6	2.1
DLL3-7	2.2
DLL3-8	1.2
DLL3-9	1.2
DLL3-10	1.4
DLL3-13	1.8
DLL3-14	5.4
DLL3-15	9.8

Example 8.3

Potency of redirecting stimulated human effector T cells against the DLL3 positive human lung carcinoma cell line SHP-77

The cytotoxic activity of DLL3xCD3 bispecific antibody constructs was analyzed in a 51-chromium (⁵¹Cr) release cytotoxicity assay using the DLL3-positive human lung carcinoma cell line SHP-77 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.

In accordance with the results of the 51-chromium release assays with stimulated enriched human CD8+ T lymphocytes as effector cells and human DLL3-transfected CHO cells as target cells, DLL3xCD3 bispecific antibody constructs of the present invention are also potent in cytotoxic activity against natural expresser target cells (see Table 6).

Table 6: EC50 values [pM] of DLL3xCD3 bispecific antibody constructs analyzed in an 18-hour 51-chromium (⁵¹Cr) release cytotoxicity assay with the DLL3-positive human lung carcinoma cell line SHP-77 as source of target cells, and stimulated enriched human CD8 T cells as effector cells.

Rows 1-10: Antibody constructs according to the invention, which bind to a DLL3 epitope comprised within the region as depicted in SEQ ID NO: 260. (Rows 1-7: Antibody constructs binding to a DLL3 epitope comprised within the EGF-3 region. Rows 8-10: Antibody constructs binding to a DLL3 epitope comprised within the EGF-4 region.) Rows 11-14: Antibody constructs binding to a DLL3 epitope which is comprised within the EGF-5/[EGF-6] region.

Row	DLL3xCD3 bispecific antibody construct	EC50 [pM]
1	DLL3-4	27
2	DLL3-5	26
3	DLL3-6	18
4	DLL3-7	23
5	DLL3-8	39
6	DLL3-9	18
7	DLL3-10	31
8	DLL3-13	22
9	DLL3-14	31
10	DLL3-15	36
11	DLL3-18	38
12	DLL3-19	142
13	DLL3-20	171
14	DLL3-21	324

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 (Milty 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 /10⁷ 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 /10⁷ cells) were added and incubated for 15 min at 4 - 8°C. The cells were washed with MACS isolation buffer (1 - 2 mL/10⁷ cells). After centrifugation (see above), supernatant was discarded and cells resuspended in MACS isolation buffer (500 μL /10⁸ cells). CD14/CD56 negative cells were then isolated using LS Columns (Milty 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 DLL3- or macaque DLL3-transfected CHO cells as target cells and distinguish them from effector cells. Briefly, cells were harvested, washed once with PBS and adjusted to 10⁶ cell/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 μL /10⁶ 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 x 10⁵ 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 DLL3-transfected CHO cells in the presence of serial dilutions of DLL3 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 DLL3xCD3 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 DLL3-transfected CHO cells

The cytotoxic activity of DLL3xCD3 bispecific antibody constructs was analyzed in a FACS-based cytotoxicity assay using CHO cells transfected with human DLL3 as target cells, and unstimulated human PBMC as effector cells. The assay was carried out as described in Example 8.4 above.

The results of the FACS-based cytotoxicity assays with unstimulated human PBMC as effector cells and human DLL3-transfected CHO cells as targets are shown in Table 7.

Table 7: EC50 values [pM] of DLL3xCD3 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 DLL3 as target cells.

Rows 1-10: Antibody constructs according to the invention, which bind to a DLL3 epitope comprised within the region as depicted in SEQ ID NO: 260. (Rows 1-7: Antibody constructs binding to a DLL3 epitope comprised within the EGF-3 region. Rows 8-10: Antibody constructs binding to a DLL3 epitope comprised within the EGF-4 region.) Rows 11-14: Antibody constructs binding to a DLL3 epitope which is comprised within the EGF-5/[EGF-6] region.

Row	DLL3xCD3 bispecific antibody construct	EC50 [pM]
1	DLL3-4	53
2	DLL3-5	36
3	DLL3-6	44
4	DLL3-7	40
5	DLL3-8	43
6	DLL3-9	43
7	DLL3-10	40
8	DLL3-13	116
9	DLL3-14	66
10	DLL3-15	57
11	DLL3-18	169
12	DLL3-19	107
13	DLL3-20	171
14	DLL3-21	85

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 the DLL3-positive lung carcinoma cell line SHP-77

The cytotoxic activity of DLL3xCD3 bispecific antibody constructs was furthermore analyzed in a FACS-based cytotoxicity assay using the DLL3-positive human lung carcinoma cell line SHP-77 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 8.

Table 8: EC₅₀ values [pM] of DLL3xCD3 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.

Rows 1-10: Antibody constructs according to the invention, which bind to a DLL3 epitope comprised within the region as depicted in SEQ ID NO: 260. (Rows 1-7: Antibody constructs binding to a DLL3 epitope comprised within the EGF-3 region. Rows 8-10: Antibody constructs binding to a DLL3 epitope comprised within the EGF-4 region.) Rows 11-14: Antibody constructs binding to a DLL3 epitope which is comprised within the EGF-5/[EGF-6] region.

Row	DLL3xCD3 bispecific antibody construct	EC ₅₀ [pM]
1	DLL3-4	44
2	DLL3-5	65
3	DLL3-6	31
4	DLL3-7	30
5	DLL3-8	24
6	DLL3-9	33
7	DLL3-10	32
8	DLL3-13	49
9	DLL3-14	65
10	DLL3-15	66
11	DLL3-18	76
12	DLL3-19	180
13	DLL3-20	1540
14	DLL3-21	770

Example 8.7

Potency of redirecting macaque T cells against macaque DLL3-expressing CHO cells

Finally, the cytotoxic activity of DLL3xCD3 bispecific antibody constructs was analyzed in a FACS-based cytotoxicity assay using CHO cells transfected with macaque (cyno) DLL3 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 DLL3-transfected CHO cells and flow cytometry based analysis of cytotoxic activity was performed as described above.

Results are shown in Table 9. Macaque T cells from cell line 4119LnPx were induced to efficiently kill macaque DLL3-transfected CHO cells by DLL3xCD3 bispecific antibody constructs according to the invention. The antibody constructs presented potently with 2-digit picomolar EC₅₀-values in this assay, confirming that they are very active in the macaque system.

Table 9: EC₅₀ values [pM] of DLL3xCD3 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 DLL3 as target cells.

Rows 1-10: Antibody constructs according to the invention, which bind to a DLL3 epitope comprised within the region as depicted in SEQ ID NO: 260. (Rows 1-7: Antibody constructs binding to a DLL3 epitope comprised within the EGF-3 region. Rows 8-10: Antibody constructs binding to a DLL3 epitope comprised within the EGF-4 region.) Rows 11-14: Antibody constructs binding to a DLL3 epitope which is comprised within the EGF-5/[EGF-6] region.

Row	DLL3xCD3 bispecific antibody construct	EC ₅₀ [pM]
1	DLL3-4	36
2	DLL3-5	42
3	DLL3-6	40
4	DLL3-7	101
5	DLL3-8	44
6	DLL3-9	58
7	DLL3-10	42
8	DLL3-13	65
9	DLL3-14	28
10	DLL3-15	32
11	DLL3-18	134
12	DLL3-19	66
13	DLL3-20	231

14	DLL3-21	86
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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 DLL3xCD3 antibody monomeric construct were 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 10 below. The DLL3xCD3 bispecific antibody constructs of the invention presented with dimer percentages of 0.0% after three freeze/thaw cycles, and with dimer percentages of ≤ 2% after 7 days of incubation at 37°C.

Table 10: Percentage of monomeric versus dimeric DLL3xCD3 bispecific antibody constructs as determined by High Performance Size Exclusion Chromatography (HP-SEC).

DLL3xCD3 bispecific antibody construct	Percentage of dimer after three freeze/thaw cycles	Percentage of dimer after 7 days of incubation at 37°C
DLL3-4	0.7	0.0
DLL3-5	1.5	0.0
DLL3-6	1.3	0.0
DLL3-7	1.2	0.0
DLL3-8	1.5	0.0
DLL3-9	1.8	0.0
DLL3-10	0.6	0.0
DLL3-13	1.6	0.0
DLL3-14	0.4	0.0
DLL3-15	1.2	0.0

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 DLL3xCD3 bispecific antibody constructs of the invention showed thermal stability with aggregation temperatures $\geq 45^{\circ}\text{C}$, as shown in Table 11 below. The group of antibody constructs binding to an epitope of DLL3 which is comprised within the EGF-4 region (as depicted in SEQ ID NO: 259) even had a thermal stability of $\geq 50^{\circ}\text{C}$, more precisely, of $\geq 54^{\circ}\text{C}$.

Table 11: Thermostability of the bispecific antibody constructs as determined by DLS (dynamic light scattering)

DLL3xCD3 bispecific antibody construct	Thermostability (DLS °C aggregation)
DLL3-4	59.3
DLL3-5	45.4
DLL3-6	58.8
DLL3-7	58.2
DLL3-8	49.8
DLL3-9	49.6
DLL3-10	52.9
DLL3-13	54.0
DLL3-14	57.0
DLL3-15	56.3

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 µg/ml. After plasma incubation the antibody constructs were compared in a 51-chromium release assay with stimulated enriched human CD8+ T cells and human DLL3-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 12 below; exemplary results for the two antibody constructs DLL-4 and DLL-14 are also shown in Figure 5. All tested antibody constructs had a very favourable plasma stability (EC_{50} plasma / EC_{50} control) of ≤ 2.5 . The group of antibody constructs binding to an epitope of DLL3 which is comprised within the EGF-4 region (as depicted in SEQ ID NO: 259) even had a plasma stability of ≤ 1.5 , more precisely, of ≤ 1.1 .

Table 12: EC₅₀ values of the antibody constructs with and without plasma incubation and calculated plasma / control value

DLL3xCD3 bispecific antibody construct	EC ₅₀ [pM]		Plasma to Control ratio (EC ₅₀ plasma/EC ₅₀ control)
	w/ plasma	w/o plasma	
DLL3-4	3.6	3.8	0.9
DLL3-5	5.4	4.2	1.3
DLL3-6	4.8	2.1	2.3
DLL3-7	2.7	2.2	1.2
DLL3-8	1.0	1.2	0.8
DLL3-9	1.2	1.2	1.0
DLL3-10	2.5	1.4	1.8
DLL3-13	2.0	1.8	1.1
DLL3-14	4.8	5.4	0.9
DLL3-15	7.8	9.8	0.8

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 13 below. All tested antibody constructs have a very favourable turbidity of ≤ 0.1 , with the exception of one construct with a turbidity slightly above 0.1. The group of antibody constructs binding to an epitope of DLL3 which is comprised within the EGF-4 region (as depicted in SEQ ID NO: 259) even have a turbidity of ≤ 0.08 .

Table 13: Turbidity of the antibody constructs after concentration to 2.5 mg/ml over night

DLL3xCD3 bispecific antibody construct	Turbidity at 2500 µg/ml [OD340]
DLL3-4	0.073
DLL3-5	0.106
DLL3-6	0.080
DLL3-7	0.089
DLL3-8	0.069
DLL3-9	0.085
DLL3-10	0.091
DLL3-13	0.075
DLL3-14	0.073
DLL3-15	0.078

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 14 below. All tested antibody constructs have a very favourable homogeneity of $\geq 80\%$ (area under the curve (= AUC) of the main peak), The group of antibody

constructs binding to an epitope of DLL3 which is comprised within the EGF-3 region (as depicted in SEQ ID NO: 258) even have a homogeneity of $\geq 90\%$.

Table 14: Protein homogeneity of the antibody constructs (% AUC of main peak)

DLL3xCD3 bispecific antibody construct	Protein homogeneity % AUC of main peak
DLL3-4	96
DLL3-5	100
DLL3-6	95
DLL3-7	93
DLL3-8	100
DLL3-9	93
DLL3-10	90
DLL3-13	100
DLL3-14	100
DLL3-15	83

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.

The antibody constructs had 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 DLL3xCD3 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 DLL3 transfected CHO cells. Effector to target cell (E:T) ratio was 10:1. The potency gap was calculated as ratio between EC50 values.

The results are shown in Table 15 below; exemplary results for the two antibody constructs DLL-4 and DLL-14 are also shown in Figure 6. Potency gaps of the tested DLL3xCD3 bispecific antibody constructs were between 0.2 and 1.0. There is hence no substantially more active dimer compared to its respective monomer.

Table 15: Potency gap between the monomeric and the dimeric isoform

DLL3xCD3 bispecific antibody construct	EC₅₀ [pM] monomer	EC₅₀ [pM] dimer	Ratio EC₅₀ monomer / EC₅₀ dimer
DLL3-4	3.8	5.7	0.7
DLL3-5	4.2	11	0.4
DLL3-6	2.1	13	0.2
DLL3-7	2.2	4.2	0.5
DLL3-8	1.2	3.4	0.4
DLL3-9	1.2	3.8	0.3
DLL3-10	1.4	1.4	1.0
DLL3-13	1.8	3.0	0.6

DLL3-14	5.4	8.7	0.6
DLL3-15	9.8	25	0.4

Example 16***In vitro* internalization assay**

Changes in the potency of the DLL3xCD3 bispecific antibody construct as a function of preincubation of the construct on the target cells in the absence of T cells were 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, but no impact was observed with the DLL3xCD3 bispecific antibody construct. The assay was carried out as follows:

T cells were counted and diluted to a concentration of 1×10^5 / ml in assay media. SHP-77 cells were counted and plated at 2500 cells per well (cpw). The antibody construct was diluted serially 1:2 (with Bravo), at a starting concentration of 100 nM. The antibody construct was 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 were plated at 25000 cpw, and the assay was incubated for 48 hours at 37°C. SHP-77 cell survival was analyzed with the Steady-Glo® system (25 µl/well). The results are shown in Figure 7 and suggest no significant internalization of the antibody construct DLL3-4 x CD3 (I2C).

Example 17**Shedding study**

In order to analyze whether the cytotoxic activity of the DLL3xCD3 bispecific antibody constructs of the invention is significantly impaired by the presence of shed DLL, the following assay was carried out: T cells were counted and diluted to a concentration of 1×10^5 / ml in assay media. SHP-77 cells were counted and diluted to a concentration of 1.25×10^5 / ml in assay media with increasing concentrations of soluble DLL3 between 0.3 nM and 12 nM. SHP-77 cells were plated at 2500 cells per well (cpw), and T cells were added at 25000 cpw. The antibody construct was diluted serially 1:2 (with Bravo), and added to the culture assay (with

Bravo). Incubation occurred for 48 hours at 37°C. SHP-77 cell survival was analyzed with the Steady-Glo® system (25 µl/well).

Example 18

Mouse xenograft efficacy study

The anti-tumor activity of an HLE DLL3xCD3 bispecific antibody construct (SEQ ID NO: 517) was tested in a model of female NOD/SCID mice which were subcutaneously injected on day 1 of the study with 5×10^6 human DLL3 positive SCLC (SHP-77 luc) or 5×10^6 human DLL3 positive melanoma (WM 266-4) cells. Effector cells (2×10^7 *in vitro* expanded and activated living human CD3+ T cells) were injected intraperitoneally on day 12. Treatment start was on day 16 (WM 266-4) or on day 18 (SHP-77 luc). The antibody construct was administered four times every five days (q5dx4) by i.v. bolus injections. The treatment groups were as follows:

- SCLC model (SHP-77 luc) / 7 mice per group
 - Vehicle-treated group with T cells
 - DLL3xCD3 bispecific antibody construct: 10 mg/kg per administration
- Melanoma model (WM266-4) / 9 mice per group
 - Vehicle-treated group with T cells
 - DLL3xCD3 bispecific antibody construct: 10 mg/kg per administration
 - DLL3xCD3 bispecific antibody construct: 2 mg/kg per administration

Tumors were measured by caliper during the study and progress evaluated by intergroup comparison of tumor volumes (TV). The tumor growth inhibition T/C [%] on day x is determined by calculating the tumor volume as $T/C (\%) = 100 \times (\text{median TV of analyzed group}) / (\text{median TV of control group})$, and the calculated values are depicted in the following table 16:

Table 16: T/C values of the mouse xenograft studies with SHP-77 luc cells and WM266-4 cells

Day of Study	T/C (%) SHP-77 model 10 mg/kg	T/C (%) WM266-4 model 10 mg/kg	T/C (%) WM266-4 model 2 mg/kg
15	103	101	101
17	92	76	77
20	64	42	47

23	50	36	38
26	52	31	35
29	34	46	40
31	33	56	55
33	30	64	75
36	24	<i>n.a</i>	<i>n.a</i>
38	19	<i>n.a</i>	<i>n.a</i>

The results are furthermore shown in Figure 8A and 8B. Significant tumor growth inhibition was shown in both tumor models and at both tested dose levels of 2 and 10 mg/kg.

Example 19

Cyno exploratory toxicology study

An exploratory toxicology study was carried out with a non half-life extended DLL3xCD3 bispecific antibody construct (SEQ ID NO: 554). Three female cynomolgus monkeys were dosed via continuous *i.v.* infusion for 16 days (5, 15, and 45 µg/kg/day for 3 days each, followed by 100 µg/kg/day for 7 days). No test article-related clinical observations, changes in body temperature, food consumption or body weight were observed.

Consistent with expectations for the pharmacology of a DLL3xCD3 bispecific antibody construct, circulating T lymphocyte populations (total T-lymphocytes, T-helper and T-cytotoxic lymphocytes, NK cells, B-lymphocytes, and CD25+ activated T-lymphocytes) were decreased on the first day of dosing and remained lower throughout the duration of the study in all animals. Activation markers (CD69 and CD25 on activated T cells) were increased on day 1, but not at later time points in the study.

To summarize, the DLL3xCD3 bispecific antibody construct was very well tolerated even at the highest dose tested (100 µg/kg/d, > 300 x EC₅₀).

Example 20

Cyno PK studys

A cyno PK study was performed with naïve male cynomolgus monkeys. Three different albumin-fused DLL3xCD3 (I2C) bispecific antibody constructs (DLL3-4, DLL3-6 and DLL3-14) were administered as *i.v.* single bolus at a concentration of 12 µg/kg. For each of the molecules a group of two animals was used.

A separate cyno PK study was performed under the same conditions, but with DLL3-4 in different Fc fusion versions.

Blood samples were collected pre-dose and at 0.05, 0.5, 1, 4, 8, 24, 48, 72, 120, 168, 240, and 336 hours post-dose. Serum was prepared for determination of serum concentrations of the molecules in an immunoassay. The assay was performed by capturing the antibody constructs via their target moiety, while an antibody directed against the CD3-binding part of the construct was used for detection. The serum concentration-time profiles were used to determine PK parameters. The pharmacokinetic parameters were determined using standard non-compartmental analysis (NCA) methods. The following PK parameters were assessed: AUC_{inf} (Area under the serum concentration- time curve), V_{ss} (volume of distribution at steady state), CL (systemic clearance) and terminal t_{1/2} (terminal half-life). For all antibody constructs, serum levels were quantifiable for all time points in all animals after their administration. No clinical observations were made in any of the treated animals.

The pharmacokinetics of the tested antibody constructs are shown in Figure 9, and the PK parameters are summarized as mean of n=2 in table 17 below.

The albumin-fused constructs showed a favorable PK profile consistent with a once or twice weekly dosing schedule in a human patient. An even more favorable PK profile supporting once weekly dosing or even every other week dosing was observed with an Fc fusion construct (scFc).

Table 17: Pharmacokinetic parameters of HLE variants of DLL3xCD3 bispecific antibody constructs in cynomolgus monkeys

Antibody construct	AUC _{inf} [ng * h / mL]	V _{ss} [mL / kg]	CL [mL / h / kg]	t _{1/2} [h]
DLL3-4 x I2C HALB	20,669	70	0.58	98

DLL3-6 x I2C HALB	20,228	67	0.59	103
DLL3-14 x I2C HALB	21,597	107	0.55	154
DLL3-4 x I2C scFc	29,746	118	0.40	213
DLL3-4 (cc) x I2C scFc	24,769	144	0.48	234
DLL3-4 x I2C hetero Fc	14,639	166	0.82	173

Table 18: Sequence listing

SEQ ID NO	DLL3 epi-tope	Designation	Format / Source	Amino acid sequence
1		DLL3-1	VH CDR1	DYGIH
2		DLL3-1	VH CDR2	VISYHGSNKYYARSVKG
3		DLL3-1	VH CDR3	EIPFGMDV
4		DLL3-1	VL CDR1	RSSQSLHSDGYNLYD
5		DLL3-1	VL CDR2	LGSNRAS
6		DLL3-1	VL CDR3	MQALQTPLT
7		DLL3-1	VH	QVQLVESGGGVVQGRSLRLSCAASGFTFSDYGIHWVRQAPGKGLEWVAVISYHGSNKYYARS VKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAREIPFGMDVWGQGTITVTVSS
8		DLL3-1	VL	DIVMTQTPLSLPVTPGEPASISCRSSQSLHSDGYNLYDLYLQKPGQSPQLLIYLGSNRASGV PDRFSGSGGTDFTLTISRVEAEDGVYYCMQALQTLTFFGGGTKVDIK
9	N-term.	DLL3-1	scFv	QVQLVESGGGVVQGRSLRLSCAASGFTFSDYGIHWVRQAPGKGLEWVAVISYHGSNKYYARS VKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAREIPFGMDVWGQGTITVTVSSGGSGGGGG SGGGSDIVMTQTPLSLPVTPGEPASISCRSSQSLHSDGYNLYDLYLQKPGQSPQLLIYLG NRASGVPDRFSGSGGTDFTLTISRVEAEDGVYYCMQALQTLTFFGGGTKVDIK

10		DLL3- 1 x12C	bispecific molecule	QVQLVESGGGVQSGRSLRLSCAASGFTFSDYGIHWVRQAPGKGLEWVAVISYHGSKYIARS VKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCAREIPFGMDVWGQTTTIVTSVSSGGSGGGG SGGGSDIVMTQTPLSLPVTPEGPASISCRSSQSLHSDGYNLDWYLGKPGQSPQLLIYLG NRASGVPDRFSGSGGTDFTLTI SRVEAEDVGVYCMQALQTPLTFGGGTVKDIKSGGGGSEV QLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNSYISYWAYWGQGLVTVSSGGG GSGGGSGGGGQTVVTQEPSTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIG GTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL
11		DLL3- 2	VH CDR1	GYMH
12		DLL3- 2	VH CDR2	WINPNSGDTNYAQKFQG
13		DLL3- 2	VH CDR3	DANIAALDAFEI
14		DLL3- 2	VL CDR1	RASQSISSYLN
15		DLL3- 2	VL CDR2	AASSLQS
16		DLL3- 2	VL CDR3	QQSYSTPLT
17		DLL3- 2	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWRQAPGQGLEWMGWINPNSGDTNYAQK FQGRVTMTTRDTSISITAYMELSRLTSDDTAVYYCARDANIAALDAFEIWGQGTMTVTVSS
18		DLL3- 2	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFS GSGGTDFTLTITSSLPEDFATYYCQQSYSTPLTFGGGKVEIK
19	N- term.	DLL3- 2	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWRQAPGQGLEWMGWINPNSGDTNYAQK FQGRVTMTTRDTSISITAYMELSRLTSDDTAVYYCARDANIAALDAFEIWGQGTMTVTVSSGGGS GGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGGTDFTLTITSSLPEDFATYYCQQSYSTPLTFGGGKVEIK

20		DLL3- 2 x12C	bispecific c molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGDTNYAQK FQGRVTMTTRDTSISTAYMELSRLTSDDTAVYYCARDANIAALDAFEIWGQGTMTVTVSSGGGGS GGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQSISSYLNWYQQKPKAPKLLIYAASS LQGVPSRFRSGSGGTDFTLTISLQPEDFATYYCQSYSTPLTFGGGTKEIKSGGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGG SGGGSGGGGQTVVTQEPSTVSPGGTTLTCGSSTGAVTSGNYPNWWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
21		DLL3- 3	VH CDR1	SYGMH
22		DLL3- 3	VH CDR2	VISYHGRDYYARSVKG
23		DLL3- 3	VH CDR3	DGATVTSYYSGMDV
24		DLL3- 3	VL CDR1	RASQGISNYLA
25		DLL3- 3	VL CDR2	LASSLQS
26		DLL3- 3	VL CDR3	QQYNFYPFPT
27		DLL3- 3	VH	QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYHGRDYYARS VKGRFTISRDNKNTLYLHMNSLRAEDTAVYYCARDGATVTSYYSGMDVWGQGTITVTVSSK
28		DLL3- 3	VL	DIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWFQQKPKAPKSLIYLASSLQSGVPSKFS GSGGTDFTLTISLQPEDFATYYCQYNFYPFPTFGPGTKVDIK
29	EGF- 1	DLL3- 3	scFv	QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYHGRDYYARS VKGRFTISRDNKNTLYLHMNSLRAEDTAVYYCARDGATVTSYYSGMDVWGQGTITVTVSSGG GGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWFQQKPKAPKSLIYL ASSLQSGVPSKFSGSGGTDFTLTISLQPEDFATYYCQYNFYPFPTFGPGTKVDIK
30		DLL3-	bispecific c	QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYHGRDYYARS VKGRFTISRDNKNTLYLHMNSLRAEDTAVYYCARDGATVTSYYSGMDVWGQGTITVTVSSGG

		3 xI2C	molecule	GGSGGGGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWFQQKPGKAPKSLIYL ASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQYNFYPTFGPGTKVDIKSGGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSG GGSGGGGGGGGQTVVTQEPSTLVSPGGTTLTCCGSTGAVTSGNYPNWVQQKPGQAPRGL IGGKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
31		DLL3- 4	VH CDR1	SYWWS
32		DLL3- 4	VH CDR2	YVYYSGTNNYNPSLKS
33		DLL3- 4	VH CDR3	IAVTGFYFDY
34		DLL3- 4	VL CDR1	RASQRVNNNNYLA
35		DLL3- 4	VL CDR2	GASSRAT
36		DLL3- 4	VL CDR3	QQYDRSPLT
37		DLL3- 4	VH	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPKGLEWIGYVYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTVAADTAVYYCASIATGTFYFDYWGGTGLVTVSS
38		DLL3- 4	VL	EIVLTQSPGTLSTLSPGERVTLSCRASQRVNNNYLAWYQQRPQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKLEIK
39	EGF- 3	DLL3- 4	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPKGLEWIGYVYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTVAADTAVYYCASIATGTFYFDYWGGTGLVTVSSGGGGGGG GGGGGSEIVLTQSPGTLSTLSPGERVTLSCRASQRVNNNYLAWYQQRPQAPRLLIYGASSRA TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKLEIK
40		DLL3- 4 xI2C	bispecific molecule	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPKGLEWIGYVYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTVAADTAVYYCASIATGTFYFDYWGGTGLVTVSSGGGGGGG GGGGGSEIVLTQSPGTLSTLSPGERVTLSCRASQRVNNNYLAWYQQRPQAPRLLIYGASSRA TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGTKLEIKSGGGGSEVQLV

				ESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSG GGSGGGGSQTVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWVQQKPGQAPRGLIGGTK FLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
41		DLL3- 5	VH CDR1	SYWWS
42		DLL3- 5	VH CDR2	YIYYSGRTNYYPSLKS
43		DLL3- 5	VH CDR3	IAVAGFFFDY
44		DLL3- 5	VL CDR1	RASQSVNKNYLA
45		DLL3- 5	VL CDR2	GASSRAT
46		DLL3- 5	VL CDR3	QQYDRSPLT
47		DLL3- 5	VH	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGIYIYSGRTNYYPSL KSRVTISIDTSKNQFSLKLSVTAADTAVYYCARIAGVAGFFFDYWGQGLTVTVSS
48		DLL3- 5	VL	EIVLTQSPGTLSPGERATLSCRASQSVNKNYLAQYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGKLEIK
49	EGF- 3	DLL3- 5	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGIYIYSGRTNYYPSL KSRVTISIDTSKNQFSLKLSVTAADTAVYYCARIAGVAGFFFDYWGQGLTVTVSSGGGGSGG GSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAQYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGKLEIK
50		DLL3- 5 x12C	bispecific molecule	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGIYIYSGRTNYYPSL KSRVTISIDTSKNQFSLKLSVTAADTAVYYCARIAGVAGFFFDYWGQGLTVTVSSGGGGSGG GSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAQYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGKLEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSG

				GGSGGGGSQT VVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTK FLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL
51		DLL3- 6	VH CDR1	SFYWS
52		DLL3- 6	VH CDR2	YIYYSGT TNYNPSLKS
53		DLL3- 6	VH CDR3	I AVAGFFFDY
54		DLL3- 6	VL CDR1	RASQSVNKNYLA
55		DLL3- 6	VL CDR2	GASSRAT
56		DLL3- 6	VL CDR3	QQYDRSPLT
57		DLL3- 6	VH	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPKGLEWIGYIYYSGT TNYNPSL KSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARI AVAGFFFDYWGQGT LTVTVSS
58		DLL3- 6	VL	EIVLTQSPGTLSPGERATLSCRASQSVNKNYLA WYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGG TKVEIK
59	EGF- 3	DLL3- 6	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPKGLEWIGYIYYSGT TNYNPSL KSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARI AVAGFFFDYWGQGT LTVTVSSGGSGGG GSGGGSEI VLTQSPGTLSPGERATLSCRASQSVNKNYLA WYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGT DFTLTISRLEPEDFAVYYCQQYDRSPLTFGGG TKVEIK
60		DLL3- 6 x12C	bispecific molecule	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPKGLEWIGYIYYSGT TNYNPSL KSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARI AVAGFFFDYWGQGT LTVTVSSGGSGGG GSGGGSEI VLTQSPGTLSPGERATLSCRASQSVNKNYLA WYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGT DFTLTISRLEPEDFAVYYCQQYDRSPLTFGGG TKVEIKSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGT LTVTVSSGGGGSG GGSGGGGSQT VVTQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTK

					FLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
61		DLL3- 7	VH CDR1		SFYWS
62		DLL3- 7	VH CDR2		YIYSGTTNYPNPSLKS
63		DLL3- 7	VH CDR3		IAVAGFFFDY
64		DLL3- 7	VL CDR1		RASQSVNKNYLA
65		DLL3- 7	VL CDR2		GASSRAT
66		DLL3- 7	VL CDR3		QQYDRSPLT
67		DLL3- 7	VH		QVQLQESGPGLVKPSQTLSTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARIAGVFFFDYWGQGLTVTVSS
68		DLL3- 7	VL		EIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGKVEIK
69	EGF- 3	DLL3- 7	scFv		QVQLQESGPGLVKPSQTLSTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARIAGVFFFDYWGQGLTVTVSSGGGGGGG GSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGKVEIK
70		DLL3- 7 x12C	bispecific molecule		QVQLQESGPGLVKPSQTLSTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARIAGVFFFDYWGQGLTVTVSSGGGGGGG GSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGGGKVEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGLTVTVSSGGGGSG GGSGGGGSQTVVTEPSLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

71		DLL3- 8	VH CDR1	SFYWS	
72		DLL3- 8	VH CDR2	YIYYSGTTNYPNPSLKS	
73		DLL3- 8	VH CDR3	IAVAGFFFDY	
74		DLL3- 8	VL CDR1	RASQSVNKNYLA	
75		DLL3- 8	VL CDR2	GASSRAT	
76		DLL3- 8	VL CDR3	QQYDRSPLT	
77		DLL3- 8	VH	QVQLQEWGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQSLSLKSSVTAADTAVYYCARIAGAGFFFDYWGQGLVTVSSK	
78		DLL3- 8	VL	EIVLTQSPGTLISLSPGERATLSCRASQSVNKNYLAAYQQKPGQAPRLLIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPSLTFGGGTKVDIK	
79	EGF- 3	DLL3- 8	scFv	QVQLQEWGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQSLSLKSSVTAADTAVYYCARIAGAGFFFDYWGQGLVTVSSGGGGGGG GGGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVNKNYLAAYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYDRSPSLTFGGGTKVDIK	
80		DLL3- 8 x12C	bispecific molecule	QVQLQEWGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQSLSLKSSVTAADTAVYYCARIAGAGFFFDYWGQGLVTVSSGGGGGGG GGGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVNKNYLAAYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYDRSPSLTFGGGTKVDIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVHRHGFNGSYISWAYWGQGLVTVSSGGGGSG GGSGGGGSGTAVTQEPSTLTVSPGGTFTLTTCGSSTGAVTSGNYPNWNVQKPGQAPRGLIGGTK FLAPGTPARFSGSLIGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL	

81		DLL3-₉	VH CDR1	SFYWS
82		DLL3-₉	VH CDR2	YIYYSGTTNYPNPSLKS
83		DLL3-₉	VH CDR3	IAVAGFFFDY
84		DLL3-₉	VL CDR1	RASQSVNKNYLA
85		DLL3-₉	VL CDR2	GASSRAT
86		DLL3-₉	VL CDR3	QQYDRSPLT
87		DLL3-₉	VH	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARIAGAGFFFDYWGQGLVTVSS
88		DLL3-₉	VL	EIVLTQSPGTLISLSPGESATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPSLTFGGGTRLEIK
89	EGF-₃	DLL3-₉	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARIAGAGFFFDYWGQGLVTVSSGGGSGGG GGGGSEIIVLTQSPGTLISLSPGESATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYDRSPSLTFGGGTRLEIK
90		DLL3-₉ x12C	bispecific molecule	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARIAGAGFFFDYWGQGLVTVSSGGGSGGG GGGGSEIIVLTQSPGTLISLSPGESATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYDRSPSLTFGGGTRLEIKSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVHRHGFNGSYISWAYWGQGLVTVSSGGGSGG GGSGGGSGTAVTQEPSTLTVSPGGTFTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLIGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

91		DLL3-10	VH CDR1	SYWWS
92		DLL3-10	VH CDR2	YIFYNGITNYPNPSLKS
93		DLL3-10	VH CDR3	IHSGSFSDY
94		DLL3-10	VL CDR1	RASQSVSRGYLA
95		DLL3-10	VL CDR2	GASSRAT
96		DLL3-10	VL CDR3	QQYDTSPIIT
97		DLL3-10	VH	QVQLQESGPGLVKPSQTLSTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFYNGITNYPNPSL KSRVTISLDTSKNQFSLKLSSTAAADTAKYYCARIHSGSFSDYWDQGTILVTSSGGGGSGG
98		DLL3-10	VL	EIVMTQSPGTLISLSPGERATLSCRASQSVSRGYLAQQKPGQAPRLLIYGASSRATDIPDRF SGSGSGTDFTLTISRLEPEDFAVYYCQQYDTSPIITFGQGTKVEIK
99	EGF-3	DLL3-10	scFv	QVQLQESGPGLVKPSQTLSTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFYNGITNYPNPSL KSRVTISLDTSKNQFSLKLSSTAAADTAKYYCARIHSGSFSDYWDQGTILVTSSGGGGSGG GGGGSEIVMTQSPGTLISLSPGERATLSCRASQSVSRGYLAQQKPGQAPRLLIYGASSRA TDIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYDTSPIITFGQGTKVEIK
100		DLL3-10 x12C	bispecific molecule	QVQLQESGPGLVKPSQTLSTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFYNGITNYPNPSL KSRVTISLDTSKNQFSLKLSSTAAADTAKYYCARIHSGSFSDYWDQGTILVTSSGGGGSGG GGGGSEIVMTQSPGTLISLSPGERATLSCRASQSVSRGYLAQQKPGQAPRLLIYGASSRA TDIPDRFSGSGTDFTLTISRLEPEDFAVYYCQQYDTSPIITFGQGTKVEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISWAYWGQGTILVTSSGGGGSG GGSGGGSGTQVVTQEPSTLTVSPGGTFTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLIGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

101		DLL3- 11	VH CDR1	NAGMS	
102		DLL3- 11	VH CDR2	RIKKNKIDGGTTDFAAPVKG	
103		DLL3- 11	VH CDR3	RGWYGDYFDY	
104		DLL3- 11	VL CDR1	RSSQSLHHSNGYNYLD	
105		DLL3- 11	VL CDR2	LGSNRRAS	
106		DLL3- 11	VL CDR3	MQALQTPFT	
107		DLL3- 11	VH	EVQLVESGGGLVKPGGSLRLSCAASGFI FNNAGMSWVRQAPGKGLEWVGRIKKNKIDGGTTDFA APVKGRFTISRDDSKNTLYLQMNSLKAEDTAVYYCTARGWYGDYFDYWGQGLTVTVSS	
108		DLL3- 11	VL	DIVMTQTPLSLPVPGEPAISCRSSQSLHHSNGYNYLDWYLQKPGQSPQLLIYLGSNRRASGV PDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQALQTPFTFGPGTKVEIK	
109	EGF- 3	DLL3- 11	scFv	EVQLVESGGGLVKPGGSLRLSCAASGFI FNNAGMSWVRQAPGKGLEWVGRIKKNKIDGGTTDFA APVKGRFTISRDDSKNTLYLQMNSLKAEDTAVYYCTARGWYGDYFDYWGQGLTVTVSSGGGGS GGGSGGGGSDIVMTQTPLSLPVPGEPAISCRSSQSLHHSNGYNYLDWYLQKPGQSPQLLI YLGSNRRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQALQTPFTFGPGTKVEIK	
110		DLL3- 11 x12C	bispecific molecule	EVQLVESGGGLVKPGGSLRLSCAASGFI FNNAGMSWVRQAPGKGLEWVGRIKKNKIDGGTTDFA APVKGRFTISRDDSKNTLYLQMNSLKAEDTAVYYCTARGWYGDYFDYWGQGLTVTVSSGGGGS GGGSGGGGSDIVMTQTPLSLPVPGEPAISCRSSQSLHHSNGYNYLDWYLQKPGQSPQLLI YLGSNRRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQALQTPFTFGPGTKVEIKSGGG GSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS SGGGSGGGGSGGGGQTAVTQEPSTLVSPGGTTLTTCGSSGTGAVTSIGNYPNWWVQKPGQAPR GLIGGTFKFLAPGTPARFSGSLLGKKAALTISGVQPEDEAEYYCVLIWYSNRWVFGGGTKLTVL	

111		DLL3-12	VH CDR1	SYDIH
112		DLL3-12	VH CDR2	VISSHGSNKNYARSVKG
113		DLL3-12	VH CDR3	DGYSGNDPFYYYYHGM DV
114		DLL3-12	VL CDR1	RASQISSYLN
115		DLL3-12	VL CDR2	AASSLQS
116		DLL3-12	VL CDR3	QQSFTTPLT
117		DLL3-12	VH	QVQLVESGGGVVQPGRSRLRLSCAASGFSFSSYDIHWVRQAPGKGLEWVAVISSHGSNKNYARS VKGRFTISRDN SKNTLYLQMNSLKAEDTAVYYCARDGYSGNDPFYYYYHGM DVWGQGT VTVS S
118		DLL3-12	VL	DIQMTQSPSSLSASVGDRTITTCRASQSISSYLNWYQQKPGKAPKLLIYAAASSLQSGVPSRFS GSGGTD FSLTISSLQPEDFATYYCQQSFTTPLTFGGGTKEIK
119	EGF-3/[4]	DLL3-12	scFv	QVQLVESGGGVVQPGRSRLRLSCAASGFSFSSYDIHWVRQAPGKGLEWVAVISSHGSNKNYARS VKGRFTISRDN SKNTLYLQMNSLKAEDTAVYYCARDGYSGNDPFYYYYHGM DVWGQGT VTVS SGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITTCRASQSISSYLNWYQQKPGKAPKLL IYAAASSLQSGVPSRFSGSGGTD FSLTISSLQPEDFATYYCQQSFTTPLTFGGGTKEIK
120		DLL3-12 x12C	bispecific molecule	QVQLVESGGGVVQPGRSRLRLSCAASGFSFSSYDIHWVRQAPGKGLEWVAVISSHGSNKNYARS VKGRFTISRDN SKNTLYLQMNSLKAEDTAVYYCARDGYSGNDPFYYYYHGM DVWGQGT VTVS SGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTITTCRASQSISSYLNWYQQKPGKAPKLL IYAAASSLQSGVPSRFSGSGGTD FSLTISSLQPEDFATYYCQQSFTTPLTFGGGTKEIKSGG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFNSYISYWAYWGQGT VTV SSGGSGGGSGGGGSGT VVTVTQEP S LTVSPGGT VTLTCGSSSTGAVTS GNYPNWVQQKPGQAP RGLIGTKFLAPGT PARFSGSLLGGKAALTL SGVQPEDEAEYCVLWYSNRWVFGGT KLTVL

121		DLL3-13	VH CDR1	SYMH
122		DLL3-13	VH CDR2	IINPSDGSTNYAQNFQG
123		DLL3-13	VH CDR3	GGNSAFYSYYDMDV
124		DLL3-13	VL CDR1	RSSQSLVYRDGNTYLS
125		DLL3-13	VL CDR2	KVSNWQS
126		DLL3-13	VL CDR3	MQGTHWPPT
127		DLL3-13	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHWVRQAPGQGLEWMGIINPSDGSTNYAQNFQGRVTMTTRDTSTNTVMELSSLRSEDTAVYVCARGNSAFYSYDMDVWGQGTITVTVSS
128		DLL3-13	VL	DVMTQSPSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRRLIYKVSNNWQSGVPDRFSGSGGTDFTLKISRVEAEDGVYFCMQGTHWPPTFGQGTKVEIK
129	EGF-4	DLL3-13	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHWVRQAPGQGLEWMGIINPSDGSTNYAQNFQGRVTMTTRDTSTNTVMELSSLRSEDTAVYVCARGNSAFYSYDMDVWGQGTITVTVSSGGGGSGGGSDVVMTQSPSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRRLIYKVSNNWQSGVPDRFSGSGGTDFTLKISRVEAEDGVYFCMQGTHWPPTFGQGTKVEIK
130		DLL3-13 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHWVRQAPGQGLEWMGIINPSDGSTNYAQNFQGRVTMTTRDTSTNTVMELSSLRSEDTAVYVCARGNSAFYSYDMDVWGQGTITVTVSSGGGGSGGGSDVVMTQSPSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRRLIYKVSNNWQSGVPDRFSGSGGTDFTLKISRVEAEDGVYFCMQGTHWPPTFGQGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGNSYISYWAYWGQGTITVTVSSGGGGSGGGSGGSGQTIVTQEPISLTVPSPGTVTLTCSGSTGAVTSIGNYPNNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL

131		DLL3-14	VH CDR1	NYMH	
132		DLL3-14	VH CDR2	IINPSDGSTSYAQKFQG	
133		DLL3-14	VH CDR3	GGNSAFYSYYDMDV	
134		DLL3-14	VL CDR1	RSSQSLVYRDGNTYLS	
135		DLL3-14	VL CDR2	KVSNWQS	
136		DLL3-14	VL CDR3	MQGTHWPPT	
137		DLL3-14	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFNYYMHWVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSS	
138		DLL3-14	VL	DVMTQTPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRRLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVYYCMQGTTHWPPTFGQGTKVEIK	
139	EGF-4	DLL3-14	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFNYYMHWVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRR LIYKVSNNWQSGVDRFSGGGSGTDFTLKISRVEAEDVGVYYCMQGTTHWPPTFGQGTKVEIK	
140		DLL3-14 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFNYYMHWVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRR LIYKVSNNWQSGVDRFSGGGSGTDFTLKISRVEAEDVGVYYCMQGTTHWPPTFGQGTKVEIKSG GGSEVQLVESGGGLVQPGLSKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTITV VSSGGSGGGSGGGSGQTVTQEPSTLVSPPGTVTLTCGSSTGAVTSGNYPNNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L	

141		DLL3-15	VH CDR1	GYIYIH
142		DLL3-15	VH CDR2	IINPSDGGSTSYGQNFQG
143		DLL3-15	VH CDR3	GGNSAFYSYYDMDV
144		DLL3-15	VL CDR1	RSSQSLAYRDGNTYLS
145		DLL3-15	VL CDR2	KVSNWQS
146		DLL3-15	VL CDR3	MQGTHWPPT
147		DLL3-15	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPQGQGLEWMGIINPSDGGSTSYGQN FQGRVTMTTRDTSNTVMELSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQTTVTVSS
148		DLL3-15	VL	DVVMTQSPSLPVTLGQPASISCRSSQSLAYRDGNTYLSWFQQRPQGQSPRRLIYKVSNNWQSGV PDRFSGSGSGTDFTLKISRVEAEDVGVYFCMQGTHWPPTFGQGTKVEIK
149	EGF-4	DLL3-15	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPQGQGLEWMGIINPSDGGSTSYGQN FQGRVTMTTRDTSNTVMELSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQTTVTVSSGGG GSGGGSGGGSDVVMTQSPSLPVTLGQPASISCRSSQSLAYRDGNTYLSWFQQRPQGQSPRR LIYKVSNNWQSGVDRFSGSGSGTDFTLKISRVEAEDVGVYFCMQGTHWPPTFGQGTKVEIK
150		DLL3-15 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPQGQGLEWMGIINPSDGGSTSYGQN FQGRVTMTTRDTSNTVMELSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQTTVTVSSGGG GSGGGSGGGSDVVMTQSPSLPVTLGQPASISCRSSQSLAYRDGNTYLSWFQQRPQGQSPRR LIYKVSNNWQSGVDRFSGSGSGTDFTLKISRVEAEDVGVYFCMQGTHWPPTFGQGTKVEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQTLVT VSSGGSGGGSGGGGSGTQVVTQEPSTLVSPPGTTVLTGSGSTGAVTSNGYPNNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L

151		DLL3-16	VH CDR1	GHYMH	
152		DLL3-16	VH CDR2	IINPSDGSSTNYAQKFQG	
153		DLL3-16	VH CDR3	GTTVVHHYSYYDMDV	
154		DLL3-16	VL CDR1	RSSQSLVYRDGNTYLT	
155		DLL3-16	VL CDR2	KVSNWQS	
156		DLL3-16	VL CDR3	MQGTHWPPT	
157		DLL3-16	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGHYMHWVRQAPGQGLEWMGIINPSDGSSTNYAQK FQGRVTMTTRDTSTSTVYMEIRSLRSEDTAVYCYCTRGTTVVHHYSYYDMDVWGQGTITVTVSS	
158		DLL3-16	VL	DVMTQTPLSLPVTLGQPASISCRSSQSLVYRDGNTYLTWFOQRPQGQSPRRLIYKVSNNWQSGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTTHWPPTFGGGTKVEIK	
159	EGF-4	DLL3-16	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGHYMHWVRQAPGQGLEWMGIINPSDGSSTNYAQK FQGRVTMTTRDTSTSTVYMEIRSLRSEDTAVYCYCTRGTTVVHHYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLTWFOQRPQGQSPRR LIYKVSNNWQSGVDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTTHWPPTFGGGTKVEIK	
160		DLL3-16 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGHYMHWVRQAPGQGLEWMGIINPSDGSSTNYAQK FQGRVTMTTRDTSTSTVYMEIRSLRSEDTAVYCYCTRGTTVVHHYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLTWFOQRPQGQSPRR LIYKVSNNWQSGVDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTTHWPPTFGGGTKVEIKSG GGSEVQLVESGGGLVQPGLSKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCYVRHGNFGNSYISYWAYWGQGTITV VSSGGSGGGSGGGGSGTQVVTQEPSTLVSPPGTVTLTCSGSTGAVTSGNYPNNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L	

161		DLL3-17	VH CDR1	NYFMH	
162		DLL3-17	VH CDR2	IINPSDGGSTSYAQNFQG	
163		DLL3-17	VH CDR3	GGNSAFYSYYDMDV	
164		DLL3-17	VL CDR1	RSSQSLVYRDGNTYLS	
165		DLL3-17	VL CDR2	RVSNWQS	
166		DLL3-17	VL CDR3	MQGTYPPT	
167		DLL3-17	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNIFYFMHWVRQAPGLGLEWMGIINPSDGGSTSYAQN FQGRVTMTTRDTSNTVMYELSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS	
168		DLL3-17	VL	DVMTQSPSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRRLIYRVSNWQSGV PDRFSGSGGTDFTLKISRVEAEDGVYFCMQGTYPPTFGQGTKVDIK	
169	EGF-4	DLL3-17	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNIFYFMHWVRQAPGLGLEWMGIINPSDGGSTSYAQN FQGRVTMTTRDTSNTVMYELSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMTQSPSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRR LIYRVSNWQSGVDRFSGSGGTDFTLKISRVEAEDGVYFCMQGTYPPTFGQGTKVDIK	
170		DLL3-17 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNIFYFMHWVRQAPGLGLEWMGIINPSDGGSTSYAQN FQGRVTMTTRDTSNTVMYELSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMTQSPSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRR LIYRVSNWQSGVDRFSGSGGTDFTLKISRVEAEDGVYFCMQGTYPPTFGQGTKVDIKSG GGSEVQLVESGGGLVQPGLSKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITV VSSGGSGGGSGGGGQTIVTQEPSTVSPGGTITLTGSGSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L	

171		DLL3-18	VH CDR1	NYGMH
172		DLL3-18	VH CDR2	VISHHGSSKYYARSVKG
173		DLL3-18	VH CDR3	DWVELVFDY
174		DLL3-18	VL CDR1	KSSQSLHSDGKTFLY
175		DLL3-18	VL CDR2	EVSNRFS
176		DLL3-18	VL CDR3	LQGIHLPFT
177		DLL3-18	VH	QVQLVESGGGAVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISHHGSSKYYARS VKGRFTISRDN SKNTLYLEMNSLRAEDTAVYYCARDWWELVFDYWGQGLTVTVSS
178		DLL3-18	VL	DIVMTQTPLSLVTPGQPASISCKSSQSLHSDGKTFLYWYLQKPGQPPQLLIYEVSNRFSGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGIHLPFTFGPGTKVEIK
179	EGF-5/[6]	DLL3-18	scFv	QVQLVESGGGAVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISHHGSSKYYARS VKGRFTISRDN SKNTLYLEMNSLRAEDTAVYYCARDWWELVFDYWGQGLTVTVSSGGGGSGGG GSGGGSDIVMTQTPLSLVTPGQPASISCKSSQSLHSDGKTFLYWYLQKPGQPPQLLIYEV SNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGIHLPFTFGPGTKVEIK
180		DLL3-18 x12C	bispecific molecule	QVQLVESGGGAVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVISHHGSSKYYARS VKGRFTISRDN SKNTLYLEMNSLRAEDTAVYYCARDWWELVFDYWGQGLTVTVSSGGGGSGGG GSGGGSDIVMTQTPLSLVTPGQPASISCKSSQSLHSDGKTFLYWYLQKPGQPPQLLIYEV SNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGIHLPFTFGPGTKVEIKSGGGGSE VQLVESGGGLVQPGGSLKSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSGG GSGGGSGGGGSGTQVVTQEPSTLTVSPGGTFTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLI GGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

181		DLL3- 19	VH CDR1	NSRMGVS	
182		DLL3- 19	VH CDR2	HIFSNDGKSYSTSLKS	
183		DLL3- 19	VH CDR3	YNYDSSGYYYSFFDY	
184		DLL3- 19	VL CDR1	RASQISSYLN	
185		DLL3- 19	VL CDR2	AASSLQS	
186		DLL3- 19	VL CDR3	QQGYSSPFT	
187		DLL3- 19	VH	QVTLKESGPM LVKPTETLTLTCTVSGFSLNSRMGVSWIRQPPGRALEWLAHIFSNDGKSYST SLKSRLTISKDTSKSQVVLTMNMDPVDATYYCARYNYDSSGYYYSFFDYWGQGLVTVSS	
188		DLL3- 19	VL	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKGKAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYYCQQGYSSPFTFGGGTKVEIK	
189	EGF- 5/[6]	DLL3- 19	scFv	QVTLKESGPM LVKPTETLTLTCTVSGFSLNSRMGVSWIRQPPGRALEWLAHIFSNDGKSYST SLKSRLTISKDTSKSQVVLTMNMDPVDATYYCARYNYDSSGYYYSFFDYWGQGLVTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKGKAPKLLIY AASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQGYSSPFTFGGGTKVEIK	
190		DLL3- 19 x12C	bispecific molecule	QVTLKESGPM LVKPTETLTLTCTVSGFSLNSRMGVSWIRQPPGRALEWLAHIFSNDGKSYST SLKSRLTISKDTSKSQVVLTMNMDPVDATYYCARYNYDSSGYYYSFFDYWGQGLVTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKGKAPKLLIY AASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQGYSSPFTFGGGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLFWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSS GGSGGGGGGGGQTVVVTQEPSLTVSPGGTTLTCGSSTGAVTSIGNYPNWVQKPGQAPRG LIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL	

191		DLL3- 20	VH CDR1	NARMGVS	
192		DLL3- 20	VH CDR2	HIFSTDEKSYSTSLKS	
193		DLL3- 20	VH CDR3	YYDSSGYYYSFFDY	
194		DLL3- 20	VL CDR1	RASQIRSYLN	
195		DLL3- 20	VL CDR2	GASNLQS	
196		DLL3- 20	VL CDR3	QQSYSSPFT	
197		DLL3- 20	VH	QVTLKESGPVLVKPTETLTLTCTVSGFSLNARMGVSWLRQPPGKALEWLAHIFSTDEKSYST SLKSRLTISKDTSKSQVVLMTNMDPVDATYYCARYYDSSGYYYSFFDYWGQGLVTVSS	
198		DLL3- 20	VL	DIQMTQSPSSLSASVGDRVTITCRASQIRSYLNWYQQKPGKAPKLLIYGASNLQSGVPSRFS GSGSGTDFTLTISSLQPEDFATYYCQQSYSSPFTFGGGTKVEIK	
199	EGF- 5/[6]	DLL3- 20	scFv	QVTLKESGPVLVKPTETLTLTCTVSGFSLNARMGVSWLRQPPGKALEWLAHIFSTDEKSYST SLKSRLTISKDTSKSQVVLMTNMDPVDATYYCARYYDSSGYYYSFFDYWGQGLVTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQIRSYLNWYQQKPGKAPKLLIY GASNLQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQSYSSPFTFGGGTKVEIK	
200		DLL3- 20 x12C	bispecific molecule	QVTLKESGPVLVKPTETLTLTCTVSGFSLNARMGVSWLRQPPGKALEWLAHIFSTDEKSYST SLKSRLTISKDTSKSQVVLMTNMDPVDATYYCARYYDSSGYYYSFFDYWGQGLVTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQIRSYLNWYQQKPGKAPKLLIY GASNLQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQSYSSPFTFGGGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLFWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNLLKTEDAVYYCVRHGNFGNSYISWAYWGQGLVTVSS GGSGGGGGGGGQTVVTVTEPSLTVSPGGTVTLTCGSSTGAVTSNYPNWWVQKPGQAPRG LIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL	

201		DLL3- 21	VH CDR1	SYIHH
202		DLL3- 21	VH CDR2	IINPSGGSKSYAQKFRG
203		DLL3- 21	VH CDR3	SMSTVTSDAFDI
204		DLL3- 21	VL CDR1	RASQISNYLN
205		DLL3- 21	VL CDR2	AASSLQS
206		DLL3- 21	VL CDR3	QQSYSAPLT
207		DLL3- 21	VH	QVQLVQSGAEVKKPGASVKVSCKASGYAFTSYIHWVRQAPGQGLEWMGIINPSGGSKSYAQK FRGRVTMTTRDTSTSTVYMEISLTSEDTAVYVCARSMSTVTSDAFDIWGQGTMTVTSS
208		DLL3- 21	VL	DIQMTQSPSSLSASVGDRTITCRASQISNYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFS GSGGTEFTLTISLQPEDFATYCYCQQSYSAPLTFGGGTKVDIK
209	EGF- 5/[6]	DLL3- 21	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYAFTSYIHWVRQAPGQGLEWMGIINPSGGSKSYAQK FRGRVTMTTRDTSTSTVYMEISLTSEDTAVYVCARSMSTVTSDAFDIWGQGTMTVTSSGGGS GGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQISNYLNWYQQKPKGAPKLLIYAASS LQSGVPSRFSGSGGTEFTLTISLQPEDFATYCYCQQSYSAPLTFGGGTKVDIK
210		DLL3- 21 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYAFTSYIHWVRQAPGQGLEWMGIINPSGGSKSYAQK FRGRVTMTTRDTSTSTVYMEISLTSEDTAVYVCARSMSTVTSDAFDIWGQGTMTVTSSGGGS GGSGGGGSDIQMTQSPSSLSASVGDRTITCRASQISNYLNWYQQKPKGAPKLLIYAASS LQSGVPSRFSGSGGTEFTLTISLQPEDFATYCYCQQSYSAPLTFGGGTKVDIKSGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYVCVRHGFNSYISYWAYWGQGTMTVTSSGGG SGGGSGGGGQTAVTQEPSTLVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGG TKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLIWYSNRWVFGGGTKLTVL

211	EGF- 3	DLL3- 4 xF12Q	bispecifi c molecule	QVQLQESGPGLVKPSQTLTCTVSGGSISSYYWWSWIRQPPGKGLEWIGYVYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTAAADTAVYYCASIATGTFYFDYWGQGTLLTVTSVSSGGSGGG GSGGGSEIVLTQSPGTLTSLSPGERVTLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTIISRLPEPDFAVYYCQYDRSPLTFGGGTKLEIKSGGGSEVQLV ESGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVHRHGFNGSYVSWWAYWGQGTLLTVTSVSSGGSGG GGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
212	EGF- 3	DLL3- 5 xF12Q	bispecifi c molecule	QVQLQESGPGLVKPSQTLTCTVSGGSISSYYWWSWIRQPPGKGLEWIGYIYSGRTNYPNPSL KSRVTISIDTSKNQFSLKLSSTAAADTAVYYCARIAGAGFFFDYWGQGTLLTVTSVSSGGSGGG GSGGGSEIVLTQSPGTLTSLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTIISRLPEPDFAVYYCQYDRSPLTFGGGTKLEIKSGGGSEVQLV ESGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVHRHGFNGSYVSWWAYWGQGTLLTVTSVSSGGSGG GGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
213	EGF- 3	DLL3- 6 xF12Q	bispecifi c molecule	QVQLQESGPGLVKPSQTLTCTVSGASISFFYWSWIRQPPGKGLEWIGYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARIAGAGFFFDYWGQGTLLTVTSVSSGGSGGG GSGGGSEIVLTQSPGTLTSLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTIISRLPEPDFAVYYCQYDRSPLTFGGGTKLEIKSGGGSEVQLV ESGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVHRHGFNGSYVSWWAYWGQGTLLTVTSVSSGGSGG GGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
214	EGF- 3	DLL3- 7 xF12Q	bispecifi c molecule	QVQLQESGPGLVKPSQTLTCTVSGASISFFYWSWIRQPPGKGLEWIGYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARIAGAGFFFDYWGQGTLLTVTSVSSGGSGGG GSGGGSEIVLTQSPGTLTSLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTIISRLPEPDFAVYYCQYDRSPLTFGGGTKLEIKSGGGSEVQLV ESGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVHRHGFNGSYVSWWAYWGQGTLLTVTSVSSGGSGG GGSGGGGQTVVTQEPSTLTVSPGGTTLTTCGSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
215	EGF- 3	DLL3- 8	bispecifi c	QVQLQEWGPGLVKPSQTLTCTVSGASISFFYWSWIRQPPGKGLEWIGYIYSGTTNYPNPSL KSRVTISVDTSKNQSLKLSSTAAADTAVYYCARIAGAGFFFDYWGQGTLLTVTSVSSGGSGGG

216	EGF- 3	DLL3- 9 xF12Q	molecule	GSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFLTITISRLPEDEFAVYQCQYDRSPLTFGGGTKVDIKSGGGGSEVQLV ESGGGLVQPGGSLRLSCAASGFTFNAYMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGFGNSYVSWWAYWGQGLVTVSSGGGSG GGSGGGGQTVVTQEPSTLTVSPGGTVTLTCSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTR FLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
217	EGF- 3	DLL3- 10 xF12Q	bispecific molecule	QVQLQESGPGLVKPSQTLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTAAATAVYYCARIAGFFFDYWGQGLVTVSSGGGGSGGG GSGGGSEIVLTQSPGTLISLSPGESATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFLTITISRLPEDEFAVYQCQYDRSPLTFGGGTRLEIKSGGGGSEVQLV ESGGGLVQPGGSLRLSCAASGFTFNAYMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGFGNSYVSWWAYWGQGLVTVSSGGGSG GGSGGGGQTVVTQEPSTLTVSPGGTVTLTCSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTR FLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
218	EGF- 4	DLL3- 13 xF12Q	bispecific molecule	QVQLQESGPGLVKPSQTLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFYNGITNYPNPSL KSRVTISLDTSKNQFSLKLSSTAAATAKYCARIHSGSFDFYWDQGLVTVSSGGGGSGGG GSGGGSEIVMTQSPGTLISLSPGERATLSCRASQSVSRGYLAWYQQKPGQAPRLLIYGASSRA TDIPDRFSGSGGTDFLTITISRLPEDEFAVYQCQYDTSPIITFGQGTKVEIKSGGGGSEVQLV ESGGGLVQPGGSLRLSCAASGFTFNAYMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGFGNSYVSWWAYWGQGLVTVSSGGGSG GGSGGGGQTVVTQEPSTLTVSPGGTVTLTCSGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTR FLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
219	EGF- 4	DLL3- 14	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHWVRQAPGQGLEWMGIINPSDGSNTYAQN FQGRVTMTTRDTSTNTVYMEISSLRSEDTAVYYCARGNSAFYSYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMTQSPSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNNWQSGVPRDFSGSGGTDFTLKISRVEAEDGVYFCMQGTHWPPTFGQGTKVEIKSG GGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNAYMNWVRQAPGKGLEWVARIRSKYNNYA TYIYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGFGNSYVSWWAYWGQGLVTV VSSGGGGSGGGGSGGQTVVTQEPSTLTVSPGGTVTLTCSGSTGAVTSGNYPNWVQQKPGQA PRGLIGGTRFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L

220	EGF- 4	DL3- 15 x12Q	bispecific molecule	<p>LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYYCMQGTHWPPFTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYCVRHGNGFNSYVSWWAYWGQGTLLVT VSSGGGGGGGGGGGSGTQVVTQEPSTLVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKPGQA PRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRQAPGQGLEWMGIINPSDGSTSYGQN FQGRVTMTTRDTSNTVTYMEISSLRSEDTAVYICARGGNSAFYSYYDMVDVWGQGTITVTVSSGGG GGGGGGGGGGSDVVMTQSPSLPVTLGQPASISCRSSQSLAYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYYCMQGTHWPPFTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYCVRHGNGFNSYVSWWAYWGQGTLLVT VSSGGGGGGGGGGGSGTQVVTQEPSTLVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKPGQA PRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p>
221	N- term.	DL3- 1 x12C -HALB variant 1	bispecific molecule -HALB variant 1	<p>QVQLVESGGGVVQSGRSLRLSCAASGFTFSDYGIHWVRQAPGKGLEWVAVISYHGSNKYYARS VKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYICAREIPFGMDVWGQGTITVTVSSGGGGGGGG SGGGSDIVMTQTPLSLPVTPEGPASISCRSSQSLHSDGYNLDWYLOKPGQSPQLLIYLG NRASGVPDRFSGGGSGTDFTLTISRVEAEDVGYYCMQALQTLTFFGGGTVKDIKSGGGGSEV QLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNSLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTITVTVSSGGG GGGGGGGGGGSGTQVVTQEPSTLVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIG GTFKFLAPGTPARFSGSLLGKKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGG SDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNPRLVRPEVDVMCT AFHDNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTCCQAADKAACLLPKLDEL RDE GKASSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLT KVHTECCGDDL ECADDRADLAKYI CENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLP SLAADFVESKD VCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEF KPLVEEPQNLIKQNCLELFEQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKH PEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFN AGTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCKCKADDKET CFAEEGKKLVAAASQAALGLHHHHH</p>

222	N-term.	DLL3-2 xI2C -HALB variant 1	bispecific molecule -HALB variant 1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPNSGDTNYAQK FQGRVTMTRDTSISITAYMELSRLTSDDTAVYYCARDANIAALDAFEIWGQGTMTVTVSSGGGGS GGGSGGGGSDIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQSYSTPLTFGGGTKEIKSGGGSEVQ LVESGGGLVQPGGSLKLSAASGFTFNKYAMNVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGG SGGGSGGGGSGTQVVTQEPSTLVSPGGTTLTTCGSSGTGAVTSGNYPNWWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGS DAHKSEVAHRFKDLEENFKALVLI AFAQYLQQCPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPELLFFAKRYKA AFTCCQAADKAACLLPKLDEL RDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLT KVTHTCCCHGDLLE CADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTLEKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALEVDETYVPKEFNA GTFTFFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAAMDDFAAFVEKCKCKADDKETC FAEEGKKLVAAASQAALGLHHHHH
223	EGF-1	DLL3-3 xI2C -HALB	bispecific molecule -HALB	QVQLVESGGGVVQPGRSRLRSCAASGFTFSSYGMHWVRQAPGKGLEWVAISYHGRDITYARS VKGRFTISRDN SKNTLYLHMNSLRAEDTAVYYCARDGATVTSYYS GMDVWGQGTITVTVSSGG GGSGGGSGGGSDIQMTQSPSSLSASVGRVTITCRASQGISNYLAWFQQKPGKAPKSLIYL ASSLQSGVPSKFSGSGGTDFTLTISSLQPEDFATYYCQYNFYPTFGPGTKVDIKSGGGGS EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSG GGSGGGSGGGGSGTQVVTQEPSTLVSPGGTTLTTCGSSGTGAVTSGNYPNWWVQQKPGQAPRGL IGGTKFLAPGTPARFSGSLLGKKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGG GGSDAHKSEVAHRFKDLEENFKALVLI AFAQYLQQCPFEDHVKL VNEVTEFAKTCVADESAE NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNPNL PRLVRPEVDVM CTAFHDNEETFLKKLYE IARRHPYFYAPELLFFAKRYKA AFTCCQAADKAACLLPKLDEL R DEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLT KVTHTCCCHGD LLECADDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVES KDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTLEKCCAAADPHECYAKVFD EFKPLVEEPQNLIKQNCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCC KHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALEVDETYVPKE

224	EGF- 3	DLL3- 4 xI2C -HALB	bispecific molecule -HALB	<p>FNAETTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCCKADDK ETCFAEEGKKLVAASQAALGLHHHHH</p> <p>QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYVYSGTTNYP KSRVTISVDTSKNQFSLKLSVTAADTAVYYCASIATGFFDYWGQGTLLTVSSGGGGGGG GGGGSEIVLTQSPGTLSPGERVTLSCRASQRVNNNYLAWYQQRPQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTIISRLPEPDFAVYQCQYDRSPLTFGGGKLEIKSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVHRHGFNGSYISYWAYWGQGTLLTVSSGGGGSG GGGGSGGTQVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG FLAPGTPARFSGSLIGGKAALTLISGVQPEDEAEYCYVLYSNRWVFGGKTLTVLPGGGSDA HKSEVAHRFKDLEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDKS LHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDVMCTAFH DNEETFLLKKYLYEIARRHPYFYAPELFFAKRYKAAFTCECCQAADKAACLLPKLDELREDEGKA SSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLECA DDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETTLKCCAAADPHECYAKVDFEFKPL VEEPQNLIKQNCLELFEQLGEYKFNQALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCKHPEA KRMPCAEEDYLSVNLQCLVLEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCCKADDKETCFA EEGKKLVAASQAALGLHHHHH</p>
225	EGF- 3	DLL3- 5 xI2C -HALB	bispecific molecule -HALB	<p>QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYSGRTNYYPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGFFDYWGQGTLLTVSSGGGGGGG GGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWEYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTIISRLPEPDFAVYQCQYDRSPLTFGGGKLEIKSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVHRHGFNGSYISYWAYWGQGTLLTVSSGGGGSG GGGGSGGTQVVTQEPSTLTVSPGGTTLTTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGG FLAPGTPARFSGSLIGGKAALTLISGVQPEDEAEYCYVLYSNRWVFGGKTLTVLPGGGSDA HKSEVAHRFKDLEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDKS LHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDVMCTAFH DNEETFLLKKYLYEIARRHPYFYAPELFFAKRYKAAFTCECCQAADKAACLLPKLDELREDEGKA SSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLECA DDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETTLKCCAAADPHECYAKVDFEFKPL</p>

226	EGF-3	DLL3-6 xI2C-HALB	bispecific molecule-HALB	VEEPQNLIKQNCSELFQGEYKFNQALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCKHPEAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDKETCFAEEGKKLVAAASQAALGLHHHHH
227	EGF-3	DLL3-7 xI2C-HALB	bispecific molecule-HALB	QVQLQESGPGLVKPSQTLSTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYSGTTNYPNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGAGFFFDYWGQGLTVTVSSGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYDRSPLTFGGGTKEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGSGGGSGGGSGGSQTVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGSDAHKSEVAHRFKDGLGEENFKALVLI AFAQLQCCPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNP NLPRLVRPEVDVMCTAFHDNEETF LKKYLYE IARRHPYFYAPEL LFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCCHGDLLECADDRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCSELFQGEYKFNQALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCKHPEAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDKETCFAEEGKKLVAAASQAALGLHHHHH
227	EGF-3	DLL3-7 xI2C-HALB	bispecific molecule-HALB	QVQLQESGPGLVKPSQTLSTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYSGTTNYPNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGAGFFFDYWGQGLTVTVSSGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYDRSPLTFGGGTKEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGSGGGSGGGSGGSQTVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGSDAHKSEVAHRFKDGLGEENFKALVLI AFAQLQCCPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNP NLPRLVRPEVDVMCTAFHDNEETF LKKYLYE IARRHPYFYAPEL LFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCCHGDLLECA

228	EGF- 3	DLL3- 8 xI2C -HALB	bispecifi c molecule -HALB	<p>DDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVLLLRRLAKTYETTLKCCAAADPHECYAKVDFEKFPL VEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEA KRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDDKETCFA EEGKKLVAASQAALGLHHHHH</p> <p>QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQLSLKSSVTAADTAVYYCARIAGVFFFDYWGQGTTLVTVSSGGGGGGG GSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGI PDRFSGSGGTDFTLTI SRLEPEDFAVYQCQYDRSPLTFGGGTKVDIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTTLTVSSGGGGSG GGSGGGGSQTVVTQEPSLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDA HKSEVAHRFKD LG EENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESAENCDKS LHTLFGDKLCTVATLRET YGEMADCCAKQEPERNECFLQHKDDNPRLVRPEVDVMCTAFH DNEETFLLKKYL YEIARRHPYFYAPEL LFFAKRYKAAFT ECCCQAADKAACIL PKLDEL RDEGKA SSAKQRLK CASLQKFGERA FKA W A VARLSQRFPAEFAEVS KLVTDLTKVHTECC HGD LLECA DDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVLLLRRLAKTYETTLKCCAAADPHECYAKVDFEKFPL VEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEA KRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDDKETCFA EEGKKLVAASQAALGLHHHHH</p>
229	EGF- 3	DLL3- 9 xI2C -HALB	bispecifi c molecule -HALB	<p>QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKSSVTAADTAVYYCARIAGVFFFDYWGQGTTLVTVSSGGGGGGG GSGGGSEIVLTQSPGTLSPGESATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGI PDRFSGSGGTDFTLTI SRLEPEDFAVYQCQYDRSPLTFGGGTRLEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTTLTVSSGGGGSG GGSGGGGSQTVVTQEPSLTVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDA HKSEVAHRFKD LG EENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESAENCDKS LHTLFGDKLCTVATLRET YGEMADCCAKQEPERNECFLQHKDDNPRLVRPEVDVMCTAFH</p>

230	EGF-3	DLL3-10 x12C - HALB	bispecific molecule -HALB	DNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDELDRDEGKA SSAKQRLKASLQKGERAFKAWAVARLSQRFPAEFAEVS KLVTDLTKVHTECCCHDGLLECA DDRADLAKY ICENQDSISSKLKECEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVLLLR LAKTYETTLKCCAAADPHECYAKVDFEFKPL VEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCCKHPEA KRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCCKADDKETCFA EEGKKLVAASQAALGLHHHHH
231	EGF-3	DLL3-11 x12C - HALB	bispecific molecule -HALB	QVQLQESGPGLVKPSQTLSTCTVSGGSISSYYWSWIRPPGKGLEWIGYIFYNGITNYPNPSL KSRVTISLDTSKNQFSLKLSSTAAATAKYYCARIHSGSFSFDYWDQGTILTVSSGGGGGGG GGGGGSEIVMTQSPGTLSPGERATLSCRASQSVSRGYLAWYQQKPGQAPRLIIYGASSRA TDIPDRFSGSGGTDTLTISRLEPEDFAVYCCQYDTSPITFGQGTKVEIKSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVSSGGGGSG GGGGGGSQTVTQEPSLTVSPGGTTLTTCGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTK FLAPGTPARFSGSLGKKAALTSLGVQPEDEAEYCYVLWYSNRWVFGGGLTVLPGGGSDA HKSEVAHRFKDLEENFKALVLI AFAQYLQCCPFEDHVKLIVNEVTEFAKTCVADESAENCDS LHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNPRLPRLVRPEVDVMCTAFH DNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDELDRDEGKA SSAKQRLKASLQKGERAFKAWAVARLSQRFPAEFAEVS KLVTDLTKVHTECCCHDGLLECA DDRADLAKY ICENQDSISSKLKECEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVLLLR LAKTYETTLKCCAAADPHECYAKVDFEFKPL VEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCCKHPEA KRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCCKADDKETCFA EEGKKLVAASQAALGLHHHHH
231	EGF-3	DLL3-11 x12C - HALB	bispecific molecule -HALB	EVQLVESGGGLVKPGGSLRLS CAASGFI FNNAGMSWVRQAPGKGLEWVGRIKNKIDGGTTDFA APVKGRFTISRDDSKNTLYLQMNSLKAEDTAVYYCTARGWYGDYFDYWGQGLTVTVSSGGGG GGGGGGGSDIVMTQTPSLPVTPEGPASISCRSSQSLHNSGNYLDWY LQKPGQSPQLLI YLGSNRASGVDRFSGSGGTDTLT LKISRVEAEDVGIYCYCMQALQTPFTFGPGTKVEIKSGGG GSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRVQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTVTVS SGGGGGGGGSGGTQTVVTQEP SLTVSPGGTTLTTCGSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLAPGTPARFSGSLGKKAALTSLGVQPEDEAEYCYVLWYSNRWVFGGGLTVLP

232	EGF- 3/[4]	DLL3- 12 x12C - HALB	bispecifi c molecule -HALB	<p>GGGGDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADES AENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVD VMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELLFFAKRYKAAFTCECCQAADKAACLLPKLDE LRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCH GDLLCADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFV ESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETTLEKCCAAADPHECYAKV FDEFKPLVEEPQNLIKQNCLEFELGEYKFQNALIVRYTKKVPQVSTPTLVEVSRNLKGVGSK CKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVP KEFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKAD DKETCFAEEGKKLVAASQAALGLHHHHH</p> <p>QVQLVESGGGVVQPGRSIRLSCAASGFSFSSYDIHWVRQAPGKGLEWVAVISSHGSNKNYARS VKGRFTISRDN SKNTLYLQMNLSLKAEDTAVYICARDYSGNDPFYYYHGMVDVWGQTTVTVS SGGGSGGGSGGGSDIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPKAPKLL IYAASSLQSGVPSRFSGSGGTDFTSLTISLQPEDFATYYCQQSFTTPTLTFGGGTKVEIKSGG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYICVRHGNFGNSYISYWAYWGQGLVTV SSGGSGGGSGGGGSGTQVVTQEPSTLTVSPGGTTLTCGSSSTGAVTSGNYPNWWVQQKPGQAP RGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVL PGGGSDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADE SAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEV DVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELLFFAKRYKAAFTCECCQAADKAACLLPKLD ELRDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECC HGDLLCADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADF VESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETTLEKCCAAADPHECYAK VFDEFKPLVEEPQNLIKQNCLEFELGEYKFQNALIVRYTKKVPQVSTPTLVEVSRNLKGVGS KCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKA DDKETCFAEEGKKLVAASQAALGLHHHHH</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHWVRQAPGQGLEWMGIINPSDGSSTNYAQN FQGRVTMTTRDTSTNTVMELSSLRSEDTAVYICARGNSAFYSYDMDVDVWGQTTVTVSSGGG GSGGGSGGGGSDVMTQSLPLPVLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRR LIYKVSNWQSGVPDRFSGSGGTDFTLKISRVEAEDGVYFCMQGTHWPTTFGGGTKVEIKSG GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYICVRHGNFGNSYISYWAYWGQGLVT</p>
233	EGF- 4	DLL3- 13 x12C - HALB	bispecifi c molecule -HALB	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHWVRQAPGQGLEWMGIINPSDGSSTNYAQN FQGRVTMTTRDTSTNTVMELSSLRSEDTAVYICARGNSAFYSYDMDVDVWGQTTVTVSSGGG GSGGGSGGGGSDVMTQSLPLPVLGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGSPRR LIYKVSNWQSGVPDRFSGSGGTDFTLKISRVEAEDGVYFCMQGTHWPTTFGGGTKVEIKSG GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYICVRHGNFGNSYISYWAYWGQGLVT</p>

234	EGF-4	DLL3-14 x12C - HALB	bispecific molecule -HALB	VSSGGGGGGGGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTFKFLAPGTPARFSGSLGGKAAALTSVGQPEDEAEYYCVLWYSNRWVFGGGTKLTV LPGGGSDAHKSEVAHRFKDLGGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVAD ESAENCDSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPE VDMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAAFTCECCQAADKAACLLPKL DELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTEC CHGDLLECADDDRADLAKYICENQDSISSKKECCEKPLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLRLAKTYETTLEKCCAAADPHECYA KVDFEFKPLVEEPQNLKQNCSELFQGEYKFNALLVRYTKVPQVSTPTLVEVSRNLGKVG SKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCKK ADDKETCFAEEGKKLVAAASQAALGLHHHHH
235	EGF-4	DLL3-15 x12C - HALB	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYMHWVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFGQRPQGSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTWHPPTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTITV VSSGGGGSGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTFKFLAPGTPARFSGSLGGKAAALTSVGQPEDEAEYYCVLWYSNRWVFGGGTKLTV LPGGGSDAHKSEVAHRFKDLGGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVAD ESAENCDSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPE VDMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAAFTCECCQAADKAACLLPKL DELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTEC CHGDLLECADDDRADLAKYICENQDSISSKKECCEKPLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFGLGMFLYEYARRHPDYSVLLRLAKTYETTLEKCCAAADPHECYA KVDFEFKPLVEEPQNLKQNCSELFQGEYKFNALLVRYTKVPQVSTPTLVEVSRNLGKVG SKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCKK ADDKETCFAEEGKKLVAAASQAALGLHHHHH

			-HALB	GGGSEVLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFNSYISYWAYWGQGTLLVT VSSGGGGGGGGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQA PRLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV LPGGGSDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVAD ESAENCDSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNPNL PRLVRPE VDVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAAACLLPKL DELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQFFPKAEFAEVSKLVTDLTKVHTEC CHGDLLECADRADLAKYICENQDSISSKLECEKEPLLEKSHCIAEVENDEMPADLP SLAAD FVESKDVCKNYAEAKDVF LGMFLYEYARRHPDYSVLLLR LAKTYETTL EKCCAAADPHECYA KVDFEFKPLVEEPQNL IKQNCLELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVG SKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDDFAAFVEKCKK ADDKETCFAEEGKKLVAASQAALGLHHHHH
236	EGF- 4	DLL3- 16 x12C - HALB	bispecifi c molecule -HALB	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGHYMHVWRQAPGQGLEWMGIINPSDGSNTYAQK FQGRVTMTTRDTSTSTVYME LRSRSEDTAVYYCTRGTTVVHYSYDMDVWGQGT TTVTVSSGGG GSGGGGGGGSDVVMQTPLSLPVTLGQPASISCRSSQSLVYRDGNTYLTW FQQRPGQSPRR LIYKVSNWQSGVPDRFSGSGGTDFTLKISRVEAEDGVYYCMQGTHWPTTFGGGTKVEIKSG GGSEVLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFNSYISYWAYWGQGTLLVT VSSGGGGGGGGGGGQTVVTQEPSTLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQKPGQA PRLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV LPGGGSDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVAD ESAENCDSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNPNL PRLVRPE VDVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAAACLLPKL DELDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQFFPKAEFAEVSKLVTDLTKVHTEC CHGDLLECADRADLAKYICENQDSISSKLECEKEPLLEKSHCIAEVENDEMPADLP SLAAD FVESKDVCKNYAEAKDVF LGMFLYEYARRHPDYSVLLLR LAKTYETTL EKCCAAADPHECYA KVDFEFKPLVEEPQNL IKQNCLELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVG SKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDDFAAFVEKCKK ADDKETCFAEEGKKLVAASQAALGLHHHHH
237	EGF- 4	DLL3- 17	bispecifi	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTNFYFMHWRQAPGLGLEWMGIINPSDGSNTYAQN FQGRVTMTTRDTSTNTVYME LSSLRSEDTAVYYCARGNSAFYSYDMDVWGQGT TTVTVSSGGG

		x12C - HALB	c molecule -HALB	GSGGGSGGGSDVVMTQSLPLPVTLQGPAISICRSSQSLVYRDGNTYLSWFQQRPQGSPRR LIYRVSNWQSGVPDRFSGSGSGTDFTLKISRVEAEDGVIYFCMQGTYPPTFGQGTQVDIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGTIVT VSSGGSGGGGGGQTVVTQEPSLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKPGQA PRGLIGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYICVLWYSNRWVFGGTKLTV LPGGGSDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVAD ESAENCDSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPE VDMCTAFHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAFTCECCQAADKAAACLLPKL DELDEGKASSAKQRLKASLQKGFGERAFKAWAVARLSQFFPKAEFAEVSKLVTDLTKVHTEC CHGDLLECADDDRADLAKYICENQDSISSKLECECEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFGLMFLEYEARHPDYSVVLLRLAKTYETTLEKCCAAADPHECYA KVDFEFKPLVEEPQNLKQNCLELFEQLGEYKFQNALLVRYTKVPQVSTPTLVEVSRNLGKVG SKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCCCK ADDKETCFAEEGKKLVAASQAALGLHHHHH
				QVQLVESGGGAVQPGRSRLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAIVSHGSSKYYARS VKGRFTISRDNKNTLYLEMNLSRAEDTAVYYCARDWWELVFDYWGGQTLVTVSSGGGGSGG GSGGGSDIVMTQTPLSLSTPGQPASISCKSSQSLHSDGKTFLYWYLOKPGQPPQLLIYEV SNRFSGVPDRFSGSGSGTDFTLKISRVEAEDGVIYCLQGIHLPTFGPGTKVEIKSGGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGNSYISYWAYWGQGTIVTVSSGG GSGGGSGGGGQTVVTQEPSLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKPGQAPRGLI GGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYICVLWYSNRWVFGGTKLTVLPGGG GSDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAEN CDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPEVDVMC TAFHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAFTCECCQAADKAAACLLPKLDELDR EGKASSAKQRLKASLQKGFGERAFKAWAVARLSQFFPKAEFAEVSKLVTDLTKVHTECCHGDL LECADDDRADLAKYICENQDSISSKLECECEKPLLEKSHCIAEVENDEMPADLPSLAADFVESK DVCKNYAEAKDVFGLMFLEYEARHPDYSVVLLRLAKTYETTLEKCCAAADPHECYAKVFFDE FKPLVEEPQNLKQNCLELFEQLGEYKFQNALLVRYTKVPQVSTPTLVEVSRNLGKVGSKCK HPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEF NAETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCCADDKE TCFAEEGKKLVAASQAALGLHHHHH
238	EGF- 5/[6]	DLL3- 18 x12C - HALB	bispecifi c molecule -HALB	

239	EGF-5/[6]	DLL3-19 x12C - HALB	bispecific molecule -HALB	QVTLKESGPMLVKPTETLTCTVSGFSLNSRMGVSWIRQPPGRALEWLAHIFSNDEKSYST SLKSRLTISKDTKSQVVLMTNMDPVDATYYCARYNDSSGYYYSFFDYWGQGLTVTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIY AASSLQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQGYSSPFTFGGGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS GGSGGGGGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRG LIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPG GGSDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESA ENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPRLVRPEVDV MCTAFHDNEETFLKKLYEIAARRHPYFYAPELLFFAKRYKAAFTGCCAADKAACLLPKLDEL RDEGKASSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHG DLLECAADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVE SKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETTLKCCAAADPHECYAKVF DEFKPLVEEPQNLIKQNCLELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKC CKHPEAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPK EFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVMDDFAAAFVEKCKKADD KETCFAEEGKKLVAAASQAALGLHHHHH
240	EGF-5/[6]	DLL3-20 x12C - HALB	bispecific molecule -HALB	QVTLKESGPVLVKPTETLTCTVSGFSLNSRMGVSWLRQPPGKALEWLAHIFSTDEKSYST SLKSRLTISKDTKSQVVLMTNMDPVDATYYCARYYDSSGYYYSFFDYWGQGLTVTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIY GASNLQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQYS SSPFTFGGGTKVEIKSGGGG SEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS GGSGGGGGGGGQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRG LIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPG GGSDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESA ENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPRLVRPEVDV MCTAFHDNEETFLKKLYEIAARRHPYFYAPELLFFAKRYKAAFTGCCAADKAACLLPKLDEL RDEGKASSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHG DLLECAADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVE SKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETTLKCCAAADPHECYAKVF DEFKPLVEEPQNLIKQNCLELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKC CKHPEAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPK

241	EGF- 5/[6]	DLL3- 21 x12C - HALB	bispecific molecule -HALB	EFNAETFTFHADICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADD KETCFAEEGKKLVAASQAALGLHHHHH QVQLVQSGAEVKKPGASVKVSCKASGYFTSYIHWVRQAPGQGLEWMGIINPSGGSKSYAQK FRGRVTMTSDTSTVYMELSSLTSEDTAVYYCARSMSTVTSDAFDIWGQTMVTVSSGGGGS GGGGGGGSDIOMTQSPSSLSASVGRVTITCRASQSI SNYLNWYQQKPKAPKLLIYAASS LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQSYSAPLTFGGGTKVDIKSGGGGSEVQ LVESSGGLVQPGSLKLSAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSSGGGG SGGGGGGGGQT VVTQEP SLTVSPGGT VTLTCGSS TGA VTS GNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGKKAALTL SGVQPEDEAEYCVLIWYSNRWVFGGGTKLT VLPGGGGS DAHKSEVAHRFKD LG EENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNP NLPRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAFT ECCCQAADKAACLLPKLDEL RDEG KASSAKQRLKCA SLQKFGERAFAKAWAVARLSQRFPAEFAEVS KLVTDLTKVHTECC HGD LLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYET TLEKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNC ELFQ LGEYKFQNALIVRYTKKVPQVSTPTLVEVSRLGKVGSKCKHP EAKRMPCAEDYLSVLNQLCVLHEKTPVSDRVT KCCTESLVNR RPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDKETC FAEEGKKLVAASQAALGLHHHHH
242	EGF- 3	DLL3- 4 xF12Q -HALB	bispecific molecule -HALB	QVQLQESGPGLVKPSSETLSITCTVSGGSISSYYWSWIRQPPGKGLEWIGYVYSGTTNYP SL KSRVTISVDTSKNQFSLKLSSTAA DTAVYYCASI AVTGFYFDYWGQGT LVTVSSGGGGSGG SGGGGSEIVLTQSPGTL SLSPGERVTLSCRASQRVNNNYLAWYQQRP GQAPRLLIYGASSRA TGI PDRFSGSGSGTDFTLTI SRLEPEDFAVYYCQQYDRSPLTFGGGTKLEIKSGGGGSEVQLV ESGGGLVQPGSLRLSCAASGFTFNSYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGT LVTVSSGGGGSG GGGGGGGQT VVTQEP SLTVSPGGT VTLTCGSS TGA VTS GNYPNWVQQKPGQAPRGLIGGTK FLAPGTPARFSGSLLGKKAALTL SGVQPEDEAEYCVLIWYSNRWVFGGGTKLT VLPGGGGS DA HKSEVAHRFKD LG EENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESAENCDKS LHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNP NLPRLVRPEVDVMCTAFH DNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAFT ECCCQAADKAACLLPKLDEL RDEGKA SSAKQRLKCA SLQKFGERAFAKAWAVARLSQRFPAEFAEVS KLVTDLTKVHTECC HGD LLECA DDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYET TLEKCCAAADPHECYAKVDFEFKPL

243	EGF-3	DLL3-5 xF12Q -HALB	bispecific molecule -HALB	VEEPQNLIKQNCLEFQIGEYKFNQALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCKHPEAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDDFAAFVEKCKCKADDKETCFAEEGKKLVAAASQAALGLHHHHH
244	EGF-3	DLL3-6 xF12Q -HALB	bispecific molecule -HALB	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGRTNYYPSLKSRTVTSIDTSKNQFSLKLSVTAADTAVYYCARIAGAGFFFDYWGQGLTVTVSSGGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYDRSPLTFGGGTKEIKSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGFGNSYVSWWAYWGQGLTVTVSSGGGGSGGGGGGGSGQTVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGSDAHKSEVAHRFKDGLGEENFKALVLI AFAQLQCCPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNP NL PRLVRPEVDVMCTAFHDNEETF LKKYLYE IARRHPYFYAPEL LFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVS KLVTDLTKVHTECC HGDLL ECADDRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLAKTYETLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCLEFQIGEYKFNQALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCKHPEAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDDFAAFVEKCKCKADDKETCFAEEGKKLVAAASQAALGLHHHHH
244	EGF-3	DLL3-6 xF12Q -HALB	bispecific molecule -HALB	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKGLEWIGYIYYSGTNTNYPNPSLKSRTVTSVDTSKNQFSLKLSVTAADTAVYYCARIAGAGFFFDYWGQGLTVTVSSGGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTFTLTISRLEPEDFAVYYCQYDRSPLTFGGGTKEIKSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGFGNSYVSWWAYWGQGLTVTVSSGGGGSGGGGGGGSGQTVTQEPSTLTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGSDAHKSEVAHRFKDGLGEENFKALVLI AFAQLQCCPFEDHVKL VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNP NL PRLVRPEVDVMCTAFHDNEETF LKKYLYE IARRHPYFYAPEL LFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVS KLVTDLTKVHTECC HGDLL ECA

245	EGF-3	DLL3-7 xF12Q -HALB	bispecific molecule -HALB	<p>DDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVLLLRRLAKTYETTLKCCAAADPHECYAKVDFEKFPL VEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEA KRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDDKETCFA EEGKKLVAASQAALGLHHHHH</p> <p>QVQLQESGPGLVKPSQTLSTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGVFFFDYWGQGTTLVTVSSGGGGGGG GGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGI PDRFSGSGGTDFTLTI SRLEPEDFAVYQCQYDRSPLTFGGGKVEIKSGGGSEVQLV ESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVHRHGFNSYVSWWAYWGQGTTLTVSSGGGGSG GGGGGGSGQTVVTQEPSTLTVSPGGTVTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLPGGGSDA HKSEVAHRFKD LG EENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESAENCDKS LHTLFGDKLCTVATLRET YGEMADCCAKQEPERNECFLQHKDDNPRLVRPEVDMCTAFH DNEETFLLKKYL YEIARRHPYFYAPEL LFFAKRYKAAFT ECCCQAADKAACIL PKLDEL RDEGKA SSAKQRLK CASLQKFGERA FKA W A VARLSQRFPKAEFAEVSKLVTDLT KVHTECC HGD LLECA DDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVLLLRRLAKTYETTLKCCAAADPHECYAKVDFEKFPL VEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEA KRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDDKETCFA EEGKKLVAASQAALGLHHHHH</p>
246	EGF-3	DLL3-8 xF12Q -HALB	bispecific molecule -HALB	<p>QVQLQEWGPGLVKPSQTLSTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGVFFFDYWGQGTTLVTVSSGGGGGGG GGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGI PDRFSGSGGTDFTLTI SRLEPEDFAVYQCQYDRSPLTFGGGKVDIKSGGGSEVQLV ESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVHRHGFNSYVSWWAYWGQGTTLTVSSGGGGSG GGGGGGSGQTVVTQEPSTLTVSPGGTVTLTCSGSTGAVTSGNYPNWVQKPGQAPRGLIGGTK FLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLPGGGSDA HKSEVAHRFKD LG EENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESAENCDKS LHTLFGDKLCTVATLRET YGEMADCCAKQEPERNECFLQHKDDNPRLVRPEVDMCTAFH</p>

247	EGF-3	DLL3-9 xF12Q -HALB	bispecific molecule -HALB	<p>DNEETFLKKYL YEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDELDRDEGKA SSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVS KLVTDLTKVHTECCCHGDLLECA DDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVLLLR LAKTYETTLKCCAAADPHECYAKVDFEFKPL VEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCCKHPEA KRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDDFAAFVEKCCCKADDKETCFA EEGKKLVAASQAALGLHHHHH</p> <p>QVQLQESGPGLVKPSQTLSTCTVSGASISSFYWSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISLDTSKNQFSLKLSVTAADTAVYYCARIAGAGFFFDYWGQGLTVTVSSGGGGSGG GGGGGSEIVLTQSPGTLSPGESATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTFTLTISRLEPEDFAVYQCQYDRSPLTFGGGTRLEIKSGGGSEVQLV ESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGFGNSYVSWWYWGQGLTVTVSSGGGGSG GGGGGGSQTVTQEPSTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTK FLAPGTPARFSGSLGKKAALTSLGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLPGGGGSDA HKSEVAFHRFKDLEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDS LHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNP NLPRVLRPEVDVMCTAFH DNEETFLKKYL YEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDELDRDEGKA SSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVS KLVTDLTKVHTECCCHGDLLECA DDRADLAKY ICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVLLLR LAKTYETTLKCCAAADPHECYAKVDFEFKPL VEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGVGSKCCKHPEA KRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDDFAAFVEKCCCKADDKETCFA EEGKKLVAASQAALGLHHHHH</p>
248	EGF-3	DLL3-10 xF12Q -HALB	bispecific molecule -HALB	<p>QVQLQESGPGLVKPSQTLSTCTVSGGSISSYYWSWIRQPPGKGLEWIGIYIFYNGITNYPNPSL KSRVTISLDTSKNQFSLKLSVTAADTAKYYCARIHSGSFSFDYWDQGLTVTVSSGGGGSGG GGGGGSEIVMTQSPGTLSPGERATLSCRASQSVSRGYLAWYQQKPGQAPRLLIYGASSRA TDIPDRFSGSGGTFTLTISRLEPEDFAVYQCQYDTSPTIFGQGTKVEIKSGGGSEVQLV ESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKG RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGFGNSYVSWWYWGQGLTVTVSSGGGGSG GGGGGGSQTVTQEPSTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTK FLAPGTPARFSGSLGKKAALTSLGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLPGGGGSDA EEGKKLVAASQAALGLHHHHH</p>

249	EGF-4	DLL3-13 xF12Q -HALB	bispecific molecule -HALB	<p>HKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESAENCCKS LHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDMCTAFH DNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTCECCQAADKAACLLPKLDELREDEGKA SSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLT KVHTECCCHGDLECA DDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETLEKCCAAADPHECYAKVDFEFKPL VEEPQNLIKQNCLEFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCKHPEA KRMPCAEYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDKETCFA EEGKKLVAASQAALGLHHHHH</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGQGLEWMGI INPSDGSSTNYAQN FQGRVTMTTRDTSNTVTYMEISSLRSEDTAVYICARGNSAFYSYYDMVDWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQSLPLVTLGQPASISCRSSQSLVYRDGNTYLSWFFQQRPGQSPRR LIYKVSNWQSGVPDRFSGSGGTFTLKISRVEAEDVGYFCMQGTHWPTTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYICVRHGNFGNSYVSWWAYWGQGTITV VSSGGSGGGSGGGSGGTQVVTQEPSTLVSPGGTTLTCGSGTGAVTSGNYPNWVQKPGQA PRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYICVLWYSNRWVFGGGTKLTV LPGGGSDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVAD ESAENCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPE VDVMCTAFHDNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTCECCQAADKAACLLPKL DELREDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLT KVHTEC CHGDLLECADRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETLEKCCAAADPHECYA KVDFEFKPLVEEPQNLIKQNCLEFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVG SKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCK ADDKETCFAEEGKKLVAASQAALGLHHHHH</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGLGLEWMGI INPSDGSSTSYAQK FQGRVTMTTRDTSNTVTYMDLSSLRSEDTAVYICARGNSAFYSYYDMVDWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQSLPLVTLGQPASISCRSSQSLVYRDGNTYLSWFFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGGTFTLKISRVEAEDVGYICMQGTHWPTTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYICVRHGNFGNSYVSWWAYWGQGTITV</p>
250	EGF-4	DLL3-14 xF12Q -HALB	bispecific molecule -HALB	<p>HKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVADESAENCCKS LHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDMCTAFH DNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTCECCQAADKAACLLPKLDELREDEGKA SSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLT KVHTECCCHGDLECA DDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETLEKCCAAADPHECYAKVDFEFKPL VEEPQNLIKQNCLEFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVGSKCKHPEA KRMPCAEYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCKADDKETCFA EEGKKLVAASQAALGLHHHHH</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGQGLEWMGI INPSDGSSTNYAQN FQGRVTMTTRDTSNTVTYMEISSLRSEDTAVYICARGNSAFYSYYDMVDWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQSLPLVTLGQPASISCRSSQSLVYRDGNTYLSWFFQQRPGQSPRR LIYKVSNWQSGVPDRFSGSGGTFTLKISRVEAEDVGYFCMQGTHWPTTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYICVRHGNFGNSYVSWWAYWGQGTITV VSSGGSGGGSGGGSGGTQVVTQEPSTLVSPGGTTLTCGSGTGAVTSGNYPNWVQKPGQA PRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYICVLWYSNRWVFGGGTKLTV LPGGGSDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKL VNEVTEFAKTCVAD ESAENCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPE VDVMCTAFHDNEETFLKKYLYE IARRHPYFYAPELLFFAKRYKAAFTCECCQAADKAACLLPKL DELREDEGKASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLT KVHTEC CHGDLLECADRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRLAKTYETLEKCCAAADPHECYA KVDFEFKPLVEEPQNLIKQNCLEFQELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLKVG SKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKCK ADDKETCFAEEGKKLVAASQAALGLHHHHH</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGLGLEWMGI INPSDGSSTSYAQK FQGRVTMTTRDTSNTVTYMDLSSLRSEDTAVYICARGNSAFYSYYDMVDWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQSLPLVTLGQPASISCRSSQSLVYRDGNTYLSWFFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGGTFTLKISRVEAEDVGYICMQGTHWPTTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYICVRHGNFGNSYVSWWAYWGQGTITV</p>

251	EGF-4	DLL3-15 xF12Q -HALB	bispecific molecule -HALB	<p>VSSGGGGGGGGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTFKFLAPGTPARFSGSLGGKAAALTSVGQPEDEAEYYCVLWYSNRWVFGGGTKLTV LPGGGSDAHKSEVAHRFKDLGGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVAD ESAENCDSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPE VDMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELLFFAKRYKAAFTCECCQAADKAACLLPKL DELRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTEC CHGDLLECADDDRADLAKYICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTTLEKCCAAADPHECYA KVFDEFKPLVEEPQNLKQNCSELFQGEYKFNALLVRYTKVPQVSTPTLVEVSRNLGKVG SKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCKK ADDKETCFAEEGKKLVAAASQAALGLHHHHHH</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWRVQAQGQGLEWMGIINPSDGSTSYGQN FQGRVTMTRDTSTNTVMELSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMTQSLPLPVTLGQPASISCRSSQSLAYRDGNTYLSWVQQRPQGSPRR LIYKVSNWQSGVDRFSGSGGTDFTLKISRVEAEDGVYFCMQGTHWPPPTFGQGTKEIKSG GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTTFNYSAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYCVRHGNGNSYVSWWAYWGQGTITVT VSSGGGGSGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTFKFLAPGTPARFSGSLGGKAAALTSVGQPEDEAEYYCVLWYSNRWVFGGGTKLTV LPGGGSDAHKSEVAHRFKDLGGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVAD ESAENCDSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLVRPE VDMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELLFFAKRYKAAFTCECCQAADKAACLLPKL DELRDEGKASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTEC CHGDLLECADDDRADLAKYICENQDSISSKKECCEKPLLEKSHCIAEVENDEMPADLPSLAAD FVESKDVCKNYAEAKDVLGMFLYEYARRHPDYSVLLRLAKTYETTTLEKCCAAADPHECYA KVFDEFKPLVEEPQNLKQNCSELFQGEYKFNALLVRYTKVPQVSTPTLVEVSRNLGKVG SKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCKK ADDKETCFAEEGKKLVAAASQAALGLHHHHHH</p>
252	-	Human DLL3	human	<p>MVSPRMSGLLSQTVILALIFLPQTRPAGVVFELQIHSGFGPGPGAPRSPCSARLPCRLLFFRVC LKPGLSEEAESPALGAALSARGPVYTEQPGAPADLPLPDGLLQVFFRDWPGTFSFIET WREELGDQIGGPAWSLLARVAGRRRLAAGGPWARDIQRAGAWELRFSYRARCEPPAVGTACTR LCRPRSAPSRGCGPLRPCAPLEDECEAPLVCRAAGSPHGFCEQPGECRCLEGWTGPLCTVPV</p>

253	-	Human DLL3 ECD	human	STSSCLSPRGPSSATTGCLVPGPGPCDGNPCANGGSCSETPRSFECTCPRGFYGLRCEVSGVT CAGGPCFNGGLCVGGADPDSAYICHCPGFGQSNCEKRVDRCSLQPCRNGGLCLDLGHALRCR CRAGFAGPRCEHDLDDCAGRACANGGTCVEGGAHRCSCALFGGRDCRERADPCAARPCAAG GRCYAHFSGLVCAACAPGYMGARCEFFVHPDGPALPAAPPGLRPGDPQRYLLPPALGLLVAAG VAGAAALLVHVRRRHSQDAGSRLLAGTPEPSVHALPDALNNLRTQEGSGDGPSSVVDWNRPE DVDPQGIYVISAPSIYAREVATPLFPLHTGRAGQRQHLFFYPSSILSVK MVSPRMSGLLSQTVILALIFLPQTRPAGVFELQIHSFGPGPGAPRSPCSARLPCRLLFFRVC LKPGLSSEEAESPICALGAALSARGPVYTEQPGAPADLPLPDGLLQVFFRDAMPGTFSFIET WREELGDQIGGPAWSLLARVAGRRRLAAGGPWARDIQRAGAWELRFSYRARCEPPAVGTACTR LCRPSAPSRCGGLRPCAPLEDECEAPLVCRAAGCSEHGFCFCEQPGECRCLEGTGPLCTVPV STSSCLSPRGPSSATTGCLVPGPGPCDGNPCANGGSCSETPRSFECTCPRGFYGLRCEVSGVT CAGGPCFNGGLCVGGADPDSAYICHCPGFGQSNCEKRVDRCSLQPCRNGGLCLDLGHALRCR CRAGFAGPRCEHDLDDCAGRACANGGTCVEGGAHRCSCALFGGRDCRERADPCAARPCAAG GRCYAHFSGLVCAACAPGYMGARCEFFVHPDGPALPAAPPGLRPGDPQRYL
254	-	Hu DLL3 N- term.	human	MVSPRMSGLLSQTVILALIFLPQTRPAGVFELQIHSFGPGPGAPRSPCSARLPCRLLFFRVC LKPGLSSEEAESPICALGAALSARGPVYTEQPGAPADLPLPDGLLQVFFRDAMPGTFSFIET WREELGDQIGGPAWSLLARVAGRRRLAAGGPWARDIQRAGAWELRFSYR
255	-	Hu DLL3 DSL dom	human	ARCEPPAVGTACTRLCRPSAPSRGCGGLRPCAPLEDECE
256	-	Hu DLL3 EGF-1	human	APLVCRAAGCSEHGFCFCEQPGECRCLEGTGPLCT
257	-	Hu DLL3 EGF-2	human	GGPGCDGNPCANGGSCSETPRSFECTCPRGFYGLRCE
258	-	Hu DLL3 EGF-3	human	SGVTCADGPCFNGGLCVGGADPDSAYICHCPGFGQSNCE
259	-	Hu DLL3	human	RVDRCSLQPCRNGGLCLDLGHALRCRCRAGFAGPRCE

		EGF-4			
260	-	Hu DLL3 EGF- 3+4	human		SGVTCADGPCFNGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQPCRNGGLCLDLIGHA LRCRCRAGFAGPRCE
261	-	Hu DLL3 EGF-5	human		DLDDCAGRACANGGTCVEGGGAHRCSCALGFGGRDCR
262	-	Hu DLL3 EGF-6	human		RADPCAARPCAHHGGRCYAHFSLVCAACAPGYMGARCE
263	-	Human DLL3 ECD x EpCA M	artificial		MVSPRMSGLLSQTVILALIFLPQTRPAGVFFELQIHSGFGPGPGAPRSPCSARLPCRLLFFRVC LKPLSEEEAAESPICALGAALSARGPVYTEQPGAPADLPLPDGLLQVFFRDWPGTFSFIIET WREELGDQIGGPAWSLLARVAGRRRLAAGGPWARDIQRAGAWELRFSYRARCEPPAVGTACTR LCRPRSAPSRGPGRLPCAPLEDECEAPLVCRAAGSPHGFCEQPGECRCLEGTGPLCTVPV STSSCLSPRGPSATTGCLVPGPGPCDGNPCANGGSCSETPRSFECTCPRGFYGLRCEVSGVT CADGPCFNGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQPCRNGGLCLDLGHALRCR CRAGFAGPRCEHDLDDCAGRACANGGTCVEGGGAHRCSCALGFGGRDCRERADPCAARPCAAG GRCYAHFSLVCAACAPGYMGARCEFFVHPDGSALPAAPPGLRPGDPQRYLSGGGSGAGVIA VIVVVVIAIVAGIVLVISRKRRMAKYEKAEIKEMGEMHRELNA
264	-	V5 x hu DLL3- DSL x EpCA M	artificial		MGWSCIIILFLVATATGVHSGKPIPNPLLGLDSTSGARCEPPAVGTACTRLCRPRSAPSRGPG LRPCAPLEDECEAPLVCRAAGSPHGFCEQPGECRCLEGTGPLCTVPVSTSSCLSPRGPSA TTGCLVPGPGPCDGNPCANGGSCSETPRSFECTCPRGFYGLRCEVSGVTCADGPCFNGLCVG GADPDSAYICHCPPGFQGSNCEKRVDRCSLQPCRNGGLCLDLGHALRCRCRAGFAGPRCEHDL DDCAGRACANGGTCVEGGGAHRCSCALGFGGRDCRERADPCAARPCAAGGRCYAHFSLVCAC APGYMGARCEFFVHPDGSALPAAPPGLRPGDPQRYLSGGGSGAGVIAIVVVVIAIVAGIV VLVISRKRRMAKYEKAEIKEMGEMHRELNA
265	-	V5 x hu DLL3- EGF1 x EpCA	artificial		MGWSCIIILFLVATATGVHSGKPIPNPLLGLDSTSGAPLVCRAAGSPHGFCEQPGECRCLEGW TGPLCTVPVSTSSCLSPRGPSATTGCLVPGPGPCDGNPCANGGSCSETPRSFECTCPRGFY LRCEVSGVTCADGPCFNGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQPCRNGGLCL DLGHALRCRCRAGFAGPRCEHDLDDCAGRACANGGTCVEGGGAHRCSCALGFGGRDCRERADP CAARPCAAGGRCYAHFSLVCAACAPGYMGARCEFFVHPDGSALPAAPPGLRPGDPQRYLSGG GGSGAGVIAIVVVVIAIVAGIVLVISRKRRMAKYEKAEIKEMGEMHRELNA

		M			MGWSCIILFLVATATGVHSGKPIPNPLLGLDSTSGGPGPCDGNPCANGGSCSETPRSFECTCP RGFYGLRCEVSGVTCADGPCFNGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQPCRN GGLCLDLGHALRCRCRAGFAGPRCEHDLDDCAGRACANGGTCVEGGAHRCSCALGFGGRDCR ERADPCAARPCAAGRCYAHFSLVCACAPGYMGARCEFPVHPDGASALPAAPPGLRPGDPQR YLSGGGGGAGVIAIVVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMGEMHRELNA
266	-	V5 x hu DLL3- EGF2 x EpCA M	artificial		MGWSCIILFLVATATGVHSGKPIPNPLLGLDSTSGSGVTCADGPCFNGLCVGGADPDSAYIC HCPPGFQGSNCEKRVDRCSLQPCRNGLCLDLGHALRCRCRAGFAGPRCEHDLDDCAGRACAN GGTCVEGGAHRCSCALGFGGRDCRERADPCAARPCAAGRCYAHFSLVCACAPGYMGARCE FPVHPDGASALPAAPPGLRPGDPQRYLSGGGGGAGVIAIVVVVIAIVAGIVVLVISRKKRM AKYEKAEIKEMGEMHRELNA
267	-	V5 x hu DLL3- EGF3 x EpCA M	artificial		MGWSCIILFLVATATGVHSGKPIPNPLLGLDSTSGRVDRCSLQPCRNGLCLDLGHALRCRCR AGFAGPRCEHDLDDCAGRACANGGTCVEGGAHRCSCALGFGGRDCRERADPCAARPCAAGGR CYAHFSLVCACAPGYMGARCEFPVHPDGASALPAAPPGLRPGDPQRYLSGGGGGAGVIAVI VVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMGEMHRELNA
268	-	V5 x hu DLL3- EGF4 x EpCA M	artificial		MGWSCIILFLVATATGVHSGKPIPNPLLGLDSTSGRVDRCSLQPCRNGLCLDLGHALRCRCR AGFAGPRCEHDLDDCAGRACANGGTCVEGGAHRCSCALGFGGRDCRERADPCAARPCAAGGR CYAHFSLVCACAPGYMGARCEFPVHPDGASALPAAPPGLRPGDPQRYLSGGGGGAGVIAVI VVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMGEMHRELNA
269	-	V5 x hu DLL3- EGF5 x EpCA M	artificial		MGWSCIILFLVATATGVHSGKPIPNPLLGLDSTSGDLDDCAGRACANGGTCVEGGAHRCSCA LGFGGRDCRERADPCAARPCAAGRCYAHFSLVCACAPGYMGARCEFPVHPDGASALPAAPP GLRPGDPQRYLSGGGGGAGVIAIVVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMGEMHR ELNA
270	-	V5 x hu DLL3- EGF6	artificial		MGWSCIILFLVATATGVHSGKPIPNPLLGLDSTSGRADPCAARPCAAGRCYAHFSGSLVCACA PGYMGARCEFPVHPDGASALPAAPPGLRPGDPQRYLSGGGGGAGVIAIVVVVIAIVAGIVV LVISRKKRMAKYEKAEIKEMGEMHRELNA

271	-	x EpCA M	cyno	<p>MVSPRMSRLLSQTVILALIFIPQARPAGVFELQIHSFGPGPGAPRSPCSARGPCRLFFRVC LKPGLSSEAAESPCALGAALSARGPVYTEQPEAPADLPLPGLLQVPPFRDAWPGTFSLI IET WREELGDQIGGPAWSLLARVTRRRRLAAGGPWARDIQRAGAWELRFSYRARCCELPAVGTACTR LCRPRSAPSRGPGGLRPCAPLEDECEAPPVCRAGCSLEHGFC EQPGE C RCLEGTG PLCMVPA STSSCLGLRGPSATTGCLVPGPGCDGNPCANGGSCSETPGSFECTCPRGFYGLRCEVSGVT CAGGPCFNGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQPCRNNGGLCLDLGHALRCR CRAGFAGPRCEHNLD CAGRACANGGTCVEGGGAHRCSCALFGGRDCRERADPCAARPCAAG GRCYAHFSGLVCA CAPGYMGRCEFPVHPDGV SALP AAPGLRPGDPQRYLLPPALGLLLV AAG VAGAALLLVHVRRRGHAQDAGSRLLAGTPEPSVHALPDALNNQRTQEGPGDVPSSSSVDWNRPE DVS RGIYVISAPSIYAREA</p>
272	-	Macaq ue DLL3 ECD	cyno	<p>MVSPRMSRLLSQTVILALIFIPQARPAGVFELQIHSFGPGPGAPRSPCSARGPCRLFFRVC LKPGLSSEAAESPCALGAALSARGPVYTEQPEAPADLPLPGLLQVPPFRDAWPGTFSLI IET WREELGDQIGGPAWSLLARVTRRRRLAAGGPWARDIQRAGAWELRFSYRARCCELPAVGTACTR LCRPRSAPSRGPGGLRPCAPLEDECEAPPVCRAGCSLEHGFC EQPGE C RCLEGTG PLCMVPA STSSCLGLRGPSATTGCLVPGPGCDGNPCANGGSCSETPGSFECTCPRGFYGLRCEVSGVT CAGGPCFNGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQPCRNNGGLCLDLGHALRCR CRAGFAGPRCEHNLD CAGRACANGGTCVEGGGAHRCSCALFGGRDCRERADPCAARPCAAG GRCYAHFSGLVCA CAPGYMGRCEFPVHPDGV SALP AAPGLRPGDPQRYLLPPALGLLLV AAG VAGAALLLVHVRRRGHAQDAGSRLLAGTPEPSVHALPDALNNQRTQEGPGDVPSSSSVDWNRPE DVS RGIYVISAPSIYAREA</p>
273	-	Ma DLL3 N- term.	cyno	<p>MVSPRMSRLLSQTVILALIFIPQARPAGVFELQIHSFGPGPGAPRSPCSARGPCRLFFRVC LKPGLSSEAAESPCALGAALSARGPVYTEQPEAPADLPLPGLLQVPPFRDAWPGTFSLI IET WREELGDQIGGPAWSLLARVTRRRRLAAGGPWARDIQRAGAWELRFSYRARCCELPAVGTACTR</p>
274	-	Ma DLL3 DSL dom.	cyno	<p>ARCELPAVGTACTR LCRPRSAPSRGPGGLRPCAPLEDECE</p>
275	-	Ma DLL3 EGF-I	cyno	<p>APPVCRAGCSLEHGFC EQPGE C RCLEGTG PLCM</p>
276	-	Ma	cyno	<p>GPFGCDGNPCANGGSCSETPGSFECTCPRGFYGLRCE</p>

		DLL3 EGF-2		
277	-	Ma DLL3 EGF-3	cyno	SGVTCADGPGCFNGGLCVGGADPDSAYICHCPPGFQGSNCE
278	-	Ma DLL3 EGF-4	cyno	RVDRCSLQPCRNGGLCLDLGHALRCRCRAGFAGPRCE
279	-	Ma DLL3 EGF-3+4	cyno	SGVTCADGPGCFNGGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQPCRNGGLCLDLGHALRCRCRAGFAGPRCE
280	-	Ma DLL3 EGF-5	cyno	NLDDCAGRACANGGTCVEGGGAHRCSALGFGRDCR
281	-	Ma DLL3 EGF-6	cyno	RADPCAARPCAHHGRCYAHFSGLVACAPGYMGSRC
282	-	Ma DLL3 ECD x EpCAM	artificial	MVSPRMSRLLSQTIVILALIFIPQARPAGVFELQIHSGPGPGAPRSPCSARGPCRLFFRVCLKPGLSSEAAEESPCALGAALSARGPVYTEQPEAPADLPNGLIQVFFRDAMPGTFSLI IETWREELGDQIGGPAWSLLARVTRRRRLAAGGPWARDIQRAGAWELRFSYRARCCELPAVGTACTR LCRPSAPSRCGPGRLPCAPLEDECEAPVCRAGCSLEHGFEQPGECRCLEGTGPLCMVPA STSSCLGLRGPSATTGCLVPGPGPCDGNPCANGGSCSETPGSFECTCPRGFYGLRCEVSGVT CADGPGCFNGGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQPCRNGGLCLDLGHALRCR CRAGFAGPRCEHNLDDCAGRACANGGTCVEGGGAHRCSALGFGRDCRERADPCAARPCAHHGRCYAHFSGLVACAPGYMGSRCFVHPDGVSAAPGLRPGDPQRYLSGGGSGAGVIA VIVVVVIAIVAGIVVLVISRKKRMAYEKAEIKEMGEMHRELNA
283	-	Human DLL1	human	MGRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGAGPPPCACRTFFRVCLKHYQASVSPPEPCTYGSAVTPVLGVDSFSLPDGGADSAFNSPIRFPFGFTWPGTFSLI IEALHTDSPDDLATENPERLISRLATQRLHTVGEESQDLHSSGRTDLKYSYRFVVCDEHYEGECS VFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGVQGR YCDECIRYPGCLHGTCQQPWQCNCQEGWGGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSYTCS CRPGYTGATCELGIDECDDPSPCKNNGGSCDTLENSYSCTCPFGFYKICELSAMTCADGPGCFNG

284	-	Human DLL4	human	GRCDSPDGGYSCRCFVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD DNVDDCASSPCANGGTCRDGVNDFSCTCPPGYTGRNCSAPVSRCEHAPCHNGATCCHERGHRYV CECARGYGGPNCQFLPELPPGPAVVDLTEKLEGQGGFPWAVCAGVILVLMILLGCAAVV CVRLRLQKHRPPADPCRGETEETMNNLANCQREKDISVSIIGATQIKNTNKKADFHGDHSDKN GFKARYPAVDYNLVQDLKGGDDTAVRDAHSKRDTKCQPQSSGEEKGTPTTLRGGEASERKRPD SGCSTSKDTKYQSVYVISEEKDECVIATEV MAAASRSASGWALLLLVALWQQAAGSGVFQLQLQEFINERGVLASGRPCEPGCRTFFRVCLK HFQAVVSPGPCTFTGTVPVLGTNSFAVRDDSSGGGRNPLQLPFNFTWPGTFSLIIEAWHAPG DDLREALPPDALISKIAIQGSLAVGQNWLLDEQTSTLRLRYSYRVICSDNYGDNCSRLCK KRNDFHGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHQNGYCSKPAECLCRPGWQGRICNE CIPHNGCRHGTCTSPWQCTCDEGWGGLFCDQDLNYCTHHSCKNGATCSNSGQRSYTCCTCRPG YTGVDCELELSECDNSPCRNNGSCKDQEDGYHCLCPGYGLHCEHSTLSCADSPCFNGGSCR ERNQGANAYACECPNFTGSNCEKKVDRCTSNPCANGGQCLNRGPSRMCRCRPGFTGTYCELHV SDCARNPCAHGGTCHDLENGLMCTCPAGFSGRRCVRTSIDACASSPCFNRACTCYTDLSTDTF VCNCPYGFVGSRCFPPGLPSPFPWAVSLGVGLAVLLVLLGMVAVRQLRLRRPDDGSREA MNNLSDFQKDNLIIPAAQLKNTNQKKELEVDCGLDKSNCGKQQNHTLDYNLAPGLGRGTMPGK FPHSDKSLGEKAPLRHSEKPECRI SAICSPRDSMYQSVCLISEERNECVIATEV
285	-	linker 1	artificial	GGGG
286	-	linker 2	artificial	GGGGS
287	-	linker 3	artificial	GGGGQ
288	-	linker 4	artificial	SGGGGS
289	-	linker 5	artificial	PGGGGS
290	-	linker 6	artificial	PGGDGS
291	-	linker 7	artificial	GGGSGGGGS
292	-	linker 8	artificial	GGGSGGGGS

293		linker 9	artificial	GGGGGGGGGGGGGGG
294	-	Hexa- his	artificial	HHHHHH
295	-	Ab156	artificial	RDWDFDVFGGGTPVGG
296	-	linear FcRn BP	artificial	QRFVTGHFGGLXPANG
297	-	linear FcRn BP-Y	artificial	QRFVTGHFGGLYPANG
298	-	linear FcRn BP-H	artificial	QRFVTGHFGGLHPANG
299		core FcRn BP-H	artificial	TGHFGGLHP
300		cyclic FcRn BP-H	artificial	QRFCTGHFGGLHPCNG
301	-	HALB	human	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNP NL PRLVRPEVDVMCTA FHDNEETFLKKLYL YEIARRHPYFYAPEL LFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEG KASSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPKAEFAEVS KLVTDLTKVHTECCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYET TLEKCCAAADPHECYAKV FDEFK PLVEEPQNL IKONCELFEOQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDKETC FAEEGKKLVAA SQAALGL
302	-	HALB variant 1	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNP NL PRLVRPEVDVMCTA FHDNEETFLKKLYL YEIARRHPYFYAPEL LFFAKRYKAAFT ECCCQAADKAACLLPKLDEL RDEG

303	-	HALB variant 2	artificial	<p>KASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA GTFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAAMDDFAAFVEKCKKADDKETC FAEEGKLVAAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQC PFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTA FHDNEETFLKKLYEIAARRHPYFYAPELFFAKRYKAFTTECCQAADKAACLLPKLDELDRDEG KASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDKETC FAEEGPKLVAAASQAALGL</p>
304	-	HALB variant 3	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQC PFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTA FHDNEETFLKKLYEIAARRHPYFYAPELFFAKRYKAFTTECCQAADKAACLLPKLDELDRDEG KASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDKETC FAEEGPHLVAAASKAALGL</p>
305	-	HALB variant 4	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQC PFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTA FHDNEETFLKKLYEIAARRHPYFYAPELFFAKRYKAFTTECCQAADKAACLLPKLDELDRDEG KASSAKQRLKASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLKCCAAADPHECYAKVDFEFK PLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP</p>

306	-	HALB variant 5	artificial	<p>EAKRMPCAEDYLSVVNLQCLVLEHKTTPVSDRVTKCCCTESLVNRRPCFSALGVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAADKAACLLPKLDELRLDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVNLQCLVLEHKTTPVSDRVTKCCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASQAALGL</p>
307	-	HALB variant 6	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAADKAACLLPKLDELRLDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVNLQCLVLEHKTTPVSDRVTKCCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPHLVAASQAALGL</p>
308	-	HALB variant 7	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECF LQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAADKAACLLPKLDELRLDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFK PLVEEPQNL IKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVNLQCLVLEHKTTPVSDRVTKCCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPHLVAASQAALGL</p>

309	-	HALB variant 8	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCC KHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASKAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCC KHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASKAALGL</p>
310	-	HALB variant 9	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCC KHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASKAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCC KHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASKAALGL</p>
311	-	HALB variant 10	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCC KHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASKAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCC KHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASKAALGL</p>
312	-	HALB variant 11	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQCPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE</p>

313	-	HALB variant 12	artificial	<p>CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA GTFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDDFAAFVEKCKCKADDKETC FAEEGPKLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDMCTA FHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA GTFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDDFAAFVEKCKCKADDKETC FAEEGPKLVAASQAALGL</p>
314	-	HALB variant 13	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDMCTA FHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA GTFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDDFAAFVEKCKCKADDKETC FAEEGPKLVAASQAALGL</p>
315	-	HALB variant 14	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDMCTA FHDNEETFLKKYLYEIARRHPYFYAPELFFAKRYKAAFTCCQAAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLRAKTYETTLKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCSELFQGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA GTFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDDDFAAFVEKCKCKADDKETC FAEEGPKLVAASQAALGL</p>

316	-	HALB variant 15	artificial	ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEGPCLVAASQAALGL DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNP NL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAAADKAACLLPKLDELDRDEG KASSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPAEFAEVS KLVTDLTKVHTECCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADIPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTL EKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCELFEQLGEYKFQNAL LVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEGPCLVAASQAALGL
317	-	HALB variant 16	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNP NL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAAADKAACLLPKLDELDRDEG KASSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPAEFAEVS KLVTDLTKVHTECCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADIPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTL EKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCELFEQLGEYKFQNAL LVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEGPCLVAASQAALGL
318	-	HALB variant 17	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNP NL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCCQAAADKAACLLPKLDELDRDEG KASSAKQRLKCSLQKFGERAFAKAWAVARLSQRFPAEFAEVS KLVTDLTKVHTECCHGDLLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADIPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTL EKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCELFEQLGEYKFQNAL LVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKCKADDDKETC FAEGPCLVAASQAALGL
319	-	HALB variant	artificial	DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNP NL PRLVRPEVDVMCTA

320	-	HALB variant 19	artificial	<p>FHDNEETFLLKKLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFK PLVEEPQNLIKONCELFEOQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP EAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEGPKLVAASKAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQSPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLLKKLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFK PLVEEPQNLIKONCELFEOQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP EAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEGPKLVAASKAALGL</p>
321	-	HALB variant 20	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLLKKLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFK PLVEEPQNLIKONCELFEOQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP EAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEGPKLVAASKAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLLKKLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFK PLVEEPQNLIKONCELFEOQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHP EAKRMPCAEEDYLSVVLNQLCVLHEKTPVSDRVTCKCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAAFVEKCCCKADDKETC FAEGPKLVAASKAALGL</p>
322	-	HALB variant 21	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFIQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLLKKLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAADKAACLLPKLDELDEG KASSAKQRLKASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTTLEKCCAAADPHECYAKVDFEFK</p>

323	-	HALB variant 22	artificial	<p>PLVEEPQNLIKQNCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA GTFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDDFAAFVEKCKKADDDKETC FAEGGKLVAAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQAPFEDHVKL VNEVTEFAKT CVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPEL LFFAKRYKAAFTCCQAAADKAACLL PKLDEL RDEG KASSAKQRLKCA SLQKFGERA FKAWA VARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDS ISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTL EKCCAAADPHECYAKVFFDEFK PLVEEPQNLIKQNCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDDFAAFVEKCKKADDDKETC FAEGGKLVAAASQAALGL</p>
324	-	HALB variant 23	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQAPFEDHVKL VNEVTEFAKT CVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPEL LFFAKRYKAAFTCCQAAADKAACLL PKLDEL RDEG KASSAKQRLKCA SLQKFGERA FKAWA VARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDS ISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTL EKCCAAADPHECYAKVFFDEFK PLVEEPQNLIKQNCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDDFAAFVEKCKKADDDKETC FAEGGPHLVAAASKAALGL</p>
325	-	HALB variant 24	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLOQAPFEDHVKL VNEVTEFAKT CVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKLYE IARRHPYFYAPEL LFFAKRYKAAFTCCQAAADKAACLL PKLDEL RDEG KASSAKQRLKCA SLQKFGERA FKAWA VARLSQRFPAEFAEVSKLVTDLTKVHTECCCHGDLLE CADDRADLAKY ICENQDS ISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTL EKCCAAADPHECYAKVFFDEFK PLVEEPQNLIKQNCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDDKETC FAEGGKLVAAASQAALGL</p>

326	-	HALB variant 25	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPHLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPHLVAASQAALGL</p>
327	-	HALB variant 26	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPHLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPHLVAASQAALGL</p>
328	-	HALB variant 27	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPHLVAASQAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE CADDRADLAKYI CENQDSI SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVWLLRLAKTYETTLEKCCAAADPHECYAKV FDEFK PLVEEPQNLIKQNCELFEQIGEYKFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCCCKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALDVDETYVPKEFNA ETFTFHADICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPHLVAASQAALGL</p>
329	-	HALB variant 28	artificial	<p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYIQQAPFEDHVKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDVMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTTECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFAKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGD LLE</p>

330	-	HALB variant 29	artificial	<p>CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHCEYAKVFDEFK PLVEEPQNLIKQNCLEFQELGEYKFQNALIVRYTKKVPQVSTPTLVEVSRNLKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASKAALGL</p> <p>DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQAPFEDHVKL VNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNL PRLVRPEVDMCTA FHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTCECCQAADKAACLLPKLDEL RDEG KASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECCHGDILLE CADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDV CKNYAEAKDVFLGMFLYEYARRHPDYSVLLLRLLAKTYETTLKCCAAADPHCEYAKVFDEFK PLVEEPQNLIKQNCLEFQELGEYKFQNALIVRYTKKVPQVSTPTLVEVSRNLKVGSKCKKHP EAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNA ETFTFHADICTLSEKERQIKKQATALVELVKHKPKATKEQLKAVMDKFAAFVEKCKKADDKETC FAEEGPKLVAASKAALGL</p>
331	-	Cross body 1 HC	artificial	<p>ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGGPSVFLF PPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYDTTPPVLDSDGSFFLYSDLTVDKSRWQQGNVFC SVMHEAL HNHYTQKSLSLSPGK</p>
332	-	Cross body 1 LC	artificial	<p>GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSN NKYAAASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTVAPTCECSDKTHTCPPCPAPELGGPSV FLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC SVMH EALHNHYTQKSLSLSPGK</p>
333	-	Cross body 2 HC	artificial	<p>ASTKGPSVFFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVTVTPSSNFGTQTYTCNVDDHKPSNTKVDKTVKPKSSDKTHTCPPCPAPEAAGGPSVFLF PPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYDTTPPVLDSDGSFFLYSDLTVDKSRWQQGNVFC SVMHEAL HNHYTQKSLSLSPGK</p>

334	-	Cross body 2 LC	artificial	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAGVETTTTPSKQSN NKYAAASSYLSLTPEQWKSHRSYSQVTHEGSTVEKTVAPTCECSEPKSSDKTHTCPPCPAPEAA GGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNHNAKTKPREEQYN SYRQVYVTLVQHDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRKEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLKSDGSGFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK
335	-	Hetero -Fc binder Fc	artificial	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLKSDGSGFFLYSK LTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK
336	-	Hetero -Fc partne r Fc	artificial	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYDTTTPVLDSDGSGFFLYSD LTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK
337	-	Maxi- body 1 target Fc	artificial	EPKSSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLKSDGSF FLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK
338	-	Maxi- body 1 CD3 Fc	artificial	EPKSSDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYDTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK
339	-	Maxi- body 2 target Fc	artificial	EPKSSDKTHTCPCPAPPEAAGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLKSDGSF FLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK
340	-	Maxi- body 2 CD3 Fc	artificial	EPKSSDKTHTCPCPAPPEAAGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRKEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYDTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK
341	-	Mono Fc	artificial	APPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYDTTTPVLDSDGSGFFLYSDLTVDKSRWQQ

					GNVFSCVMHEALHNHYTQKSLSLSPGK
342	-	CDR-L1 of F6A	artificial		GSSTGAVTSGYYPN
343		CDR-L2 of F6A	artificial		GTKFLAP
344		CDR-L3 of F6A	artificial		ALWYSNRWV
345		CDR-H1 of F6A	artificial		IYAMN
346		CDR-H2 of F6A	artificial		RIRSKYNNYATYYADSVKS
347		CDR-H3 of F6A	artificial		HGNFGNSYVSFFAY
348		VH of F6A	artificial		EVQLVESGGGLVQPGGSLKLSCAASGFTFN IYAMNWVRQAPGKLEWVARIRSKYNNYATYYA DSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGLVTVSS
349		VL of F6A	artificial		QTVVTQEPSTLTVSPGGTTLTSGVQPEDEAEYYCALWYSNRWVFGGGLTKLTVL FSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGLTKLTVL
350		VH-VL of F6A	artificial		EVQLVESGGGLVQPGGSLKLSCAASGFTFN IYAMNWVRQAPGKLEWVARIRSKYNNYATYYA DSVKSRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSFFAYWGQGLVTVSSG GGSGGGGGGGGQTVVTQEPSTLTVSPGGTTLTSGVQPEDEAEYYCALWYSNRWVQKPGQAPRGL IGGTKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCALWYSNRWVFGGGLTKLTVL
351		CDR-L1 of H2C	artificial		GSSTGAVTSGYYPN
352		CDR-L2 of H2C	artificial		GTKFLAP

353		CDR-L3 of H2C	artificial	ALWYSNRWV	
354		CDR-H1 of H2C	artificial	KYAMN	
355		CDR-H2 of H2C	artificial	RIRSKYNNYATYYADSVKD	
356		CDR-H3 of H2C	artificial	HGNFGNSYISYWAY	
357		VH of H2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSS	
358		VL of H2C	artificial	QTVVTQEPSTVSPGGTVTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGTKLTVL	
359		VH-VL of H2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQGLTVTVSSG GGSGGGGGGSGQTAVTQEPSTVSPGGTVTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGTKLTVL	
360		CDR-L1 of H1E	artificial	GSSTGAVTSGYYPN	
361		CDR-L2 of H1E	artificial	GTKFLAP	
362		CDR-L3 of H1E	artificial	ALWYSNRWV	
363		CDR-H1 of H1E	artificial	SYAMN	

364		CDR-H2 of H1E	artificial	RIRSKYNNYATYYADSVKG
365		CDR-H3 of H1E	artificial	HGNFGNSYLSFWAY
366		VH of H1E	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNLIKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGTLLTVSS
367		VL of H1E	artificial	QTVVTQEPSTLVSPGGTVTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
368		VH-VL of H1E	artificial	EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNLIKTEDTAVYYCVRHGNFGNSYLSFWAYWGQGTLLTVSSG GGSGGGGGGGGQTVVTQEPSTLVSPGGTVTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
369		CDR-L1 of G4H	artificial	GSSTGAVTSGYYPN
370		CDR-L2 of G4H	artificial	GTKFLAP
371		CDR-L3 of G4H	artificial	ALWYSNRWV
372		CDR-H1 of G4H	artificial	RYAMN
373		CDR-H2 of G4H	artificial	RIRSKYNNYATYYADSVKG
374		CDR-H3 of G4H	artificial	HGNFGNSYLSYFAY

375		VH of G4H	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGLTVTVSS
376		VL of G4H	artificial	QTVVTQEPSLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
377		VH-VL of G4H	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSYFAYWGQGLTVTVSSG GGSGGGGGGGGQTVVTQEPSLTVSPGGTIVTLTCGSSTGAVTSGYYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
378		CDR-L1 of A2J	artificial	RSSTGAVTSGYYPN
379		CDR-L2 of A2J	artificial	ATDMRPS
380		CDR-L3 of A2J	artificial	ALWYSNRWV
381		CDR-H1 of A2J	artificial	VYAMN
382		CDR-H2 of A2J	artificial	RIRSKYNNYATYYADSVKK
383		CDR-H3 of A2J	artificial	HGNFGNSYLSWYAY
384		VH of A2J	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWYAYWGQGLTVTVSS
385		VL of A2J	artificial	QTVVTQEPSLTVSPGGTIVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
386		VH-VL of A2J	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYLSWYAYWGQGLTVTVSSG GGSGGGGGGGGQTVVTQEPSLTVSPGGTIVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGL

				IGATDMRPSGTPARFSGSLGKGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
387	CDR-L1 of E1L	artificial		GSSTGAVTSGYYPN
388	CDR-L2 of E1L	artificial		GTKFLAP
389	CDR-L3 of E1L	artificial		ALWYSNRWV
390	CDR-H1 of E1L	artificial		KYAMN
391	CDR-H2 of E1L	artificial		RIRSKYNNYATYYADSVKS
392	CDR-H3 of E1L	artificial		HGNFGNSYTSYYAY
393	VH of E1L	artificial		EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPKGLEWVARIRSKYNNYATYYA DSVKSRTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGLTVTVSS
394	VL of E1L	artificial		QTVVTQEPSTLTVSPGGTVTLTCGSSSTGAVTSGYYPNWVQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGKGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
395	VH-VL of E1L	artificial		EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPKGLEWVARIRSKYNNYATYYA DSVKSRTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYTSYYAYWGQGLTVTVSSG GGSGGGGGSGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSSTGAVTSGYYPNWVQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGKGKAAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
396	CDR-L1 of E2M	artificial		RSSTGAVTSGYYPN
397	CDR-L2 of E2M	artificial		ATDMRPS

398	CDR-L3 of E2M	artificial	ALWYSNRWV
399	CDR-H1 of E2M	artificial	GYAMN
400	CDR-H2 of E2M	artificial	RIRSKYNNYATYYADSVKE
401	CDR-H3 of E2M	artificial	HRNFGNSYLSWFAY
402	VH of E2M	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVHRNFGNSYLSWFAYWGQGLTVTVSS
403	VL of E2M	artificial	QTVVTQEPSTLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGLIGATDMRPSGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
404	VH-VL of E2M	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKERFTISRDDSKNTAYLQMNNLKTEDTAVYYCVHRNFGNSYLSWFAYWGQGLTVTVSSG GGSGGGGGGGSGTQVVTQEPSTLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQAPRGL IGATDMRPSGTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
405	CDR-L1 of F7O	artificial	GSSTGAVTSGYYPN
406	CDR-L2 of F7O	artificial	GTKFLAP
407	CDR-L3 of F7O	artificial	ALWYSNRWV
408	CDR-H1 of F7O	artificial	VYAMN

409		CDR-H2 of F70	artificial	RIRSKYNNYATYYADSVKK
410		CDR-H3 of F70	artificial	HGNFGNSYISWWAY
411		VH of F70	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLLTVSS
412		VL of F70	artificial	QTVVTQEPSTLVSPGGTTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
413		VH-VL of F70	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKKRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISWWAYWGQGTLLTVSSG GGSGGGGGGGGQTVVTQEPSTLVSPGGTTLTCGSSSTGAVTSGYYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL
414		CDR-L1 of F12Q	artificial	GSSTGAVTSGNYPN
415		CDR-L2 of F12Q	artificial	GTKFLAP
416		CDR-L3 of F12Q	artificial	VLWYSNRWV
417		CDR-H1 of F12Q	artificial	SYAMN
418		CDR-H2 of F12Q	artificial	RIRSKYNNYATYYADSVKG
419		CDR-H3 of F12Q	artificial	HGNFGNSYVSWWAY

420		VH of F12Q	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGLTVTVSS
421		VL of F12Q	artificial	QTVVTQEPSLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
422		VH-VL of F12Q	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGLTVTVSSG GGSGGGGGGGGQTVVTQEPSLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
423		CDR-L1 of I2C	artificial	GSSTGAVTSGNYPN
424		CDR-L2 of I2C	artificial	GTKFLAP
425		CDR-L3 of I2C	artificial	VLWYSNRWV
426		CDR-H1 of I2C	artificial	KYAMN
427		CDR-H2 of I2C	artificial	RIRSKYNNYATYYADSVKD
428		CDR-H3 of I2C	artificial	HGNFGNSYISYWAY
429		VH of I2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS
430		VL of I2C	artificial	QTVVTQEPSLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
431		VH-VL of I2C	artificial	EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSG GGSGGGGGGGGQTVVTQEPSLTVSPGGTIVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGL

				IGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
432		VH of F12q	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVHRHGFNGSYVSWWAYWGQGLTVTVSS
433		VL of F12q	artificial	QTVVTQEPSTLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPAR FSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
434		VH-VL of F12q	artificial	EVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVHRHGFNGSYVSWWAYWGQGLTVTVSSG GGSGGGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGL IGGTFKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
435		DLL3-4-001 (G44C)	VH	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTAAADTAVYYCASIAVTGFYFDYWGGQGLTVTVSS
436		DLL3-4-001 (G234C)	VL	EIVLTQSPGTLVSLSPGERVTLSCRASQVRVNNNYLAWYQQRPGQAPRLLIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYYCQYDRSPLTFGCGTKLEIK
437		DLL3-4-001 (G44C-G243C)	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTAAADTAVYYCASIAVTGFYFDYWGGQGLTVTVSSGGGGSGGG GSGGGSEIVLTQSPGTLVSLSPGERVTLSCRASQVRVNNNYLAWYQQRPGQAPRLLIYGASSRA TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYDRSPLTFGCGTKLEIK
438		DLL3-4-001 (CC)x12C	bispecific molecule	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGYVYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSSTAAADTAVYYCASIAVTGFYFDYWGGQGLTVTVSSGGGGSGGG GSGGGSEIVLTQSPGTLVSLSPGERVTLSCRASQVRVNNNYLAWYQQRPGQAPRLLIYGASSRA TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYDRSPLTFGCGTKLEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK RFTISRDDSKNTAYLQMNSLKTEDTAVYYCVHRHGFNGSYISWAYWGQGLTVTVSSGGGGSG GGSGGGGSGTQVVTQEPSTLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGG FLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

439		DLL3- 14 - D55E	VH- CDR2	IINPSEGSTSYAQKFQG
440		DLL3- 14 - G56A	VH- CDR2	IINPSDASTSYAQKFQG
441		DLL3- 14 - D171E	VL- CDR1	RSSQSLVYREGNTYLS
442		DLL3- 14 - G172A	VL- CDR1	RSSQSLVYRDANTYLS
443		DLL3- 14 - N173Q	VL- CDR1	RSSQSLVYRDGQTYLS
444		DLL3- 14 - T174A	VL- CDR1	RSSQSLVYRDGNAYLS
445		DLL3- 14 - L43Q	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPSDGSSTSYAQK FQGRVTMTTRDTSNTVTYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
446		DLL3- 14 - D55E	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPSEGSTSYAQK FQGRVTMTTRDTSNTVTYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
447		DLL3- 14 - G56A	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPSDASTSYAQK FQGRVTMTTRDTSNTVTYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
448		DLL3- 14 - L43Q- D55E	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPSEGSTSYAQK FQGRVTMTTRDTSNTVTYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS

449	DLL3-14-L43Q-G56A	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGQGLEWMGIINPSDASTSYAQK FQGRVTMTTRDTSNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
450	DLL3-14-G44C	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
451	DLL3-14-L43Q-G44C	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGQCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
452	DLL3-14-G44C-D55E	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLCLEWMGIINPSEGSTSYAQK FQGRVTMTTRDTSNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
453	DLL3-14-G44C-G56A	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLCLEWMGIINPSDASTSYAQK FQGRVTMTTRDTSNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
454	DLL3-14-L43Q-G44C-D55E	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGQCLEWMGIINPSEGSTSYAQK FQGRVTMTTRDTSNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
455	DLL3-14-L43Q-G44C-G56A	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGQCLEWMGIINPSDASTSYAQK FQGRVTMTTRDTSNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMDVWGQGTITVTVSS
456	DLL3-14-	VL	DVMTQTPLSLPVTLGQPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGGTDFTLKISRVEAEDVGVYYCMQGTHTWPPFTFGQGTKVEIK

		D171E		
457		DLL3-14-G172A	VL	DVVMQTPLSLPVTILGQPASISCRSSQSLVYRDANTYLSWFQQRPQGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPPTFGQGTKVEIK
458		DLL3-14-N173Q	VL	DVVMQTPLSLPVTILGQPASISCRSSQSLVYRDGQTYLSWFQQRPQGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPPTFGQGTKVEIK
459		DLL3-14-T174A	VL	DVVMQTPLSLPVTILGQPASISCRSSQSLVYRDGNAYLSWFQQRPQGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPPTFGQGTKVEIK
460		DLL3-14-G208S	VL	DVVMQTPLSLPVTILGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPPTFGQGTKVEIK
461		DLL3-14-D171E-G208S	VL	DVVMQTPLSLPVTILGQPASISCRSSQSLVYREGNTYLSWFQQRPQGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPPTFGQGTKVEIK
462		DLL3-14-G172A-G208S	VL	DVVMQTPLSLPVTILGQPASISCRSSQSLVYRDANTYLSWFQQRPQGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPPTFGQGTKVEIK
463		DLL3-14-Q243C	VL	DVVMQTPLSLPVTILGQPASISCRSSQSLVYRDGNTYLSWFQQRPQGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPPTFGCGTKVEIK
464		DLL3-14-D171E-Q243C	VL	DVVMQTPLSLPVTILGQPASISCRSSQSLVYREGNTYLSWFQQRPQGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPPTFGCGTKVEIK
465		DLL3-14-G172A-Q243C	VL	DVVMQTPLSLPVTILGQPASISCRSSQSLVYRDANTYLSWFQQRPQGQSPRRLLIYKVSNNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPPTFGCGTKVEIK

466	DLL3-14 - N173Q Q243C	VL	DVVMQTPLSLPVTGLQPASISCRSSQSLVYRDGQTYLSWFQQRPGQSPRRLIYKVSNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVYCMQGTHWPPTFGCGTKVEIK
467	DLL3-14 - T174A-Q243C	VL	DVVMQTPLSLPVTGLQPASISCRSSQSLVYRDGNAYLSWFQQRPGQSPRRLIYKVSNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVYCMQGTHWPPTFGCGTKVEIK
468	DLL3-14 - G208S-Q243C	VL	DVVMQTPLSLPVTGLQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVYCMQGTHWPPTFGCGTKVEIK
469	DLL3-14 - D171E-G208S-Q243C	VL	DVVMQTPLSLPVTGLQPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRRLIYKVSNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVYCMQGTHWPPTFGCGTKVEIK
470	DLL3-14 - G172A - G208S-Q243C	VL	DVVMQTPLSLPVTGLQPASISCRSSQSLVYRDANTYLSWFQQRPGQSPRRLIYKVSNWQSGV PDRFSGGGSGTDFTLKISRVEAEDVGVYCMQGTHWPPTFGCGTKVEIK
471	DLL3-14 -001	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYIMHWVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDPDRFSGGGSGTDFTLKISRVEAEDVGVYCMQGTHWPPTFGQGTKEIK
472	DLL3-14 -002	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYIMHWVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQPASISCRSSQSLVYRDANTYLSWFQQRPGQSPRR LIYKVSNWQSGVDPDRFSGGGSGTDFTLKISRVEAEDVGVYCMQGTHWPPTFGQGTKEIK

473	DLL3-14 -003	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMVWQGGTTTTSVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQGPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTWHPPPTFGQGTKEIK
474	DLL3-14 -004	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMVWQGGTTTTSVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQGPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTWHPPPTFGQGTKEIK
475	DLL3-14 -005	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMVWQGGTTTTSVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQGPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTWHPPPTFGQGTKEIK
476	DLL3-14 -006	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMVWQGGTTTTSVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQGPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTWHPPPTFGQGTKEIK
477	DLL3-14 -007	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLGLEWMGIINPSEGSTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMVWQGGTTTTSVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQGPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTWHPPPTFGQGTKEIK
478	DLL3-14 -008	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLGLEWMGIINPSDASTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMVWQGGTTTTSVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQGPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTWHPPPTFGQGTKEIK
479	DLL3-14 -009	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMVWQGGTTTTSVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQGPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTWHPPPTFGQGTKEIK
480	DLL3-14 -010	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLGLEWMGIINPSEGSTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMVWQGGTTTTSVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQGPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTWHPPPTFGQGTKEIK
481	DLL3-14 -011	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWRQAPGLGLEWMGIINPSDASTSYAQK FQGRVTMTRDTSNTVMYMDLSSLRSEDTAVYICARGNSAFYSYYDMVWQGGTTTTSVSSGGG

482	DLL3-14 -012 (CC)	scFv	GSGGGSGGGSDVVMQTPLSLPVTGLQPASISCRSSQSLVYRDANTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDTLTKISRVEAEDGVYYCMQGTHWPPTFGCGTKVEIK QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHWRQAPGLCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMVWQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTGLQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDTLTKISRVEAEDGVYYCMQGTHWPPTFGCGTKVEIK
483	DLL3-14 -013	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHWRQAPGLCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMVWQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTGLQPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDTLTKISRVEAEDGVYYCMQGTHWPPTFGCGTKVEIK
484	DLL3-14 -014	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHWRQAPGLCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMVWQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTGLQPASISCRSSQSLVYRDANTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDTLTKISRVEAEDGVYYCMQGTHWPPTFGCGTKVEIK
485	DLL3-14 -015	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHWRQAPGLCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMVWQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTGLQPASISCRSSQSLVYRDGQTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDTLTKISRVEAEDGVYYCMQGTHWPPTFGCGTKVEIK
486	DLL3-14 -016	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHWRQAPGLCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMVWQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTGLQPASISCRSSQSLVYRDGNAYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDTLTKISRVEAEDGVYYCMQGTHWPPTFGCGTKVEIK
487	DLL3-14 -017	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHWRQAPGLCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMVWQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTGLQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDTLTKISRVEAEDGVYYCMQGTHWPPTFGCGTKVEIK
488	DLL3-14 -018	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHWRQAPGQCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMVWQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTGLQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDTLTKISRVEAEDGVYYCMQGTHWPPTFGCGTKVEIK
489	DLL3-14 -019	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHWRQAPGLCLEWMGIINPSEGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGGNSAFYSYYDMVWQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTGLQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDTLTKISRVEAEDGVYYCMQGTHWPPTFGCGTKVEIK

490	DLL3-14 -020	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLCLEWMGIINPSDASTSYAQK FQGRVTMTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDTLTKISRVEAEDGVYYCMQGTTHWPPTFGCGTKVEIK
491	DLL3-14 -021	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQCLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDTLTKISRVEAEDGVYYCMQGTTHWPPTFGCGTKVEIK
492	DLL3-14 -022	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQCLEWMGIINPSEGSTSYAQK FQGRVTMTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDTLTKISRVEAEDGVYYCMQGTTHWPPTFGCGTKVEIK
493	DLL3-14 -023	scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQCLEWMGIINPSDASTSYAQK FQGRVTMTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDANTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDTLTKISRVEAEDGVYYCMQGTTHWPPTFGCGTKVEIK
494	DLL3-14 -001 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDTLTKISRVEAEDGVYYCMQGTTHWPPTFGCGTKVEIKSG GGSEVQLVESGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTILVT VSSGGSGGGSGGGGQTIVTQEPISLTVPSTVPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTFKFLAPGTPARFSGSLGGKAALTLGSVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L
495	DLL3-14 -002 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDANTYLSWFQQRPGQSPRR LIYKVSNWQSGVPRDFSGGGSGTDTLTKISRVEAEDGVYYCMQGTTHWPPTFGCGTKVEIKSG GGSEVQLVESGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTILVT VSSGGSGGGSGGGGQTIVTQEPISLTVPSTVPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQA

496	DLL3-14 -003 x12C	bispecific molecule	<p>PRGLIGGTKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYMHVVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTITVT VSSGGSGGGSGGGSGQTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p>
497	DLL3-14 -004 x12C	bispecific molecule	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYMHVVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTITVT VSSGGSGGGSGGGSGQTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p>
498	DLL3-14 -005 x12C	bispecific molecule	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYMHVVRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGNSYISYWAYWGQGTITVT VSSGGSGGGSGGGSGQTVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p>
499	DLL3-14 -006 x12C	bispecific molecule	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYMHVVRQAPGQGLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA</p>

500	DLL3-14-007 x12C	bispecific molecule	<p> TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLVT VSSGGGGGGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTV L </p> <p> QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHVVRQAPGLGLEWMGIINPSEGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYVCARGNSAFYSYYDMDVWGQGTTLTVSSGGG GSGGGGGGGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDGVYYCMQGTHWPTTFGQGTKEIKSG GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLVT VSSGGGGGGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTV L </p>
501	DLL3-14-008 x12C	bispecific molecule	<p> QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHVVRQAPGLGLEWMGIINPDSASTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYVCARGNSAFYSYYDMDVWGQGTTLTVSSGGG GSGGGGGGGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDGVYYCMQGTHWPTTFGQGTKEIKSG GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLVT VSSGGGGGGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTV L </p>
502	DLL3-14-009 x12C	bispecific molecule	<p> QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHVVRQAPGQGLEWMGIINPSDGSSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYVCARGNSAFYSYYDMDVWGQGTTLTVSSGGG GSGGGGGGGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDGVYYCMQGTHWPTTFGQGTKEIKSG GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLVT VSSGGGGGGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTV L </p>
503	DLL3-14-010 x12C	bispecific molecule	<p> QVQLVQSGAEVKKPGASVKVSCKASGYFTFTNYYMHVVRQAPGQGLEWMGIINPSEGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYVCARGNSAFYSYYDMDVWGQGTTLTVSSGGG GSGGGGGGGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRR </p>

504	DLL3-14-011 x12C	bispecific molecule	LIYKVSNWQSGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQGTHWPPTFGQGTKEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTLLTVSSGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
505	DLL3-14-012 (CC) x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLCLEWMGIINPSDGSTSYAQKFQGRVTMTTRDTSNTVYMDLSSLRSEDTAVYVCARGGNSAFYSYYDMVDWVGQGTITVSSGGGGGGGGGGSDVVMQTPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQGTHWPPTFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTLLTVSSGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
506	DLL3-14-013 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLCLEWMGIINPSDGSTSYAQKFQGRVTMTTRDTSNTVYMDLSSLRSEDTAVYVCARGGNSAFYSYYDMVDWVGQGTITVSSGGGGGGGGGGSDVVMQTPLSLPVTLGQPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRRLIYKVSNWQSGVPDRFSGSGGTDFTLKISRVEAEDVGYYCMQGTHWPPTFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTLLTVSSGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

507	DLL3-14 -014 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLCLEWMGIINPSDGSSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGCGTKVEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTITV VSSGGSGGGSGGGSGGTQVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L
508	DLL3-14 -015 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLCLEWMGIINPSDGSSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGCGTKVEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTITV VSSGGSGGGSGGGSGGTQVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L
509	DLL3-14 -016 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLCLEWMGIINPSDGSSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGCGTKVEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTITV VSSGGSGGGSGGGSGGTQVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L
510	DLL3-14 -017 x12C	bispecific molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGLCLEWMGIINPSDGSSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTQPLSLPVTGLQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGCGTKVEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQGTITV VSSGGSGGGSGGGSGGTQVVTQEPSTLTVSPGGTTLTLCGSSTGAVTSGNYPNWVQKPGQA

511	DLL3-14 -018 x12C	bispecific molecule	<p>PRGLIGGTKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p> <p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGCLLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGCGTKVEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITV VSSGGSGGGSGGGSGTQVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p>
512	DLL3-14 -019 x12C	bispecific molecule	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGCLLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGCGTKVEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITV VSSGGSGGGSGGGSGTQVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p>
513	DLL3-14 -020 x12C	bispecific molecule	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGCLLEWMGIINPSDASTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGCGTKVEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTITV VSSGGSGGGSGGGSGTQVVTQEPSTLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPGQA PRGLIGGTKFLAPGTPARFSGSLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV L</p>
514	DLL3-14 -021 x12C	bispecific molecule	<p>QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGCLLEWMGIINPSDGSTSYAQK FQGRVTMTRDTSNTVYMDLSSLRSEDTAVYYCARGNSAFYSYYDMVWGQGTITVTVSSGGG GGGGSGGGSDVVMQTQPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVYCMQGTTHWPTFGCGTKVEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA</p>

515	DLL3-14 -022 x12C	bispecific molecule	<p> TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLVT VSSGGGGGGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTFKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTV L </p> <p> QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHVVRQAPGQCLEWMGIINPSEGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYICARGNSAFYSYDMDVWGQGTTLTVSSGGG GSGGGGGGGGGGGGGGGGGTQPLSLPVTGLQGPASISCRSSQSLVYREGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGSGGTDFTLKISRVEAEDGVYCMQGTHWPTFGCGTKVEIKSG GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLVT VSSGGGGGGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTFKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTV L </p>
516	DLL3-14 -023 x12C	bispecific molecule	<p> QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHVVRQAPGQCLEWMGIINPDSASTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYICARGNSAFYSYDMDVWGQGTTLTVSSGGG GSGGGGGGGGGGGGGGGGGTQPLSLPVTGLQGPASISCRSSQSLVYRDANTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGSGGTDFTLKISRVEAEDGVYCMQGTHWPTFGCGTKVEIKSG GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLVT VSSGGGGGGGGGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTFKFLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTV L </p>
517	DLL3-4 x12C -scFc	bispecific c HLE molecule	<p> QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYVYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYICASIATGTFYFDYWGQGTTLTVSSGGGGGGGG GSGGGGSEIVLTQSPGTLSPGERVTLSCRASQVRNNNYLAWYQQRPQAPRLLIYGASSRA TGI PDRFSGSGGTDFTLTISRLEPEDFAVYCCQYDRSPLTFGGGKLEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTTLTVSSGGGGSG GGGGGGGGGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGK FLAPGTPARFSGSLGGKAAATLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYIT </p>

				LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGSGGGSGGGSGGGSGGGSGGGSGGGG SDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTTLPSSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
518	DLL3- 4 xI2C - scFc_d elGK	bispecific c HLE molecule	QVQLQESGPGLVKPSETLSLTCTVSGGISISSYYWSWIRQPPGKGLEWIGYVYYSGTTNYPNSL KSRVTISVDTSKNQFSLKLSVTAADTA VYCASIAVTGYFDYWGGTLVTVSSGGSGGGG GSGGGSEIVLTQSPGTLSLSPGERVTLSCRASQRVNNNYLAWYQORPGQAPRLLIYGASSRA TGIPDRFGSGSGTDFTLTI SRLEPEDFAVYCYCQYDRSPLTFGGGTKLEIKSGGGSEVQLV ESGGGLVPGGSLKLSCAAAGFTFNKYAMNWVRQAPGKGLEVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISWAYWGQGTLLTVSSGGGGSG GGSGGGGSQT VVTQEPSSLTVSPGGTVTLCGSSSTGAVTSIGNYPNWVQOKPGQAPRGLIGGTK FLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTH TCPGPCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGSGGGSGGGSGGGSGGGSGGGSGGGSD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQ VYTTLPSSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	
519	DLL3- 4-001 (CC) xI2C - scFc	bispecific c HLE molecule	QVQLQESGPGLVKPSETLSLTCTVSGGISISSYYWSWIRQPPGKCLEWIGYVYYSGTTNYPNSL KSRVTISVDTSKNQFSLKLSVTAADTA VYCASIAVTGYFDYWGGTLVTVSSGGSGGGG GSGGGSEIVLTQSPGTLSLSPGERVTLSCRASQRVNNNYLAWYQORPGQAPRLLIYGASSRA TGIPDRFGSGSGTDFTLTI SRLEPEDFAVYCYCQYDRSPLTFGCGTKLEIKSGGGSEVQLV ESGGGLVPGGSLKLSCAAAGFTFNKYAMNWVRQAPGKGLEVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISWAYWGQGTLLTVSSGGGGSG GGSGGGGSQT VVTQEPSSLTVSPGGTVTLCGSSSTGAVTSIGNYPNWVQOKPGQAPRGLIGGTK FLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCYVLWYSNRWVFGGGTKLTVLGGGGDKTH TCPGPCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWOOGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGG	

520	DLL3-4-001 (CC) x12C -scFc₋delG₋K	bispecific c HLE molecule	<p>SDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKCLEWIGVYYSGTTNYPNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCASIAVTGFYFDYWGQGLTIVTVSSGGSGGGGSGGGGSEIVLTQSPGTLSPGERVTLSCRASQRVNNYLAWYQQRPQGAPRLLIYGASSRATGIPDRFSGSGGTDFTLTIISRLPEPDFAVYYCQYDRSPLTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTIVTVSSGGGSGGGSGGGSQTVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p> <p>QVQLQESGPGLVKPSETLSLTCTVSGASISFFYWSWIRQPPGKLEWIGIYYSGTTNYPNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARIAGFFFDYWGQGLTIVTVSSGGSGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTIISRLPEPDFAVYYCQYDRSPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTIVTVSSGGGSGGGSGGGSQTVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>
521	DLL3-6 x12C -scFc	bispecific c HLE molecule	<p>QVQLQESGPGLVKPSETLSLTCTVSGASISFFYWSWIRQPPGKLEWIGIYYSGTTNYPNPSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARIAGFFFDYWGQGLTIVTVSSGGSGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTIISRLPEPDFAVYYCQYDRSPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFGNSYISYWAYWGQGLTIVTVSSGGGSGGGSGGGSQTVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK</p>

522	DLL3- 6 xI2C - scFc_d eIGK	bispecifi c HLE molecule	PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYFSWIRQPPGKGLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGFFFDYWGQGLTVTVSSGGGGSGGG GGGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTIISRLPEPEFAVYYCQYDRSPLTFGGGTKEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSG GGGGGGSGTAVTQEPSTLTVSPGGTTLTTCGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTK FLAPGTPARFSGSLIGGKAALTLTSGVQPEDEAEYCYVLWYSNRWVFGGGLTKLTVLGGGDKTH TCPGPCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGSD KTHTCPCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKL TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
523	DLL3- 6-001 (CC) xI2C - scFc	bispecifi c HLE molecule	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYFSWIRQPPGKCLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGFFFDYWGQGLTVTVSSGGGGSGGG GGGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDFTLTIISRLPEPEFAVYYCQYDRSPLTFGGGTKEIKSGGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSG GGGGGGSGTAVTQEPSTLTVSPGGTTLTTCGSTGAVTSGNYPNWVQQKPGQAPRGLIGGTK FLAPGTPARFSGSLIGGKAALTLTSGVQPEDEAEYCYVLWYSNRWVFGGGLTKLTVLGGGDKTH TCPGPCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVD KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYS KLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

524	DLL3-6-001 (CC) x12C - scFc_d elGK	bispecific HLE molecule	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKCLEWIGIYIYSGTTNYPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGFFFDYWGQGLTVTVSSGGGGGGG GSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGI PDRFSGSGGTDFTLTI SRLEPEDFAVYCCQYDRSPLTFGCGTKVEIKSGGGSEVQLV ESGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGLTVTVSSGGGGSG GSGGGGGQTVTQEPSTLTVSPGGTVTLTCGSTGAVTSGNYPNWVQQKPGQAPRGLIGTK FLAPGTPARFSGSLGGAALTL SGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK KTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK
525	DLL3-14 x12C - scFc	bispecific HLE molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFNYYMHWRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVMTQTPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVPDRFSGGGSGTDFTLKISRVEAEDVGYVCMQGTHTWPTTFGQGTKEIKSG GGGSEVQLVESGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGSYISYWAYWGQGLTVT VSSGGGGSGGGSGGGQTVTQEPSTLTVSPGGTVTLTCGSTGAVTSGNYPNWVQQKPGQA PRGLIGGTFKFLAPGTPARFSGSLGGAALTL SGVQPEDEAEYCVLWYSNRWVFGGGTKLTV LGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSG GGGSGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT I SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK
526	DLL3-14	bispecific HLE molecule	QVQLVQSGAEVKKPGASVKVSCKASGYTFNYYMHWRQAPGLGLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYYCARGNSAFYSYDMDVWGQGTITVTVSSGGG

		x12C - scFc_d elGK	molecule	GSGGGSGGGSDVVMQTPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDFTLKISRVEAEDVGYVCMQGTHWPPTFGQGTKEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTLV VSSGGSGGGGGGSGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKPGQA PRGLIGGKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCVLWYSNRWVFGGKTLTV LGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGSGGGGGSGGGGGSGGGGG GGGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISK AKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
527		DLL3- 14 -012 (CC) x12C - scFc	bispecific c HLE molecule	QVQLVQSGAEVKKPGASVKVSCKASGYFTFNYYMHVVRQAPGLCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYVCARGNSAFYSYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDFTLKISRVEAEDVGYVCMQGTHWPPTFGCGTKEIKSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNGFNSYISYWAYWGQGTLV VSSGGSGGGGGGSGTQVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKPGQA PRGLIGGKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYCVLWYSNRWVFGGKTLTV LGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGSGGGGGSGGGGG GGGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT ISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
528		DLL3- 14 -012 (CC) x12C-	bispecific c HLE molecule	QVQLVQSGAEVKKPGASVKVSCKASGYFTFNYYMHVVRQAPGLCLEWMGIINPSDGSTSYAQK FQGRVTMTTRDTSTNTVYMDLSSLRSEDTAVYVCARGNSAFYSYDMDVWGQGTITVTVSSGGG GSGGGSGGGSDVVMQTPLSLPVTLGQPASISCRSSQSLVYRDGNTYLSWFQQRPGQSPRR LIYKVSNWQSGVDRFSGGGSGTDFTLKISRVEAEDVGYVCMQGTHWPPTFGCGTKEIKSG

			GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYA TYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVT VSSGGSGGGGGGSGTQVVTQEPSTLVSPPGTVTLTCGSGTGAVTSGNYPNWWQKPGQA PRLIGGTFKFLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTV LGGGDKTHTCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGGGGGGGGGGGGGG GGGGGSDKTHTCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
529	DLL3- 6-001 (CC)	VH	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKCLEWIGIYIYSGTTNPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGAGFFFDYWGQGLTVTVSS
530	DLL3- 6-001 (CC)	VL	EIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF SGSGSGTDFTLTISRLEPEDFAVYYCQQYDRSPLTFGCGTKVEIK
531	DLL3- 6-001 (CC)	scFv	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKCLEWIGIYIYSGTTNPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGAGFFFDYWGQGLTVTVSSGGGGGG GSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYDRSPLTFGCGTKVEIK
532	DLL3- 6-001 (CC) x12C	bispecific molecule	QVQLQESGPGLVKPSSETLSLTCTVSGASISSFYWSWIRQPPGKCLEWIGIYIYSGTTNPNPSL KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARIAGAGFFFDYWGQGLTVTVSSGGGGGG GSGGGSEIVLTQSPGTLSPGERATLSCRASQSVNKNYLAWYQQKPGQAPRLLIYGASSRA TGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYDRSPLTFGCGTKVEIKSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGGSG GGSGGGSGTQVVTQEPSTLVSPPGTVTLTCGSGTGAVTSGNYPNWWQKPGQAPRGLIGGTK FLAPGTPARFSGSLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

533	Fc monom er-1 +c/-g	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQOGNVFSCSVMHREALHNHYTQKSLSLSPGK
534	Fc monom er-2 +c/-g/ delGK	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQOGNVFSCSVMHREALHNHYTQKSLSLSP
535	Fc monom er-3 -c/+g	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQOGNVFSCSVMHREALHNHYTQKSLSLSPGK
536	Fc monom er-4 -c/+g/ delGK	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQOGNVFSCSVMHREALHNHYTQKSLSLSP
537	Fc monom er-5 -c/-g	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQOGNVFSCSVMHREALHNHYTQKSLSLSPGK
538	Fc monom er-6 -c/-g/ delGK	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQOGNVFSCSVMHREALHNHYTQKSLSLSP
539	Fc monom er-7 +c/+g	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQOGNVFSCSVMHREALHNHYTQKSLSLSPGK
540	Fc monom	DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP

	er-8 +c/+g/ delGK		QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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542	scFc-2		DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
543	scFc-3		DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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			YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP
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546	scFc-6		DKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP
547	scFc-7		DKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSF FLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
548	scFc-8		DKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSFFLYSK LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSFFL YKSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP

549		(G ₄ S) ₄ linker			GGGSGGGSGGGSGGGGS
550		(G ₄ S) ₅ linker			GGGSGGGSGGGSGGGSGGGGS
551		(G ₄ S) ₆ linker			GGGSGGGSGGGSGGGSGGGSGGGGS
552		(G ₄ S) ₇ linker			GGGSGGGSGGGSGGGSGGGSGGGSGGGGS
553		(G ₄ S) ₈ linker			GGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGGS
554		DLL3- 22	bispecific molecule		QVQLQESGPGLVKPSSETLSLTCTVSGDSISYYW ^{WT} WIRQPPGKGLEWIGYIYYSGTTNYPNPSLKSRVTISVDTSKS QFSLKLSVTAADTA ^Y Y ^C ASIAVRGFFFDYWGQGT ^{LV} TVSSGGSGGGSGGGSEIVLTQSPGTLSLSPGERA TLSCRASQSVSSSYLA ^W YQQKPGQAPRI ^{LI} YGASTRATGIPDRFSGSGGTDT ^{FTLT} ISRLEPEDFA ^V Y ^C QQYGT ^S PLT ^{FT} GGGT ^{KVE} IKRSGGGSEVQ ^{LV} ESGGGLVQPGGSLKLSCAASG ^{FT} FNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMN ^N LKTEDTA ^V Y ^C VRHGNFGNSYISYWAYWGQGT ^{LV} TVSSGGSGGG GGSGGGSGQTVVTQEP ^{SL} TVSPGGTV ^{LT} TCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG ^{TK} FLAPGTPARFSGSL LGKKAALTLSGVQPEDEAEY ^C VLWYSNRWVFGGT ^{TKLT} VLHHHHHH

SEQUENCE LISTING

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<150> US 62/199,930

<151> 2015-07-31

<150> US 62/290,896

<151> 2016-02-03

<160> 554

<170> PatentIn version 3.5

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Arg Ser Ser Gln Ser Leu Leu His Ser Asp Gly Tyr Asn Tyr Leu Asp
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Leu Gly Ser Asn Arg Ala Ser
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Met Gln Ala Leu Gln Thr Pro Leu Thr
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr His Gly Ser Asn Lys Tyr Tyr Ala Arg Ser Val
50 55 60

Lys 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 Arg Glu Ile Pro Phe Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp 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 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

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

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<400> 9

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Ser Gly Arg
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr His Gly Ser Asn Lys Tyr Tyr Ala Arg Ser Val
50 55 60

Lys 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 Arg Glu Ile Pro Phe Gly Met Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro
130 135 140

Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
145 150 155 160

Leu Leu His Ser Asp Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys
165 170 175

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
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Cys Met Gln Ala Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
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 Ser Gly Arg
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr His Gly Ser Asn Lys Tyr Tyr Ala Arg Ser Val
 50 55 60

Lys 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 Arg Glu Ile Pro Phe Gly Met Asp Val Trp Gly Gln Gly Thr Thr
 100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 115 120 125

Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 130 135 140

Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 145 150 155 160

Leu Leu His Ser Asp Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys
 165 170 175

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
 180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 195 200 205

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

Cys Met Gln Ala Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 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

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Gly Tyr Tyr Met His
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1 5 10 15

Gly

<210> 13
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 13

Asp Ala Asn Ile Ala Ala Leu Asp Ala Phe Glu Ile
1 5 10

<210> 14
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<400> 14

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

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Ala Ala Ser Ser Leu Gln Ser
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<210> 16
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<212> PRT
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<400> 16

Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1 5

<210> 17
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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 Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Asn Ile Ala Ala Leu Asp Ala Phe Glu Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

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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

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Asn Ile Ala Ala Leu Asp Ala Phe Glu Ile Trp Gly
100 105 110

Gln Gly Thr Met 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 Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 20
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 20

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 Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Asn Ile Ala Ala Leu Asp Ala Phe Glu Ile Trp Gly
100 105 110

Gln Gly Thr Met 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 Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 210 215 220

Gln Gln Ser Tyr Ser Thr Pro Leu 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> 21
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 21

Ser Tyr Gly Met His
1 5

<210> 22
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 22

Val Ile Ser Tyr His Gly Arg Asp Thr Tyr Tyr Ala Arg Ser Val Lys
1 5 10 15

Gly

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 23

Asp Gly Ala Thr Val Thr Ser Tyr Tyr Tyr Ser Gly Met Asp Val
1 5 10 15

<210> 24
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 24

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala
1 5 10

<210> 25
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 25

Leu Ala Ser Ser Leu Gln Ser
1 5

<210> 26
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 26

Gln Gln Tyr Asn Phe Tyr Pro Phe Thr
1 5

<210> 27
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 27

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 His Gly Arg Asp Thr Tyr Tyr Ala Arg Ser Val
 50 55 60

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

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Gly Ala Thr Val Thr Ser Tyr Tyr Tyr Ser Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Lys
 115 120 125

<210> 28
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 28

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

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 29
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 29

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 His Gly Arg Asp Thr Tyr Tyr Ala Arg Ser Val
 50 55 60

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

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ala Thr Val Thr Ser Tyr Tyr Tyr Ser 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 Gly Ile Ser Asn Tyr Leu Ala Trp Phe Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile Tyr Leu Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly Ser 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 Tyr Asn Phe Tyr Pro Phe Thr Phe Gly Pro Gly
225 230 235 240

Thr Lys Val Asp Ile Lys
245

<210> 30

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 30

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 His Gly Arg Asp Thr Tyr Tyr Ala Arg Ser Val
50 55 60

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

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ala Thr Val Thr Ser Tyr Tyr Tyr Ser 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 Gly Ile Ser Asn Tyr Leu Ala Trp Phe Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile Tyr Leu Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly Ser 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 Tyr Asn Phe Tyr Pro Phe Thr Phe Gly Pro Gly
 225 230 235 240

Thr Lys Val Asp 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> 31
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 31

Ser Tyr Tyr Trp Ser
1 5

<210> 32
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 32

Tyr Val Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 33
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 33

Ile Ala Val Thr Gly Phe Tyr Phe Asp Tyr
1 5 10

<210> 34
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 34

Arg Ala Ser Gln Arg Val Asn Asn Asn Tyr Leu Ala
1 5 10

<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 35

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 36
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 36

Gln Gln Tyr Asp Arg Ser Pro Leu Thr
1 5

<210> 37
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 37

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 Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

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

Leu Val Thr Val Ser Ser
115

<210> 38
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 38

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Asn Asn Asn
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg 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 Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 39
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 39

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 Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Ser
115 120 125

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys

<210> 40
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 40

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 Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
 210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
 275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
 290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

<210> 41
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 41

Ser Tyr Tyr Trp Ser
1 5

<210> 42
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 42

Tyr Ile Tyr Tyr Ser Gly Arg Thr Asn Tyr Tyr Pro Ser Leu Lys Ser
1 5 10 15

<210> 43
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 43

Ile Ala Val Ala Gly Phe Phe Phe Asp Tyr
1 5 10

<210> 44

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 44

Arg Ala Ser Gln Ser Val Asn Lys Asn Tyr Leu Ala
1 5 10

<210> 45

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 45

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 46

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 46

Gln Gln Tyr Asp Arg Ser Pro Leu Thr
1 5

<210> 47

<211> 118

<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 Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Arg Thr Asn Tyr Tyr Pro Ser Leu Lys
50 55 60

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

Leu Val Thr Val Ser Ser
115

<210> 48

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 48

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 Asn Lys 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 Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 49
<211> 241
<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 Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Arg Thr Asn Tyr Tyr Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Ile 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 Ile Ala Val Ala Gly Phe Phe 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 Ser
115 120 125

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys

<210> 50

<211> 496

<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 Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Arg Thr Asn Tyr Tyr Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Ile 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 51
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 51

Ser Phe Tyr Trp Ser
 1 5

<210> 52
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 52

Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn 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

Ile Ala Val Ala Gly Phe Phe Phe Asp Tyr
 1 5 10

<210> 54
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 54

Arg Ala Ser Gln Ser Val Asn Lys Asn Tyr Leu Ala
1 5 10

<210> 55
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 55

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 56
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 56

Gln Gln Tyr Asp Arg Ser Pro Leu Thr
1 5

<210> 57
<211> 118
<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 Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Phe
20 25 30

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

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

Leu Val Thr Val Ser Ser
115

<210> 58
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 58

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 Asn Lys 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 Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 59
<211> 241
<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 Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 60
<211> 496
<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 Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

<210> 61
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 61

Ser Phe Tyr Trp Ser
1 5

<210> 62
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 62

Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 63
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 63

Ile Ala Val Ala Gly Phe Phe Phe Asp Tyr
1 5 10

<210> 64
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 64

Arg Ala Ser Gln Ser Val Asn Lys Asn Tyr Leu Ala
1 5 10

<210> 65

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 65

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 66

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 66

Gln Gln Tyr Asp Arg Ser Pro Leu Thr
1 5

<210> 67

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 67

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

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

Leu Val Thr Val Ser Ser
115

<210> 68
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 68

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 Asn Lys 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 Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 69
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 69

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
 180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
 210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 225 230 235 240

Lys

<210> 70
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 70

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 Ala Ser Ile Ser Ser Phe
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
 290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 71
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 71

Ser Phe Tyr Trp Ser
1 5

<210> 72
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 72

Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 73
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 73

Ile Ala Val Ala Gly Phe Phe Phe Asp Tyr
1 5 10

<210> 74
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 74

Arg Ala Ser Gln Ser Val Asn Lys Asn Tyr Leu Ala
1 5 10

<210> 75
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 75

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 76
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 76

Gln Gln Tyr Asp Arg Ser Pro Leu Thr
1 5

<210> 77
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 77

Gln Val Gln Leu Gln Glu Trp Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

Leu Val Thr Val Ser Ser Lys
115

<210> 78

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 78

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 Asn Lys 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 Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 79
 <211> 241
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 79

Gln Val Gln Leu Gln Glu Trp Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Phe
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

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

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile
225 230 235 240

Lys

<210> 80
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 80

Gln Val Gln Leu Gln Glu Trp Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 81

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 81

Ser Phe Tyr Trp Ser
1 5

<210> 82

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 82

Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 83

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 83

Ile Ala Val Ala Gly Phe Phe Phe Asp Tyr
1 5 10

<210> 84

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 84

Arg Ala Ser Gln Ser Val Asn Lys Asn Tyr Leu Ala
1 5 10

<210> 85

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 85

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 86

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 86

Gln Gln Tyr Asp Arg Ser Pro Leu Thr
1 5

<210> 87

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 87

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

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

Leu Val Thr Val Ser Ser
115

<210> 88
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 88

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Lys 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 Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 89
<211> 241
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 89

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
225 230 235 240

Lys

<210> 90
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 90

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
 130 135 140

Ser Leu Ser Pro Gly Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
 180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
 210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
 225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
 275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
 290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 91
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 91

Ser 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 Asn Gly Ile Thr Asn 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

Ile His Ser Gly Ser Phe Ser Phe Asp Tyr
1 5 10

<210> 94
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 94

Arg Ala Ser Gln Ser Val Ser Arg Gly Tyr Leu Ala
1 5 10

<210> 95
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 95

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 96

Gln Gln Tyr Asp Thr Ser Pro Ile Thr
1 5

<210> 97
<211> 118
<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 Gly Ser Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Ile Phe Tyr Asn Gly Ile Thr Asn Tyr 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 Ser Ser Val Thr Ala Ala Asp Thr Ala Lys Tyr Tyr Cys Ala
85 90 95

Arg Ile His Ser Gly Ser Phe Ser Phe Asp Tyr Trp Asp Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 98
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 98

Glu Ile Val Met 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 Arg Gly
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 Asp 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 Asp Thr Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 99
<211> 241
<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 Gly Ser Ile Ser Ser Tyr
 20 25 30

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

Gly Tyr Ile Phe Tyr Asn Gly Ile Thr Asn Tyr 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 Ser Ser Val Thr Ala Ala Asp Thr Ala Lys Tyr Tyr Cys Ala
 85 90 95

Arg Ile His Ser Gly Ser Phe Ser Phe Asp Tyr Trp Asp 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 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu
 130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Ser Val Ser Arg Gly Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
 210 215 220

Tyr Asp Thr Ser Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 225 230 235 240

Lys

<210> 100
 <211> 496
 <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 Gly Ser Ile Ser Ser Tyr
 20 25 30

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

Gly Tyr Ile Phe Tyr Asn Gly Ile Thr Asn Tyr 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 Ser Ser Val Thr Ala Ala Asp Thr Ala Lys Tyr Tyr Cys Ala
 85 90 95

Arg Ile His Ser Gly Ser Phe Ser Phe Asp Tyr Trp Asp 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 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu
 130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Ser Arg Gly Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Thr Ser Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 101
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 101

Asn Ala Gly Met Ser
 1 5

<210> 102
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 102

Arg Ile Lys Asn Lys Ile Asp Gly Gly Thr Thr Asp Phe Ala Ala Pro
1 5 10 15

Val Lys Gly

<210> 103

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 103

Arg Gly Trp Tyr Gly Asp Tyr Phe Asp Tyr
1 5 10

<210> 104

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 104

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 105

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 105

Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 106
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 106

Met Gln Ala Leu Gln Thr Pro Phe Thr
1 5

<210> 107
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 107

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 Ile Phe Asn Asn Ala
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Arg Ile Lys Asn Lys Ile Asp Gly Gly Thr Thr Asp Phe Ala Ala
50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Ala Arg Gly Trp Tyr Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 108
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 108

Asp Ile Val Met Thr Gln Thr 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 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Met Gln Ala
 85 90 95

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

<210> 109
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 109

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 Ile Phe Asn Asn Ala
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Arg Ile Lys Asn Lys Ile Asp Gly Gly Thr Thr Asp Phe Ala Ala
50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Ala Arg Gly Trp Tyr Gly Asp Tyr 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 Val Met Thr Gln Thr Pro
130 135 140

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

Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp
165 170 175

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly
180 185 190

Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
195 200 205

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

Gly Ile Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly
 225 230 235 240

Pro Gly Thr Lys Val Glu Ile Lys
 245

<210> 110
 <211> 503
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 110

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 Ile Phe Asn Asn Ala
 20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Gly Arg Ile Lys Asn Lys Ile Asp Gly Gly Thr Thr Asp Phe Ala Ala
 50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
 85 90 95

Tyr Cys Thr Ala Arg Gly Trp Tyr Gly Asp Tyr 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 Val Met Thr Gln Thr Pro
 130 135 140

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

Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp
 165 170 175

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly
 180 185 190

Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
 195 200 205

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

Gly Ile Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly
 225 230 235 240

Pro Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val
 245 250 255

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 260 265 270

Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met
 275 280 285

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
 290 295 300

Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val
 305 310 315 320

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
 325 330 335

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

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
 355 360 365

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln
 385 390 395 400

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
 405 410 415

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
 420 425 430

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

Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
 450 455 460

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
 465 470 475 480

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
 485 490 495

Gly Thr Lys Leu Thr Val Leu
 500

<210> 111
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 111

Ser Tyr Asp Ile His
 1 5

<210> 112
 <211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 112

Val	Ile	Ser	Ser	His	Gly	Ser	Asn	Lys	Asn	Tyr	Ala	Arg	Ser	Val	Lys
1				5					10					15	

Gly

<210> 113
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 113

Asp	Gly	Tyr	Ser	Gly	Asn	Asp	Pro	Phe	Tyr	Tyr	Tyr	Tyr	His	Gly	Met
1				5					10					15	

Asp Val

<210> 114
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 114

Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn
1				5					10	

<210> 115
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 115

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 116

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 116

Gln Gln Ser Phe Thr Thr Pro Leu Thr
1 5

<210> 117

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 117

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 Ser Phe Ser Ser Tyr
20 25 30

Asp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Ser His Gly Ser Asn Lys Asn Tyr Ala Arg Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ser Gly Asn Asp Pro Phe Tyr Tyr Tyr Tyr His
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<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 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 Ser Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Thr Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 119
<211> 249
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 119

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 Ser Phe Ser Ser Tyr
20 25 30

Asp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Ser His Gly Ser Asn Lys Asn Tyr Ala Arg Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ser Gly Asn Asp Pro Phe Tyr Tyr Tyr Tyr His
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
130 135 140

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

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
180 185 190

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 210 215 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Thr Thr Pro Leu Thr Phe
 225 230 235 240

Gly Gly Gly Thr Lys Val Glu Ile Lys
 245

<210> 120
 <211> 504
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 120

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 Ser Phe Ser Ser Tyr
 20 25 30

Asp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Ser His Gly Ser Asn Lys Asn Tyr Ala Arg Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Gly Tyr Ser Gly Asn Asp Pro Phe Tyr Tyr Tyr Tyr His
 100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
130 135 140

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

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
180 185 190

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
210 215 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Thr Thr Pro Leu Thr Phe
225 230 235 240

Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu
245 250 255

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
260 265 270

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
275 280 285

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
290 295 300

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
305 310 315 320

Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala
325 330 335

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

Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala
355 360 365

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr
385 390 395 400

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
405 410 415

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
420 425 430

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

Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
450 455 460

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
465 470 475 480

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
485 490 495

Gly Gly Thr Lys Leu Thr Val Leu
500

<210> 121
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 121

Ser Tyr Tyr Met His
1 5

<210> 122
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 122

Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Asn Phe Gln
1 5 10 15

Gly

<210> 123
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 123

Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
1 5 10

<210> 124
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 124

Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Asn Thr Tyr Leu Ser
1 5 10 15

<210> 125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 125

Lys Val Ser Asn Trp Gln Ser
1 5

<210> 126

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 126

Met Gln Gly Thr His Trp Pro Pro Thr
1 5

<210> 127

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 127

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

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 128
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 128

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 129
<211> 250
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 129

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

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 130
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 130

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

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 131
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 131

Asn Tyr Tyr Met His
1 5

<210> 132

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 132

Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 133

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 133

Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
1 5 10

<210> 134

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 134

Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Asn Thr Tyr Leu Ser
1 5 10 15

<210> 135

<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 135

Lys Val Ser Asn Trp Gln Ser
1 5

<210> 136
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 136

Met Gln Gly Thr His Trp Pro Pro Thr
1 5

<210> 137
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 137

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 138
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 138

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 139
<211> 250

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 139

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 140
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 140

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 141

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 141

Gly Tyr Tyr Ile His
1 5

<210> 142

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 142

Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Gly Gln Asn Phe Gln
1 5 10 15

Gly

<210> 143

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 143

Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
1 5 10

<210> 144

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 144

Arg Ser Ser Gln Ser Leu Ala Tyr Arg Asp Gly Asn Thr Tyr Leu Ser
1 5 10 15

<210> 145
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 145

Lys Val Ser Asn Trp Gln Ser
1 5

<210> 146
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 146

Met Gln Gly Thr His Trp Pro Pro Thr
1 5

<210> 147
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 147

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 Gly Tyr
20 25 30

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

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Gly Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 148
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 148

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Ala Tyr Arg
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 149
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 149

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 Gly Tyr
 20 25 30

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

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Gly Gln Asn Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
 130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
 145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Ala Tyr Arg Asp Gly Asn Thr Tyr Leu
 165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 150
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 150

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 Gly Tyr
20 25 30

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

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Gly Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Ala Tyr Arg Asp Gly Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 151
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 151

Gly His Tyr Met His
1 5

<210> 152

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 152

Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 153

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 153

Gly Thr Thr Val Val His Tyr Ser Tyr Tyr Asp Met Asp Val
1 5 10

<210> 154

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 154

Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Asn Thr Tyr Leu Thr
1 5 10 15

<210> 155
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 155

Lys Val Ser Asn Trp Gln Ser
 1 5

<210> 156
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 156

Met Gln Gly Thr His Trp Pro Pro Thr
 1 5

<210> 157
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 157

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 Gly His
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Gly Thr Thr Val Val His Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 158
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 158

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Asn Thr Tyr Leu Thr Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly 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

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 159
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 159

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 Gly His
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Thr Arg Gly Thr Thr Val Val His Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
 130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
 145 150 155 160

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

Thr Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 160
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 160

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 Gly His
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Gly Thr Thr Val Val His Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Thr Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
 500 505

<210> 161
 <211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 161

Asn Tyr Phe Met His
1 5

<210> 162
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 162

Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Asn Phe Gln
1 5 10 15

Gly

<210> 163
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 163

Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
1 5 10

<210> 164
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 164

Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Asn Thr Tyr Leu Ser
 1 5 10 15

<210> 165
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 165

Arg Val Ser Asn Trp Gln Ser
 1 5

<210> 166
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 166

Met Gln Gly Thr Tyr Trp Pro Pro Thr
 1 5

<210> 167
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 167

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 Asn Tyr
 20 25 30

Phe Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 168
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 168

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Arg Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Met Gln Gly
85 90 95

Thr Tyr Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 169
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 169

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 Asn Tyr
20 25 30

Phe Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Arg Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr Tyr Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
245 250

<210> 170
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 170

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 Asn Tyr
20 25 30

Phe Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Arg Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr Tyr Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
 500 505

<210> 171
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 171

Asn Tyr Gly Met His
1 5

<210> 172
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 172

Val Ile Ser His His Gly Ser Ser Lys Tyr Tyr Ala Arg Ser Val Lys
1 5 10 15

Gly

<210> 173
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 173

Asp Trp Trp Glu Leu Val Phe Asp Tyr
1 5

<210> 174
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 174

Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Phe Leu Tyr
1 5 10 15

<210> 175

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 175

Glu Val Ser Asn Arg Phe Ser
1 5

<210> 176

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 176

Leu Gln Gly Ile His Leu Pro Phe Thr
1 5

<210> 177

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 177

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn 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 His His Gly Ser Ser Lys Tyr Tyr Ala Arg Ser Val
 50 55 60

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

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Trp Trp Glu Leu Val Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 178
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 178

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
 35 40 45

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

Asp Arg Phe Ser Gly Ser Gly 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 Leu Gln Gly
 85 90 95

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

<210> 179
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 179

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn 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 His His Gly Ser Ser Lys Tyr Tyr Ala Arg Ser Val
50 55 60

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

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Trp Glu Leu 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 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu
130 135 140

Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln
145 150 155 160

Ser Leu Leu His Ser Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln
165 170 175

Lys Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg
180 185 190

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
210 215 220

Tyr Cys Leu Gln Gly Ile His Leu Pro Phe Thr Phe Gly Pro Gly Thr
225 230 235 240

Lys Val Glu Ile Lys
245

<210> 180
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 180

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn 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 His His Gly Ser Ser Lys Tyr Tyr Ala Arg Ser Val
50 55 60

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

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Trp Glu Leu 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 Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu
130 135 140

Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln
145 150 155 160

Ser Leu Leu His Ser Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln
165 170 175

Lys Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg
180 185 190

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
210 215 220

Tyr Cys Leu Gln Gly Ile His Leu Pro Phe Thr Phe Gly Pro Gly Thr
225 230 235 240

Lys Val Glu 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> 181
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 181

Asn Ser Arg Met Gly Val Ser
1 5

<210> 182
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 182

His Ile Phe Ser Asn Asp Gly Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 183
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 183

Tyr Asn Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe Asp Tyr
1 5 10 15

<210> 184
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 184

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 1 5 10

<210> 185
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 185

Ala Ala Ser Ser Leu Gln Ser
 1 5

<210> 186
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 186

Gln Gln Gly Tyr Ser Ser Pro Phe Thr
 1 5

<210> 187
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 187

Gln Val Thr Leu Lys Glu Ser Gly Pro Met Leu Val Lys Pro Thr Glu
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ser
 20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Gly Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Tyr Asn Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 188
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 188

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 Gly Tyr Ser Ser Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 189
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 189

Gln Val Thr Leu Lys Glu Ser Gly Pro Met Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ser
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Gly Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Tyr Asn Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe
100 105 110

Asp 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 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

Ser Leu Gln Ser Gly Val Pro 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 Gly Tyr Ser Ser Pro Phe Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 190
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 190

Gln Val Thr Leu Lys Glu Ser Gly Pro Met Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ser
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Gly Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Tyr Asn Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe
100 105 110

Asp 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 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

Ser Leu Gln Ser Gly Val Pro 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 Gly Tyr Ser Ser Pro Phe Thr Phe Gly Gly
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> 191
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 191

Asn Ala Arg Met Gly Val Ser
1 5

<210> 192
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 192

His Ile Phe Ser Thr Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 193
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 193

Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe Asp Tyr
1 5 10 15

<210> 194
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 194

Arg Ala Ser Gln Ser Ile Arg Ser Tyr Leu Asn
1 5 10

<210> 195
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 195

Gly Ala Ser Asn Leu Gln Ser
1 5

<210> 196
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 196

Gln Gln Ser Tyr Ser Ser Pro Phe Thr
1 5

<210> 197
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 197

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Leu Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Thr Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 198
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 198

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 Arg 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 Gly Ala Ser Asn 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 Ser Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 199
 <211> 247
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 199

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Leu Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Thr Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe
 100 105 110

Asp 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 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 Arg Ser Tyr Leu Asn Trp Tyr
 165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly Ala Ser
180 185 190

Asn Leu Gln Ser Gly Val Pro 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 Tyr Ser Ser Pro Phe Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 200
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 200

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Leu Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Thr Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe
100 105 110

Asp 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 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 Arg Ser Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly Ala Ser
180 185 190

Asn Leu Gln Ser Gly Val Pro 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 Tyr Ser Ser Pro Phe Thr Phe Gly Gly
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> 201

<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 201

Ser Tyr Tyr Ile His
1 5

<210> 202
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 202

Ile Ile Asn Pro Ser Gly Gly Ser Lys Ser Tyr Ala Gln Lys Phe Arg
1 5 10 15

Gly

<210> 203
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 203

Ser Met Ser Thr Val Thr Ser Asp Ala Phe Asp Ile
1 5 10

<210> 204
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 204

Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 205
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 205

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 206
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 206

Gln Gln Ser Tyr Ser Ala Pro Leu Thr
1 5

<210> 207
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 207

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 Ala Phe Thr Ser Tyr
20 25 30

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

Gly Ile Ile Asn Pro Ser Gly Gly Ser Lys Ser Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Met Ser Thr Val Thr Ser Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 208
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 208

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 Asn 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 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 Ala Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 209
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 209

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 Ala Phe Thr Ser Tyr
20 25 30

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

Gly Ile Ile Asn Pro Ser Gly Gly Ser Lys Ser Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Met Ser Thr Val Thr Ser Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met 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 Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Ser Tyr Ser Ala Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240

Asp Ile Lys

<210> 210
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 210

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 Ala Phe Thr Ser Tyr
20 25 30

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

Gly Ile Ile Asn Pro Ser Gly Gly Ser Lys Ser Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Met Ser Thr Val Thr Ser Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met 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 Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Ser Tyr Ser Ala Pro Leu 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> 211
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 211

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 Ile Ser Ser Tyr
 20 25 30

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

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
 130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
 165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 212
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 212

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 Ile Ser Ser Tyr
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Arg Thr Asn Tyr Tyr Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Ile 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
 290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 213
 <211> 496

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 213

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

<210> 214
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 214

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 215
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 215

Gln Val Gln Leu Gln Glu Trp Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

<210> 216
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 216

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 217
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 217

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 Tyr
20 25 30

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

Gly Tyr Ile Phe Tyr Asn Gly Ile Thr Asn Tyr 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 Ser Ser Val Thr Ala Ala Asp Thr Ala Lys Tyr Tyr Cys Ala
85 90 95

Arg Ile His Ser Gly Ser Phe Ser Phe Asp Tyr Trp Asp 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 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Ser Arg Gly Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
 210 215 220

Tyr Asp Thr Ser Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
 275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
 290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

<210> 218
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 218

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

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 219
<211> 505
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 219

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 220
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 220

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 Gly Tyr
20 25 30

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

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Gly Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Ala Tyr Arg Asp Gly Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 221
 <211> 1096
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 221

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Ser Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Tyr His Gly Ser Asn Lys Tyr Tyr Ala Arg Ser Val
 50 55 60

Lys 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 Arg Glu Ile Pro Phe Gly Met Asp Val Trp Gly Gln Gly Thr Thr
 100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 115 120 125

Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro
 130 135 140

Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 145 150 155 160

Leu Leu His Ser Asp Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys
 165 170 175

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

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

Cys Met Gln Ala Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
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 Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val
 500 505 510

Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val
 515 520 525

Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His
 530 535 540

Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala
 545 550 555 560

Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly
 565 570 575

Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met
 580 585 590

Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu
 595 600 605

Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu
610 615 620

Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu
625 630 635 640

Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala
645 650 655

Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu
660 665 670

Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp
675 680 685

Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys
690 695 700

Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala
705 710 715 720

Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val
725 730 735

Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His
740 745 750

Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr
755 760 765

Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys
770 775 780

Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn
785 790 795 800

Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu
805 810 815

Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu
820 825 830

Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val
835 840 845

Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys
850 855 860

Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp
865 870 875 880

Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn
885 890 895

Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu
900 905 910

Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu
915 920 925

Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys
930 935 940

His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val
945 950 955 960

Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp
965 970 975

Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys
980 985 990

Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn
995 1000 1005

Ala Gly Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu
1010 1015 1020

Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val
1025 1030 1035

Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Ala Met
 1040 1045 1050

Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp
 1055 1060 1065

Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala
 1070 1075 1080

Ser Gln Ala Ala Leu Gly Leu His His His His His His
 1085 1090 1095

<210> 222
 <211> 1095
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 222

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 Gly Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Thr Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Ala Asn Ile Ala Ala Leu Asp Ala Phe Glu Ile Trp Gly
 100 105 110

Gln Gly Thr Met 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 Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Ser Tyr Ser Thr Pro Leu 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 Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala
500 505 510

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
515 520 525

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
530 535 540

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
545 550 555 560

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
565 570 575

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
580 585 590

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
595 600 605

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
610 615 620

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
625 630 635 640

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
645 650 655

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
660 665 670

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
675 680 685

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
690 695 700

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
705 710 715 720

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
725 730 735

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
740 745 750

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
755 760 765

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
770 775 780

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
785 790 795 800

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
805 810 815

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
820 825 830

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
835 840 845

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
850 855 860

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
865 870 875 880

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
885 890 895

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
900 905 910

Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
915 920 925

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
930 935 940

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
945 950 955 960

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
965 970 975

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
 980 985 990

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
 995 1000 1005

Gly Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys
 1010 1015 1020

Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys
 1025 1030 1035

His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Ala Met Asp
 1040 1045 1050

Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys
 1055 1060 1065

Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser
 1070 1075 1080

Gln Ala Ala Leu Gly Leu His His His His His His
 1085 1090 1095

<210> 223
 <211> 1098
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 223

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 His Gly Arg Asp Thr Tyr Tyr Ala Arg Ser Val
50 55 60

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

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ala Thr Val Thr Ser Tyr Tyr Tyr Ser 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 Gly Ile Ser Asn Tyr Leu Ala Trp Phe Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile Tyr Leu Ala Ser Ser
180 185 190

Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly Ser 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 Tyr Asn Phe Tyr Pro Phe Thr Phe Gly Pro Gly
225 230 235 240

Thr Lys Val Asp 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 Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser
500 505 510

Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala
515 520 525

Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu
530 535 540

Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys
545 550 555 560

Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu
565 570 575

Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly
580 585 590

Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys
595 600 605

Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg
610 615 620

Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr
625 630 635 640

Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe
645 650 655

Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe
660 665 670

Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys
675 680 685

Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg
690 695 700

Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala
705 710 715 720

Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala
725 730 735

Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys
740 745 750

Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala
755 760 765

Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu
770 775 780

Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val
785 790 795 800

Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe
805 810 815

Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val
820 825 830

Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr
835 840 845

Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu
850 855 860

Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val
865 870 875 880

Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys
885 890 895

Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn
900 905 910

Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro
915 920 925

Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys
930 935 940

Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu
945 950 955 960

Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val
965 970 975

Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg
980 985 990

Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu
995 1000 1005

Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu
1010 1015 1020

Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu
1025 1030 1035

Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala
1040 1045 1050

Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala
1055 1060 1065

Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
1070 1075 1080

Ala Ala Ser Gln Ala Ala Leu Gly Leu His His His His His His
1085 1090 1095

<210> 224
<211> 1093
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 224

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 Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
 1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
 1070 1075 1080

Ala Leu Gly Leu His His His His His His
 1085 1090

<210> 225
 <211> 1093
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 225

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 Ile Ser Ser Tyr
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Arg Thr Asn Tyr Tyr Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Ile 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
 500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
 530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
 995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
 1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
 1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
 1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
 1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
 1070 1075 1080

Ala Leu Gly Leu His His His His His His
 1085 1090

<210> 226
 <211> 1093
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 226

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 Ala Ser Ile Ser Ser Phe
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
 290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
1070 1075 1080

Ala Leu Gly Leu His His His His His His
1085 1090

<210> 227
<211> 1093
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 227

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 Ala Ser Ile Ser Ser Phe
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
 130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
 180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
 210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
 275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
 290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
1070 1075 1080

Ala Leu Gly Leu His His His His His His
 1085 1090

<210> 228
 <211> 1093
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 228

Gln Val Gln Leu Gln Glu Trp Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Phe
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

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

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
 500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
 530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
 565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
 580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
1070 1075 1080

Ala Leu Gly Leu His His His His His His
1085 1090

<210> 229
<211> 1093
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 229

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
 500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
1070 1075 1080

Ala Leu Gly Leu His His His His His His
1085 1090

<210> 230
<211> 1093
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 230

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 Tyr
20 25 30

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

Gly Tyr Ile Phe Tyr Asn Gly Ile Thr Asn Tyr 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 Ser Ser Val Thr Ala Ala Asp Thr Ala Lys Tyr Tyr Cys Ala
85 90 95

Arg Ile His Ser Gly Ser Phe Ser Phe Asp Tyr Trp Asp 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 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Ser Arg Gly Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Thr Ser Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
 500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
 530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
 565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
 580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
 595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
 610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
 625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
 645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
 660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
1070 1075 1080

Ala Leu Gly Leu His His His His His His
1085 1090

<210> 231
 <211> 1100
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 231

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 Ile Phe Asn Asn Ala
 20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Gly Arg Ile Lys Asn Lys Ile Asp Gly Gly Thr Thr Asp Phe Ala Ala
 50 55 60

Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr
 85 90 95

Tyr Cys Thr Ala Arg Gly Trp Tyr Gly Asp Tyr 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 Val Met Thr Gln Thr Pro
 130 135 140

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

Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp
 165 170 175

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly
180 185 190

Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
195 200 205

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

Gly Ile Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly
225 230 235 240

Pro Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu Val
245 250 255

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
260 265 270

Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met
275 280 285

Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
290 295 300

Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val
305 310 315 320

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr
325 330 335

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

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
355 360 365

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr Gln
385 390 395 400

Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys
405 410 415

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val
420 425 430

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

Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly
450 455 460

Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala
465 470 475 480

Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly
485 490 495

Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp Ala His
500 505 510

Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe
515 520 525

Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro
530 535 540

Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys
545 550 555 560

Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His
565 570 575

Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr
580 585 590

Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn
595 600 605

Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu
610 615 620

Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu
625 630 635 640

Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro
645 650 655

Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala
660 665 670

Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu
675 680 685

Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys
690 695 700

Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe
705 710 715 720

Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu
725 730 735

Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr
740 745 750

Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp
755 760 765

Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu
770 775 780

Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala
785 790 795 800

Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala
805 810 815

Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys
820 825 830

Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro
835 840 845

Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr
850 855 860

Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala
865 870 875 880

Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu
885 890 895

Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe
900 905 910

Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser
915 920 925

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

Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp
945 950 955 960

Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr
965 970 975

Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn
980 985 990

Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro
995 1000 1005

Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys
1010 1015 1020

Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu
1025 1030 1035

Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 1040 1045 1050

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys
 1055 1060 1065

Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys
 1070 1075 1080

Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His His His
 1085 1090 1095

His His
 1100

<210> 232
 <211> 1101
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 232

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 Ser Phe Ser Ser Tyr
 20 25 30

Asp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Ser Ser His Gly Ser Asn Lys Asn Tyr Ala Arg Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Gly Tyr Ser Gly Asn Asp Pro Phe Tyr Tyr Tyr Tyr His
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
130 135 140

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

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
180 185 190

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
195 200 205

Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
210 215 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Thr Thr Pro Leu Thr Phe
225 230 235 240

Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser Glu
245 250 255

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
260 265 270

Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala
275 280 285

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
290 295 300

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
305 310 315 320

Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala
325 330 335

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

Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala
355 360 365

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val Thr
385 390 395 400

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
405 410 415

Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp
420 425 430

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

Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
450 455 460

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
465 470 475 480

Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly
485 490 495

Gly Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp Ala
500 505 510

His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn
515 520 525

Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys
530 535 540

Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala
545 550 555 560

Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu
565 570 575

His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu
580 585 590

Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg
595 600 605

Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg
610 615 620

Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn
625 630 635 640

Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His
645 650 655

Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys
660 665 670

Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu
675 680 685

Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala
690 695 700

Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala
705 710 715 720

Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala
725 730 735

Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His
740 745 750

Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala
755 760 765

Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys
770 775 780

Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile
785 790 795 800

Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala
805 810 815

Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala
820 825 830

Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His
835 840 845

Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu
850 855 860

Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr
865 870 875 880

Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn
885 890 895

Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys
900 905 910

Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val
915 920 925

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

Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu
945 950 955 960

Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys
965 970 975

Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val
980 985 990

Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val
995 1000 1005

Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile
1010 1015 1020

Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
1025 1030 1035

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln
1040 1045 1050

Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys
1055 1060 1065

Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys
1070 1075 1080

Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His His
1085 1090 1095

His His His
1100

<210> 233
<211> 1102
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 233

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

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp
500 505 510

Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu
515 520 525

Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln
530 535 540

Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe
545 550 555 560

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser
565 570 575

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg
580 585 590

Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu
595 600 605

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro
610 615 620

Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp
625 630 635 640

Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg
645 650 655

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr
660 665 670

Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys
675 680 685

Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser
690 695 700

Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg
705 710 715 720

Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys
725 730 735

Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val
740 745 750

His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg
755 760 765

Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser
770 775 780

Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys
785 790 795 800

Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu
805 810 815

Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu
820 825 830

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

His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr
850 855 860

Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys
865 870 875 880

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
 885 890 895

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
 900 905 910

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
 915 920 925

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

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
 945 950 955 960

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
 965 970 975

Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
 980 985 990

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
 995 1000 1005

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 1010 1015 1020

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr
 1025 1030 1035

Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu
 1040 1045 1050

Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys
 1055 1060 1065

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly
 1070 1075 1080

Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His
 1085 1090 1095

His His His His
1100

<210> 234
<211> 1102
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 234

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp
 500 505 510

Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu
 515 520 525

Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln
 530 535 540

Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe
 545 550 555 560

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser
 565 570 575

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg
 580 585 590

Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu
595 600 605

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro
610 615 620

Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp
625 630 635 640

Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg
645 650 655

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr
660 665 670

Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys
675 680 685

Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser
690 695 700

Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg
705 710 715 720

Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys
725 730 735

Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val
740 745 750

His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg
755 760 765

Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser
770 775 780

Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys
785 790 795 800

Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu
805 810 815

Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu
820 825 830

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

His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr
850 855 860

Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys
865 870 875 880

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
885 890 895

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
900 905 910

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
915 920 925

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

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
945 950 955 960

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
965 970 975

Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
980 985 990

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
995 1000 1005

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
1010 1015 1020

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr
 1025 1030 1035

Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu
 1040 1045 1050

Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys
 1055 1060 1065

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly
 1070 1075 1080

Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His
 1085 1090 1095

His His His His
 1100

<210> 235
 <211> 1102
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 235

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 Gly Tyr
 20 25 30

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

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Gly Gln Asn Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Ala Tyr Arg Asp Gly Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp
500 505 510

Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu
515 520 525

Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln
530 535 540

Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe
545 550 555 560

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser
565 570 575

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg
580 585 590

Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu
595 600 605

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro
610 615 620

Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp
625 630 635 640

Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg
645 650 655

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr
660 665 670

Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys
675 680 685

Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser
690 695 700

Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg
705 710 715 720

Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys
725 730 735

Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val
740 745 750

His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg
755 760 765

Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser
770 775 780

Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys
785 790 795 800

Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu
805 810 815

Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu
820 825 830

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

His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr
850 855 860

Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys
865 870 875 880

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
885 890 895

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
900 905 910

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
915 920 925

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

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
 945 950 955 960

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
 965 970 975

Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
 980 985 990

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
 995 1000 1005

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 1010 1015 1020

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr
 1025 1030 1035

Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu
 1040 1045 1050

Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys
 1055 1060 1065

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly
 1070 1075 1080

Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His
 1085 1090 1095

His His His His
 1100

<210> 236
 <211> 1102
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 236

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 Gly His
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Gly Thr Thr Val Val His Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Thr Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp
500 505 510

Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu
515 520 525

Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln
530 535 540

Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe
545 550 555 560

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser
565 570 575

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg
580 585 590

Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu
595 600 605

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro
610 615 620

Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp
625 630 635 640

Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg
645 650 655

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr
660 665 670

Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys
675 680 685

Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser
690 695 700

Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg
705 710 715 720

Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys
725 730 735

Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val
740 745 750

His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg
755 760 765

Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser
770 775 780

Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys
785 790 795 800

Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu
805 810 815

Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu
820 825 830

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

His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr
850 855 860

Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys
 865 870 875 880

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
 885 890 895

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
 900 905 910

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
 915 920 925

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

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
 945 950 955 960

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
 965 970 975

Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
 980 985 990

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
 995 1000 1005

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 1010 1015 1020

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr
 1025 1030 1035

Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu
 1040 1045 1050

Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys
 1055 1060 1065

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly
 1070 1075 1080

Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His
 1085 1090 1095

His His His His
 1100

<210> 237
 <211> 1102
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 237

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 Asn Tyr
 20 25 30

Phe Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Asn Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Arg Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr Tyr Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp
 500 505 510

Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu
 515 520 525

Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln
 530 535 540

Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe
 545 550 555 560

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser
565 570 575

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg
580 585 590

Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu
595 600 605

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro
610 615 620

Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp
625 630 635 640

Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg
645 650 655

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr
660 665 670

Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys
675 680 685

Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser
690 695 700

Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg
705 710 715 720

Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys
725 730 735

Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val
740 745 750

His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg
755 760 765

Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser
770 775 780

Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys
785 790 795 800

Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu
805 810 815

Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu
820 825 830

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

His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr
850 855 860

Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys
865 870 875 880

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
885 890 895

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
900 905 910

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
915 920 925

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

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
945 950 955 960

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
965 970 975

Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
980 985 990

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
 995 1000 1005

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 1010 1015 1020

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr
 1025 1030 1035

Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu
 1040 1045 1050

Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys
 1055 1060 1065

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly
 1070 1075 1080

Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His
 1085 1090 1095

His His His His
 1100

<210> 238
 <211> 1097
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 238

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn 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 His His Gly Ser Ser Lys Tyr Tyr Ala Arg Ser Val
50 55 60

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

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Trp Glu Leu 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 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu
130 135 140

Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln
145 150 155 160

Ser Leu Leu His Ser Asp Gly Lys Thr Phe Leu Tyr Trp Tyr Leu Gln
165 170 175

Lys Pro Gly Gln Pro Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg
180 185 190

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
210 215 220

Tyr Cys Leu Gln Gly Ile His Leu Pro Phe Thr Phe Gly Pro Gly Thr
225 230 235 240

Lys Val Glu 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 Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu
500 505 510

Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu
515 520 525

Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp
530 535 540

His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val
545 550 555 560

Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe
565 570 575

Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu
580 585 590

Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe
595 600 605

Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro
610 615 620

Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe
625 630 635 640

Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr
645 650 655

Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr
660 665 670

Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu
675 680 685

Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu
690 695 700

Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp
705 710 715 720

Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu
725 730 735

Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys
740 745 750

His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys
755 760 765

Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys
770 775 780

Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu
785 790 795 800

Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val
805 810 815

Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe
820 825 830

Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser
835 840 845

Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu
850 855 860

Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe
865 870 875 880

Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln
885 890 895

Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala
900 905 910

Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr
915 920 925

Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys
930 935 940

Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser
945 950 955 960

Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser
965 970 975

Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro
980 985 990

Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe
995 1000 1005

Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser
1010 1015 1020

Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu
1025 1030 1035

Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val
1040 1045 1050

Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp
1055 1060 1065

Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala
1070 1075 1080

Ala Ser Gln Ala Ala Leu Gly Leu His His His His His His
1085 1090 1095

<210> 239
<211> 1099
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 239

Gln Val Thr Leu Lys Glu Ser Gly Pro Met Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ser
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Gly Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Tyr Asn Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe
100 105 110

Asp 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 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

Ser Leu Gln Ser Gly Val Pro 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 Gly Tyr Ser Ser Pro Phe Thr Phe Gly Gly
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 Pro Gly Gly Gly Gly Ser Asp Ala His Lys
 500 505 510

Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys
 515 520 525

Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe
 530 535 540

Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr
 545 550 555 560

Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr
 565 570 575

Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr
 580 585 590

Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu
 595 600 605

Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val
 610 615 620

Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu
 625 630 635 640

Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr
645 650 655

Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala
660 665 670

Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro
675 680 685

Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln
690 695 700

Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys
705 710 715 720

Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe
725 730 735

Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu
740 745 750

Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu
755 760 765

Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys
770 775 780

Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu
785 790 795 800

Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp
805 810 815

Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp
820 825 830

Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp
835 840 845

Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr
850 855 860

Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys
865 870 875 880

Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile
885 890 895

Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln
900 905 910

Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr
915 920 925

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

Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr
945 950 955 960

Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro
965 970 975

Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg
980 985 990

Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys
995 1000 1005

Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr
1010 1015 1020

Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val
1025 1030 1035

Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys
1040 1045 1050

Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
1055 1060 1065

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu
 1070 1075 1080

Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His His His His
 1085 1090 1095

His

<210> 240
 <211> 1099
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 240

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
 20 25 30

Arg Met Gly Val Ser Trp Leu Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala His Ile Phe Ser Thr Asp Glu Lys Ser Tyr Ser Thr Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Ser Phe Phe
 100 105 110

Asp 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 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 Arg Ser Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly Ala Ser
180 185 190

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

Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys
515 520 525

Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe
530 535 540

Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr
545 550 555 560

Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr
565 570 575

Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr
580 585 590

Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu
595 600 605

Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val
610 615 620

Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu
625 630 635 640

Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr
645 650 655

Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala
660 665 670

Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro
675 680 685

Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln
690 695 700

Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys
705 710 715 720

Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe
725 730 735

Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu
740 745 750

Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu
755 760 765

Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys
770 775 780

Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu
785 790 795 800

Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp
805 810 815

Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp
820 825 830

Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp
835 840 845

Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr
850 855 860

Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys
865 870 875 880

Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile
885 890 895

Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln
900 905 910

Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr
915 920 925

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

Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr
945 950 955 960

Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro
965 970 975

Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg
980 985 990

Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys
 995 1000 1005

Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr
 1010 1015 1020

Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val
 1025 1030 1035

Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys
 1040 1045 1050

Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 1055 1060 1065

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu
 1070 1075 1080

Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His His His His
 1085 1090 1095

His

<210> 241
 <211> 1095
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 241

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 Ala Phe Thr Ser Tyr
 20 25 30

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

Gly Ile Ile Asn Pro Ser Gly Gly Ser Lys Ser Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Met Ser Thr Val Thr Ser Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met 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 Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Ser Tyr Ser Ala Pro Leu 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 Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala
500 505 510

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
515 520 525

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
530 535 540

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
545 550 555 560

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
565 570 575

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
580 585 590

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
595 600 605

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
610 615 620

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
625 630 635 640

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
645 650 655

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
660 665 670

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
675 680 685

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
690 695 700

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
705 710 715 720

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
725 730 735

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
740 745 750

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
755 760 765

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
770 775 780

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
785 790 795 800

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
805 810 815

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
820 825 830

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
835 840 845

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
850 855 860

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
865 870 875 880

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
885 890 895

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
900 905 910

Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
915 920 925

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
930 935 940

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
945 950 955 960

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
965 970 975

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
980 985 990

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
995 1000 1005

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys
1010 1015 1020

Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys
1025 1030 1035

His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp
1040 1045 1050

Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys
1055 1060 1065

Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser
1070 1075 1080

Gln Ala Ala Leu Gly Leu His His His His His His
1085 1090 1095

<210> 242
<211> 1093
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 242

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 Ile Ser Ser Tyr
20 25 30

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

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
 1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
 1070 1075 1080

Ala Leu Gly Leu His His His His His His
 1085 1090

<210> 243
 <211> 1093
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 243

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 Ile Ser Ser Tyr
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Arg Thr Asn Tyr Tyr Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Ile 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
 500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
 530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
 995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
 1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
 1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
 1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
 1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
 1070 1075 1080

Ala Leu Gly Leu His His His His His His
 1085 1090

<210> 244
 <211> 1093
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 244

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 Ala Ser Ile Ser Ser Phe
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
 930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
 945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
 965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
 980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
 995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
 1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
 1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
 1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
 1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
 1070 1075 1080

Ala Leu Gly Leu His His His His His His
 1085 1090

<210> 245
 <211> 1093
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 245

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 Ala Ser Ile Ser Ser Phe
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
 130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
 180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
 210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
 275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
 290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
1070 1075 1080

Ala Leu Gly Leu His His His His His His
 1085 1090

<210> 246
 <211> 1093
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 246

Gln Val Gln Leu Gln Glu Trp Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Ser Phe
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

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

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
 500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
 530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
 565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
 580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
 1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
 1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
 1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
 1070 1075 1080

Ala Leu Gly Leu His His His His His His
 1085 1090

<210> 247
 <211> 1093
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 247

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 Ala Ser Ile Ser Ser Phe
 20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Ser
115 120 125

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Ser Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
 500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
1070 1075 1080

Ala Leu Gly Leu His His His His His His
1085 1090

<210> 248
<211> 1093
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 248

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 Tyr
20 25 30

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

Gly Tyr Ile Phe Tyr Asn Gly Ile Thr Asn Tyr 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 Ser Ser Val Thr Ala Ala Asp Thr Ala Lys Tyr Tyr Cys Ala
85 90 95

Arg Ile His Ser Gly Ser Phe Ser Phe Asp Tyr Trp Asp 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 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Ser Arg Gly Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Thr Ser Pro Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Ser Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Val Ser Trp Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Pro Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu Val Ala His Arg
 500 505 510

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 515 520 525

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
 530 535 540

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 545 550 555 560

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
 565 570 575

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
 580 585 590

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
 595 600 605

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
 610 615 620

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
 625 630 635 640

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
 645 650 655

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
 660 665 670

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
675 680 685

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
690 695 700

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
705 710 715 720

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
725 730 735

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
740 745 750

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
755 760 765

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
770 775 780

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
785 790 795 800

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
805 810 815

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
820 825 830

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
835 840 845

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
850 855 860

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
865 870 875 880

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
885 890 895

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
900 905 910

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
915 920 925

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
930 935 940

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
945 950 955 960

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
965 970 975

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
980 985 990

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
995 1000 1005

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
1010 1015 1020

Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
1025 1030 1035

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
1040 1045 1050

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
1055 1060 1065

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala
1070 1075 1080

Ala Leu Gly Leu His His His His His His
1085 1090

<210> 249
 <211> 1102
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 249

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

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Asn Tyr Ala Gln Asn Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
 130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
 145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp
500 505 510

Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu
515 520 525

Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln
530 535 540

Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe
545 550 555 560

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser
565 570 575

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg
580 585 590

Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu
595 600 605

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro
610 615 620

Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp
625 630 635 640

Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg
645 650 655

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr
660 665 670

Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys
675 680 685

Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser
690 695 700

Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg
705 710 715 720

Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys
725 730 735

Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val
740 745 750

His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg
755 760 765

Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser
770 775 780

Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys
785 790 795 800

Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu
805 810 815

Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu
820 825 830

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

His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr
850 855 860

Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys
865 870 875 880

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
885 890 895

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
900 905 910

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
915 920 925

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

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
945 950 955 960

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
965 970 975

Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
980 985 990

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
995 1000 1005

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
1010 1015 1020

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr
1025 1030 1035

Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu
 1040 1045 1050

Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys
 1055 1060 1065

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly
 1070 1075 1080

Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His
 1085 1090 1095

His His His His
 1100

<210> 250
 <211> 1102
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 250

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ser Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp
500 505 510

Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu
515 520 525

Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln
530 535 540

Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe
545 550 555 560

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser
565 570 575

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg
580 585 590

Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu
595 600 605

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro
610 615 620

Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp
625 630 635 640

Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg
645 650 655

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr
660 665 670

Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys
675 680 685

Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser
690 695 700

Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg
705 710 715 720

Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys
725 730 735

Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val
740 745 750

His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg
755 760 765

Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser
770 775 780

Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys
785 790 795 800

Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu
805 810 815

Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu
820 825 830

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

His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr
850 855 860

Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys
865 870 875 880

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
885 890 895

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
900 905 910

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
915 920 925

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

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
945 950 955 960

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
965 970 975

Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
980 985 990

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
995 1000 1005

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
1010 1015 1020

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr
1025 1030 1035

Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu
1040 1045 1050

Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys
1055 1060 1065

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly
1070 1075 1080

Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His
1085 1090 1095

His His His His
1100

<210> 251
<211> 1102
<212> PRT
<213> Homo sapiens

<400> 251

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 Gly Tyr
20 25 30

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

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Gly Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn 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 Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Ser Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Ala Tyr Arg Asp Gly Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Phe Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser

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

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Pro Gly Gly Gly Gly Ser Asp
 500 505 510

Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu
 515 520 525

Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln
 530 535 540

Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe
 545 550 555 560

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser
 565 570 575

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg
 580 585 590

Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu
 595 600 605

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro
 610 615 620

Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp
 625 630 635 640

Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg
 645 650 655

His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr
 660 665 670

Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys

675					680					685					
Leu	Leu	Pro	Lys	Leu	Asp	Glu	Leu	Arg	Asp	Glu	Gly	Lys	Ala	Ser	Ser
690						695					700				
Ala	Lys	Gln	Arg	Leu	Lys	Cys	Ala	Ser	Leu	Gln	Lys	Phe	Gly	Glu	Arg
705					710					715					720
Ala	Phe	Lys	Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	Pro	Lys
				725					730					735	
Ala	Glu	Phe	Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys	Val
			740					745					750		
His	Thr	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp	Arg
		755					760					765			
Ala	Asp	Leu	Ala	Lys	Tyr	Ile	Cys	Glu	Asn	Gln	Asp	Ser	Ile	Ser	Ser
	770					775					780				
Lys	Leu	Lys	Glu	Cys	Cys	Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His	Cys
785						790					795				800
Ile	Ala	Glu	Val	Glu	Asn	Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	Ser	Leu
				805					810					815	
Ala	Ala	Asp	Phe	Val	Glu	Ser	Lys	Asp	Val	Cys	Lys	Asn	Tyr	Ala	Glu
			820					825					830		
Ala	Lys	Asp	Val	Phe	Leu	Gly	Met	Phe	Leu	Tyr	Glu	Tyr	Ala	Arg	Arg
		835					840					845			
His	Pro	Asp	Tyr	Ser	Val	Val	Leu	Leu	Leu	Arg	Leu	Ala	Lys	Thr	Tyr
	850					855					860				
Glu	Thr	Thr	Leu	Glu	Lys	Cys	Cys	Ala	Ala	Ala	Asp	Pro	His	Glu	Cys
865					870					875					880
Tyr	Ala	Lys	Val	Phe	Asp	Glu	Phe	Lys	Pro	Leu	Val	Glu	Glu	Pro	Gln
				885					890					895	

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
900 905 910

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
915 920 925

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

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala
945 950 955 960

Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu
965 970 975

Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu
980 985 990

Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr
995 1000 1005

Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
1010 1015 1020

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr
1025 1030 1035

Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu
1040 1045 1050

Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys
1055 1060 1065

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly
1070 1075 1080

Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu His His
1085 1090 1095

His His His His

1100

<210> 252
<211> 618
<212> PRT
<213> Homo sapiens

<400> 252

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

Ala Leu Ile Phe Leu Pro Gln Thr Arg Pro Ala Gly Val Phe Glu Leu
20 25 30

Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
35 40 45

Pro Cys Ser Ala Arg Leu Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
50 55 60

Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
65 70 75 80

Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Gly Ala
85 90 95

Pro Ala Pro Asp Leu Pro Leu Pro Asp Gly Leu Leu Gln Val Pro Phe
100 105 110

Arg Asp Ala Trp Pro Gly Thr Phe Ser Phe Ile Ile Glu Thr Trp Arg
115 120 125

Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro Ala Trp Ser Leu Leu Ala
130 135 140

Arg Val Ala Gly Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145 150 155 160

Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg Ala
165 170 175

Arg Cys Glu Pro Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys Arg
180 185 190

Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys Ala
195 200 205

Pro Leu Glu Asp Glu Cys Glu Ala Pro Leu Val Cys Arg Ala Gly Cys
210 215 220

Ser Pro Glu His Gly Phe Cys Glu Gln Pro Gly Glu Cys Arg Cys Leu
225 230 235 240

Glu Gly Trp Thr Gly Pro Leu Cys Thr Val Pro Val Ser Thr Ser Ser
245 250 255

Cys Leu Ser Pro Arg Gly Pro Ser Ser Ala Thr Thr Gly Cys Leu Val
260 265 270

Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser
275 280 285

Cys Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe
290 295 300

Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro
305 310 315 320

Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala
325 330 335

Tyr Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys
340 345 350

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
355 360 365

Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
370 375 380

Gly Pro Arg Cys Glu His Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys
385 390 395 400

Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser
405 410 415

Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro
420 425 430

Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe
435 440 445

Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ala Arg Cys
450 455 460

Glu Phe Pro Val His Pro Asp Gly Ala Ser Ala Leu Pro Ala Ala Pro
465 470 475 480

Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu Leu Pro Pro Ala
485 490 495

Leu Gly Leu Leu Val Ala Ala Gly Val Ala Gly Ala Ala Leu Leu Leu
500 505 510

Val His Val Arg Arg Arg Gly His Ser Gln Asp Ala Gly Ser Arg Leu
515 520 525

Leu Ala Gly Thr Pro Glu Pro Ser Val His Ala Leu Pro Asp Ala Leu
530 535 540

Asn Asn Leu Arg Thr Gln Glu Gly Ser Gly Asp Gly Pro Ser Ser Ser
545 550 555 560

Val Asp Trp Asn Arg Pro Glu Asp Val Asp Pro Gln Gly Ile Tyr Val
565 570 575

Ile Ser Ala Pro Ser Ile Tyr Ala Arg Glu Val Ala Thr Pro Leu Phe
580 585 590

Pro Pro Leu His Thr Gly Arg Ala Gly Gln Arg Gln His Leu Leu Phe
595 600 605

Pro Tyr Pro Ser Ser Ile Leu Ser Val Lys
610 615

<210> 253
<211> 492
<212> PRT
<213> Homo sapiens

<400> 253

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

Ala Leu Ile Phe Leu Pro Gln Thr Arg Pro Ala Gly Val Phe Glu Leu
20 25 30

Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
35 40 45

Pro Cys Ser Ala Arg Leu Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
50 55 60

Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
65 70 75 80

Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Gly Ala
85 90 95

Pro Ala Pro Asp Leu Pro Leu Pro Asp Gly Leu Leu Gln Val Pro Phe
100 105 110

Arg Asp Ala Trp Pro Gly Thr Phe Ser Phe Ile Ile Glu Thr Trp Arg
115 120 125

Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro Ala Trp Ser Leu Leu Ala
130 135 140

Arg Val Ala Gly Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145 150 155 160

Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg Ala
165 170 175

Arg Cys Glu Pro Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys Arg
180 185 190

Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys Ala
195 200 205

Pro Leu Glu Asp Glu Cys Glu Ala Pro Leu Val Cys Arg Ala Gly Cys
210 215 220

Ser Pro Glu His Gly Phe Cys Glu Gln Pro Gly Glu Cys Arg Cys Leu
225 230 235 240

Glu Gly Trp Thr Gly Pro Leu Cys Thr Val Pro Val Ser Thr Ser Ser
245 250 255

Cys Leu Ser Pro Arg Gly Pro Ser Ser Ala Thr Thr Gly Cys Leu Val
260 265 270

Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser
275 280 285

Cys Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe
290 295 300

Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro
305 310 315 320

Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala
325 330 335

Tyr Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys
340 345 350

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
355 360 365

Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
370 375 380

Gly Pro Arg Cys Glu His Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys

385 390 395 400
 Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser
 405 410 415
 Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro
 420 425 430
 Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe
 435 440 445
 Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ala Arg Cys
 450 455 460
 Glu Phe Pro Val His Pro Asp Gly Ala Ser Ala Leu Pro Ala Ala Pro
 465 470 475 480
 Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu
 485 490

 <210> 254
 <211> 175
 <212> PRT
 <213> Homo sapiens

 <400> 254

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

 Ala Leu Ile Phe Leu Pro Gln Thr Arg Pro Ala Gly Val Phe Glu Leu
 20 25 30

 Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
 35 40 45

 Pro Cys Ser Ala Arg Leu Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
 50 55 60

 Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
 65 70 75 80

Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Gly Ala
85 90 95

Pro Ala Pro Asp Leu Pro Leu Pro Asp Gly Leu Leu Gln Val Pro Phe
100 105 110

Arg Asp Ala Trp Pro Gly Thr Phe Ser Phe Ile Ile Glu Thr Trp Arg
115 120 125

Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro Ala Trp Ser Leu Leu Ala
130 135 140

Arg Val Ala Gly Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145 150 155 160

Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg
165 170 175

<210> 255
<211> 40
<212> PRT
<213> Homo sapiens

<400> 255

Ala Arg Cys Glu Pro Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys
1 5 10 15

Arg Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys
20 25 30

Ala Pro Leu Glu Asp Glu Cys Glu
35 40

<210> 256
<211> 34
<212> PRT
<213> Homo sapiens

<400> 256

Ala Pro Leu Val Cys Arg Ala Gly Cys Ser Pro Glu His Gly Phe Cys
1 5 10 15

Glu Gln Pro Gly Glu Cys Arg Cys Leu Glu Gly Trp Thr Gly Pro Leu
 20 25 30

Cys Thr

<210> 257
 <211> 37
 <212> PRT
 <213> Homo sapiens

<400> 257

Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser Cys
 1 5 10 15

Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe Tyr
 20 25 30

Gly Leu Arg Cys Glu
 35

<210> 258
 <211> 40
 <212> PRT
 <213> Homo sapiens

<400> 258

Ser Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys
 1 5 10 15

Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro
 20 25 30

Gly Phe Gln Gly Ser Asn Cys Glu
 35 40

<210> 259
 <211> 37
 <212> PRT
 <213> Homo sapiens

<400> 259

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys

1 5 10 15

Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
 20 25 30

Gly Pro Arg Cys Glu
 35

<210> 260
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 260

Ser Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys
 1 5 10 15

Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro
 20 25 30

Gly Phe Gln Gly Ser Asn Cys Glu Lys Arg Val Asp Arg Cys Ser Leu
 35 40 45

Gln Pro Cys Arg Asn Gly Gly Leu Cys Leu Asp Leu Gly His Ala Leu
 50 55 60

Arg Cys Arg Cys Arg Ala Gly Phe Ala Gly Pro Arg Cys Glu
 65 70 75

<210> 261
 <211> 37
 <212> PRT
 <213> Homo sapiens

<400> 261

Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly Thr Cys
 1 5 10 15

Val Glu Gly Gly Gly Ala His Arg Cys Ser Cys Ala Leu Gly Phe Gly
 20 25 30

Gly Arg Asp Cys Arg

35

<210> 262
<211> 37
<212> PRT
<213> Homo sapiens

<400> 262

Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys
1 5 10 15

Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met
20 25 30

Gly Ala Arg Cys Glu
35

<210> 263
<211> 548
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 263

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

Ala Leu Ile Phe Leu Pro Gln Thr Arg Pro Ala Gly Val Phe Glu Leu
20 25 30

Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
35 40 45

Pro Cys Ser Ala Arg Leu Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
50 55 60

Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
65 70 75 80

Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Gly Ala
85 90 95

Pro Ala Pro Asp Leu Pro Leu Pro Asp Gly Leu Leu Gln Val Pro Phe
100 105 110

Arg Asp Ala Trp Pro Gly Thr Phe Ser Phe Ile Ile Glu Thr Trp Arg
115 120 125

Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro Ala Trp Ser Leu Leu Ala
130 135 140

Arg Val Ala Gly Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145 150 155 160

Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg Ala
165 170 175

Arg Cys Glu Pro Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys Arg
180 185 190

Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys Ala
195 200 205

Pro Leu Glu Asp Glu Cys Glu Ala Pro Leu Val Cys Arg Ala Gly Cys
210 215 220

Ser Pro Glu His Gly Phe Cys Glu Gln Pro Gly Glu Cys Arg Cys Leu
225 230 235 240

Glu Gly Trp Thr Gly Pro Leu Cys Thr Val Pro Val Ser Thr Ser Ser
245 250 255

Cys Leu Ser Pro Arg Gly Pro Ser Ser Ala Thr Thr Gly Cys Leu Val
260 265 270

Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser
275 280 285

Cys Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe
290 295 300

Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro
 305 310 315 320

Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala
 325 330 335

Tyr Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys
 340 345 350

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
 355 360 365

Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
 370 375 380

Gly Pro Arg Cys Glu His Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys
 385 390 395 400

Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser
 405 410 415

Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro
 420 425 430

Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe
 435 440 445

Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ala Arg Cys
 450 455 460

Glu Phe Pro Val His Pro Asp Gly Ala Ser Ala Leu Pro Ala Ala Pro
 465 470 475 480

Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu Ser Gly Gly Gly
 485 490 495

Gly Ser Gly Ala Gly Val Ile Ala Val Ile Val Val Val Ile Ala
 500 505 510

Ile Val Ala Gly Ile Val Val Leu Val Ile Ser Arg Lys Lys Arg Met
 515 520 525

Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu Met Gly Glu Met His Arg
 530 535 540

Glu Leu Asn Ala
 545

<210> 264
 <211> 408
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 264

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
 20 25 30

Thr Ser Gly Ala Arg Cys Glu Pro Pro Ala Val Gly Thr Ala Cys Thr
 35 40 45

Arg Leu Cys Arg Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu
 50 55 60

Arg Pro Cys Ala Pro Leu Glu Asp Glu Cys Glu Ala Pro Leu Val Cys
 65 70 75 80

Arg Ala Gly Cys Ser Pro Glu His Gly Phe Cys Glu Gln Pro Gly Glu
 85 90 95

Cys Arg Cys Leu Glu Gly Trp Thr Gly Pro Leu Cys Thr Val Pro Val
 100 105 110

Ser Thr Ser Ser Cys Leu Ser Pro Arg Gly Pro Ser Ser Ala Thr Thr
 115 120 125

Gly Cys Leu Val Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala
 130 135 140

Asn Gly Gly Ser Cys Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys
 145 150 155 160

Pro Arg Gly Phe Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys
 165 170 175

Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp
 180 185 190

Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser
 195 200 205

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

Gly Gly Leu Cys Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg
 225 230 235 240

Ala Gly Phe Ala Gly Pro Arg Cys Glu His Asp Leu Asp Asp Cys Ala
 245 250 255

Gly Arg Ala Cys Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala
 260 265 270

His Arg Cys Ser Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu
 275 280 285

Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys
 290 295 300

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

Gly Ala Arg Cys Glu Phe Pro Val His Pro Asp Gly Ala Ser Ala Leu
 325 330 335

Pro Ala Ala Pro Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu
 340 345 350

Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile Ala Val Ile Val Val
 355 360 365

Val Val Ile Ala Ile Val Ala Gly Ile Val Val Leu Val Ile Ser Arg
 370 375 380

Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu Met Gly
 385 390 395 400

Glu Met His Arg Glu Leu Asn Ala
 405

<210> 265
 <211> 368
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 265

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
 20 25 30

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

Gly Phe Cys Glu Gln Pro Gly Glu Cys Arg Cys Leu Glu Gly Trp Thr
 50 55 60

Gly Pro Leu Cys Thr Val Pro Val Ser Thr Ser Ser Cys Leu Ser Pro
 65 70 75 80

Arg Gly Pro Ser Ser Ala Thr Thr Gly Cys Leu Val Pro Gly Pro Gly
 85 90 95

Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser Cys Ser Glu Thr
 100 105 110

Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe Tyr Gly Leu Arg
115 120 125

Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly
130 135 140

Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His
145 150 155 160

Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys Arg Val Asp Arg
165 170 175

Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys Leu Asp Leu Gly
180 185 190

His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala Gly Pro Arg Cys
195 200 205

Glu His Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly
210 215 220

Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser Cys Ala Leu Gly
225 230 235 240

Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro Cys Ala Ala Arg
245 250 255

Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe Ser Gly Leu Val
260 265 270

Cys Ala Cys Ala Pro Gly Tyr Met Gly Ala Arg Cys Glu Phe Pro Val
275 280 285

His Pro Asp Gly Ala Ser Ala Leu Pro Ala Ala Pro Pro Gly Leu Arg
290 295 300

Pro Gly Asp Pro Gln Arg Tyr Leu Ser Gly Gly Gly Gly Ser Gly Ala
305 310 315 320

Gly Val Ile Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly
325 330 335

Ile Val Val Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu
340 345 350

Lys Ala Glu Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
355 360 365

<210> 266
<211> 310
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 266

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
20 25 30

Thr Ser Gly Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly
35 40 45

Gly Ser Cys Ser Glu Thr Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg
50 55 60

Gly Phe Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp
65 70 75 80

Gly Pro Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp
85 90 95

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

Glu Lys Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly
115 120 125

Leu Cys Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly
130 135 140

Phe Ala Gly Pro Arg Cys Glu His Asp Leu Asp Asp Cys Ala Gly Arg
 145 150 155 160

Ala Cys Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg
 165 170 175

Cys Ser Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala
 180 185 190

Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala
 195 200 205

His Phe Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ala
 210 215 220

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

Ala Pro Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu Ser Gly
 245 250 255

Gly Gly Gly Ser Gly Ala Gly Val Ile Ala Val Ile Val Val Val Val
 260 265 270

Ile Ala Ile Val Ala Gly Ile Val Val Leu Val Ile Ser Arg Lys Lys
 275 280 285

Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu Met Gly Glu Met
 290 295 300

His Arg Glu Leu Asn Ala
 305 310

<210> 267
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 267

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
20 25 30

Thr Ser Gly Ser Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly
35 40 45

Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His
50 55 60

Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys Arg Val Asp Arg
65 70 75 80

Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys Leu Asp Leu Gly
85 90 95

His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala Gly Pro Arg Cys
100 105 110

Glu His Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly
115 120 125

Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser Cys Ala Leu Gly
130 135 140

Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro Cys Ala Ala Arg
145 150 155 160

Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe Ser Gly Leu Val
165 170 175

Cys Ala Cys Ala Pro Gly Tyr Met Gly Ala Arg Cys Glu Phe Pro Val
180 185 190

His Pro Asp Gly Ala Ser Ala Leu Pro Ala Ala Pro Pro Gly Leu Arg
195 200 205

Pro Gly Asp Pro Gln Arg Tyr Leu Ser Gly Gly Gly Gly Ser Gly Ala
 210 215 220

Gly Val Ile Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala Gly
 225 230 235 240

Ile Val Val Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu
 245 250 255

Lys Ala Glu Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
 260 265 270

<210> 268
 <211> 231
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 268

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
 20 25 30

Thr Ser Gly Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly
 35 40 45

Gly Leu Cys Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala
 50 55 60

Gly Phe Ala Gly Pro Arg Cys Glu His Asp Leu Asp Asp Cys Ala Gly
 65 70 75 80

Arg Ala Cys Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His
 85 90 95

Arg Cys Ser Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg
 100 105 110

Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr
115 120 125

Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly
130 135 140

Ala Arg Cys Glu Phe Pro Val His Pro Asp Gly Ala Ser Ala Leu Pro
145 150 155 160

Ala Ala Pro Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu Ser
165 170 175

Gly Gly Gly Gly Ser Gly Ala Gly Val Ile Ala Val Ile Val Val Val
180 185 190

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

Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu Met Gly Glu
210 215 220

Met His Arg Glu Leu Asn Ala
225 230

<210> 269
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 269

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
20 25 30

Thr Ser Gly Asp Leu Asp Asp Cys Ala Gly Arg Ala Cys Ala Asn Gly
35 40 45

Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser Cys Ala Leu
50 55 60

Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro Cys Ala Ala
65 70 75 80

Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe Ser Gly Leu
85 90 95

Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ala Arg Cys Glu Phe Pro
100 105 110

Val His Pro Asp Gly Ala Ser Ala Leu Pro Ala Ala Pro Pro Gly Leu
115 120 125

Arg Pro Gly Asp Pro Gln Arg Tyr Leu Ser Gly Gly Gly Gly Ser Gly
130 135 140

Ala Gly Val Ile Ala Val Ile Val Val Val Val Ile Ala Ile Val Ala
145 150 155 160

Gly Ile Val Val Leu Val Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr
165 170 175

Glu Lys Ala Glu Ile Lys Glu Met Gly Glu Met His Arg Glu Leu Asn
180 185 190

Ala

<210> 270
<211> 155
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 270

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
20 25 30

Thr Ser Gly Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly
35 40 45

Gly Arg Cys Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala Pro
50 55 60

Gly Tyr Met Gly Ala Arg Cys Glu Phe Pro Val His Pro Asp Gly Ala
65 70 75 80

Ser Ala Leu Pro Ala Ala Pro Pro Gly Leu Arg Pro Gly Asp Pro Gln
85 90 95

Arg Tyr Leu Ser Gly Gly Gly Gly Ser Gly Ala Gly Val Ile Ala Val
100 105 110

Ile Val Val Val Val Ile Ala Ile Val Ala Gly Ile Val Val Leu Val
115 120 125

Ile Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys
130 135 140

Glu Met Gly Glu Met His Arg Glu Leu Asn Ala
145 150 155

<210> 271
<211> 587
<212> PRT
<213> *Macaca fascicularis*

<400> 271

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

Ala Leu Ile Phe Ile Pro Gln Ala Arg Pro Ala Gly Val Phe Glu Leu
20 25 30

Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
35 40 45

Pro Cys Ser Ala Arg Gly Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
50 55 60

Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
65 70 75 80

Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Glu Ala
85 90 95

Pro Ala Pro Asp Leu Pro Leu Pro Asn Gly Leu Leu Gln Val Pro Phe
100 105 110

Arg Asp Ala Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Thr Trp Arg
115 120 125

Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro Ala Trp Ser Leu Leu Ala
130 135 140

Arg Val Thr Arg Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145 150 155 160

Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg Ala
165 170 175

Arg Cys Glu Leu Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys Arg
180 185 190

Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys Ala
195 200 205

Pro Leu Glu Asp Glu Cys Glu Ala Pro Pro Val Cys Arg Ala Gly Cys
210 215 220

Ser Leu Glu His Gly Phe Cys Glu Gln Pro Gly Glu Cys Arg Cys Leu
225 230 235 240

Glu Gly Trp Thr Gly Pro Leu Cys Met Val Pro Ala Ser Thr Ser Ser
245 250 255

Cys Leu Gly Leu Arg Gly Pro Ser Ser Ala Thr Thr Gly Cys Leu Val

260

265

270

Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser
 275 280 285

Cys Ser Glu Thr Pro Gly Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe
 290 295 300

Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro
 305 310 315 320

Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala
 325 330 335

Tyr Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys
 340 345 350

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
 355 360 365

Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
 370 375 380

Gly Pro Arg Cys Glu His Asn Leu Asp Asp Cys Ala Gly Arg Ala Cys
 385 390 395 400

Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser
 405 410 415

Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro
 420 425 430

Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe
 435 440 445

Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ser Arg Cys
 450 455 460

Glu Phe Pro Val His Pro Asp Gly Val Ser Ala Leu Pro Ala Ala Pro
 465 470 475 480

Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu Leu Pro Pro Ala
485 490 495

Leu Gly Leu Leu Val Ala Ala Gly Val Ala Gly Ala Ala Leu Leu Leu
500 505 510

Val His Val Arg Arg Arg Gly His Ala Gln Asp Ala Gly Ser Arg Leu
515 520 525

Leu Ala Gly Thr Pro Glu Pro Ser Val His Ala Leu Pro Asp Ala Leu
530 535 540

Asn Asn Gln Arg Thr Gln Glu Gly Pro Gly Asp Val Pro Ser Ser Ser
545 550 555 560

Val Asp Trp Asn Arg Pro Glu Asp Val Asp Ser Arg Gly Ile Tyr Val
565 570 575

Ile Ser Ala Pro Ser Ile Tyr Ala Arg Glu Ala
580 585

<210> 272
<211> 492
<212> PRT
<213> Macaca fascicularis

<400> 272

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

Ala Leu Ile Phe Ile Pro Gln Ala Arg Pro Ala Gly Val Phe Glu Leu
20 25 30

Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
35 40 45

Pro Cys Ser Ala Arg Gly Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
50 55 60

Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
65 70 75 80

Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Glu Ala
85 90 95

Pro Ala Pro Asp Leu Pro Leu Pro Asn Gly Leu Leu Gln Val Pro Phe
100 105 110

Arg Asp Ala Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Thr Trp Arg
115 120 125

Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro Ala Trp Ser Leu Leu Ala
130 135 140

Arg Val Thr Arg Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145 150 155 160

Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg Ala
165 170 175

Arg Cys Glu Leu Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys Arg
180 185 190

Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys Ala
195 200 205

Pro Leu Glu Asp Glu Cys Glu Ala Pro Pro Val Cys Arg Ala Gly Cys
210 215 220

Ser Leu Glu His Gly Phe Cys Glu Gln Pro Gly Glu Cys Arg Cys Leu
225 230 235 240

Glu Gly Trp Thr Gly Pro Leu Cys Met Val Pro Ala Ser Thr Ser Ser
245 250 255

Cys Leu Gly Leu Arg Gly Pro Ser Ser Ala Thr Thr Gly Cys Leu Val
260 265 270

Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser
275 280 285

Cys Ser Glu Thr Pro Gly Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe
290 295 300

Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro
305 310 315 320

Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala
325 330 335

Tyr Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys
340 345 350

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
355 360 365

Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
370 375 380

Gly Pro Arg Cys Glu His Asn Leu Asp Asp Cys Ala Gly Arg Ala Cys
385 390 395 400

Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser
405 410 415

Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro
420 425 430

Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe
435 440 445

Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ser Arg Cys
450 455 460

Glu Phe Pro Val His Pro Asp Gly Val Ser Ala Leu Pro Ala Ala Pro
465 470 475 480

Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu
485 490

<210> 273

<211> 175

<212> PRT
<213> Macaca fascicularis

<400> 273

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

Ala Leu Ile Phe Ile Pro Gln Ala Arg Pro Ala Gly Val Phe Glu Leu
20 25 30

Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
35 40 45

Pro Cys Ser Ala Arg Gly Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
50 55 60

Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
65 70 75 80

Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Glu Ala
85 90 95

Pro Ala Pro Asp Leu Pro Leu Pro Asn Gly Leu Leu Gln Val Pro Phe
100 105 110

Arg Asp Ala Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Thr Trp Arg
115 120 125

Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro Ala Trp Ser Leu Leu Ala
130 135 140

Arg Val Thr Arg Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145 150 155 160

Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg
165 170 175

<210> 274
<211> 40
<212> PRT
<213> Macaca fascicularis

<400> 274

Ala Arg Cys Glu Leu Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys
1 5 10 15

Arg Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys
20 25 30

Ala Pro Leu Glu Asp Glu Cys Glu
35 40

<210> 275

<211> 34

<212> PRT

<213> Macaca fascicularis

<400> 275

Ala Pro Pro Val Cys Arg Ala Gly Cys Ser Leu Glu His Gly Phe Cys
1 5 10 15

Glu Gln Pro Gly Glu Cys Arg Cys Leu Glu Gly Trp Thr Gly Pro Leu
20 25 30

Cys Met

<210> 276

<211> 37

<212> PRT

<213> Macaca fascicularis

<400> 276

Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser Cys
1 5 10 15

Ser Glu Thr Pro Gly Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe Tyr
20 25 30

Gly Leu Arg Cys Glu
35

<210> 277

<211> 40

<212> PRT
<213> Macaca fascicularis

<400> 277

Ser Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys
1 5 10 15

Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro
20 25 30

Gly Phe Gln Gly Ser Asn Cys Glu
35 40

<210> 278
<211> 37
<212> PRT
<213> Macaca fascicularis

<400> 278

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
1 5 10 15

Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
20 25 30

Gly Pro Arg Cys Glu
35

<210> 279
<211> 78
<212> PRT
<213> Macaca fascicularis

<400> 279

Ser Gly Val Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Leu Cys
1 5 10 15

Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys His Cys Pro Pro
20 25 30

Gly Phe Gln Gly Ser Asn Cys Glu Lys Arg Val Asp Arg Cys Ser Leu
35 40 45

Gln Pro Cys Arg Asn Gly Gly Leu Cys Leu Asp Leu Gly His Ala Leu
 50 55 60

Arg Cys Arg Cys Arg Ala Gly Phe Ala Gly Pro Arg Cys Glu
 65 70 75

<210> 280
 <211> 37
 <212> PRT
 <213> *Macaca fascicularis*

<400> 280

Asn Leu Asp Asp Cys Ala Gly Arg Ala Cys Ala Asn Gly Gly Thr Cys
 1 5 10 15

Val Glu Gly Gly Gly Ala His Arg Cys Ser Cys Ala Leu Gly Phe Gly
 20 25 30

Gly Arg Asp Cys Arg
 35

<210> 281
 <211> 37
 <212> PRT
 <213> *Macaca fascicularis*

<400> 281

Arg Ala Asp Pro Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys
 1 5 10 15

Tyr Ala His Phe Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met
 20 25 30

Gly Ser Arg Cys Glu
 35

<210> 282
 <211> 548
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 282

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

Ala Leu Ile Phe Ile Pro Gln Ala Arg Pro Ala Gly Val Phe Glu Leu
20 25 30

Gln Ile His Ser Phe Gly Pro Gly Pro Gly Pro Gly Ala Pro Arg Ser
35 40 45

Pro Cys Ser Ala Arg Gly Pro Cys Arg Leu Phe Phe Arg Val Cys Leu
50 55 60

Lys Pro Gly Leu Ser Glu Glu Ala Ala Glu Ser Pro Cys Ala Leu Gly
65 70 75 80

Ala Ala Leu Ser Ala Arg Gly Pro Val Tyr Thr Glu Gln Pro Glu Ala
85 90 95

Pro Ala Pro Asp Leu Pro Leu Pro Asn Gly Leu Leu Gln Val Pro Phe
100 105 110

Arg Asp Ala Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Thr Trp Arg
115 120 125

Glu Glu Leu Gly Asp Gln Ile Gly Gly Pro Ala Trp Ser Leu Leu Ala
130 135 140

Arg Val Thr Arg Arg Arg Arg Leu Ala Ala Gly Gly Pro Trp Ala Arg
145 150 155 160

Asp Ile Gln Arg Ala Gly Ala Trp Glu Leu Arg Phe Ser Tyr Arg Ala
165 170 175

Arg Cys Glu Leu Pro Ala Val Gly Thr Ala Cys Thr Arg Leu Cys Arg
180 185 190

Pro Arg Ser Ala Pro Ser Arg Cys Gly Pro Gly Leu Arg Pro Cys Ala
195 200 205

Pro Leu Glu Asp Glu Cys Glu Ala Pro Pro Val Cys Arg Ala Gly Cys
 210 215 220

Ser Leu Glu His Gly Phe Cys Glu Gln Pro Gly Glu Cys Arg Cys Leu
 225 230 235 240

Glu Gly Trp Thr Gly Pro Leu Cys Met Val Pro Ala Ser Thr Ser Ser
 245 250 255

Cys Leu Gly Leu Arg Gly Pro Ser Ser Ala Thr Thr Gly Cys Leu Val
 260 265 270

Pro Gly Pro Gly Pro Cys Asp Gly Asn Pro Cys Ala Asn Gly Gly Ser
 275 280 285

Cys Ser Glu Thr Pro Gly Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe
 290 295 300

Tyr Gly Leu Arg Cys Glu Val Ser Gly Val Thr Cys Ala Asp Gly Pro
 305 310 315 320

Cys Phe Asn Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala
 325 330 335

Tyr Ile Cys His Cys Pro Pro Gly Phe Gln Gly Ser Asn Cys Glu Lys
 340 345 350

Arg Val Asp Arg Cys Ser Leu Gln Pro Cys Arg Asn Gly Gly Leu Cys
 355 360 365

Leu Asp Leu Gly His Ala Leu Arg Cys Arg Cys Arg Ala Gly Phe Ala
 370 375 380

Gly Pro Arg Cys Glu His Asn Leu Asp Asp Cys Ala Gly Arg Ala Cys
 385 390 395 400

Ala Asn Gly Gly Thr Cys Val Glu Gly Gly Gly Ala His Arg Cys Ser
 405 410 415

Cys Ala Leu Gly Phe Gly Gly Arg Asp Cys Arg Glu Arg Ala Asp Pro

420

425

430

Cys Ala Ala Arg Pro Cys Ala His Gly Gly Arg Cys Tyr Ala His Phe
 435 440 445

Ser Gly Leu Val Cys Ala Cys Ala Pro Gly Tyr Met Gly Ser Arg Cys
 450 455 460

Glu Phe Pro Val His Pro Asp Gly Val Ser Ala Leu Pro Ala Ala Pro
 465 470 475 480

Pro Gly Leu Arg Pro Gly Asp Pro Gln Arg Tyr Leu Ser Gly Gly Gly
 485 490 495

Gly Ser Gly Ala Gly Val Ile Ala Val Ile Val Val Val Val Ile Ala
 500 505 510

Ile Val Ala Gly Ile Val Val Leu Val Ile Ser Arg Lys Lys Arg Met
 515 520 525

Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu Met Gly Glu Met His Arg
 530 535 540

Glu Leu Asn Ala
 545

<210> 283
 <211> 723
 <212> PRT
 <213> Homo sapiens

<400> 283

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

Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe
 20 25 30

Val Asn Lys Lys Gly Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly
 35 40 45

Ala Gly Pro Pro Pro Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu
50 55 60

Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly
65 70 75 80

Ser Ala Val Thr Pro Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp
85 90 95

Gly Gly Gly Ala Asp Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe
100 105 110

Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His
115 120 125

Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile
130 135 140

Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser
145 150 155 160

Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg
165 170 175

Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys
180 185 190

Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly
195 200 205

Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro
210 215 220

Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro
225 230 235 240

Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu
245 250 255

Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp
260 265 270

Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp
275 280 285

Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr Cys
290 295 300

Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr
305 310 315 320

Thr Gly Ala Thr Cys Glu Leu Gly Ile Asp Glu Cys Asp Pro Ser Pro
325 330 335

Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser Cys
340 345 350

Thr Cys Pro Pro Gly Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met
355 360 365

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

Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe
385 390 395 400

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

Gly Ala Lys Cys Val Asp Leu Gly Asp Ala Tyr Leu Cys Arg Cys Gln
420 425 430

Ala Gly Phe Ser Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala
435 440 445

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

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

Pro Val Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys
485 490 495

His Glu Arg Gly His Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr Gly
500 505 510

Gly Pro Asn Cys Gln Phe Leu Leu Pro Glu Leu Pro Pro Gly Pro Ala
515 520 525

Val Val Asp Leu Thr Glu Lys Leu Glu Gly Gln Gly Gly Pro Phe Pro
530 535 540

Trp Val Ala Val Cys Ala Gly Val Ile Leu Val Leu Met Leu Leu Leu
545 550 555 560

Gly Cys Ala Ala Val Val Val Cys Val Arg Leu Arg Leu Gln Lys His
565 570 575

Arg Pro Pro Ala Asp Pro Cys Arg Gly Glu Thr Glu Thr Met Asn Asn
580 585 590

Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly
595 600 605

Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp
610 615 620

His Ser Ala Asp Lys Asn Gly Phe Lys Ala Arg Tyr Pro Ala Val Asp
625 630 635 640

Tyr Asn Leu Val Gln Asp Leu Lys Gly Asp Asp Thr Ala Val Arg Asp
645 650 655

Ala His Ser Lys Arg Asp Thr Lys Cys Gln Pro Gln Gly Ser Ser Gly
660 665 670

Glu Glu Lys Gly Thr Pro Thr Thr Leu Arg Gly Gly Glu Ala Ser Glu
675 680 685

Arg Lys Arg Pro Asp Ser Gly Cys Ser Thr Ser Lys Asp Thr Lys Tyr
690 695 700

Gln Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Val Ile Ala
705 710 715 720

Thr Glu Val

<210> 284
<211> 685
<212> PRT
<213> Homo sapiens

<400> 284

Met Ala Ala Ala Ser Arg Ser Ala Ser Gly Trp Ala Leu Leu Leu Leu
1 5 10 15

Val Ala Leu Trp Gln Gln Arg Ala Ala Gly Ser Gly Val Phe Gln Leu
20 25 30

Gln Leu Gln Glu Phe Ile Asn Glu Arg Gly Val Leu Ala Ser Gly Arg
35 40 45

Pro Cys Glu Pro Gly Cys Arg Thr Phe Phe Arg Val Cys Leu Lys His
50 55 60

Phe Gln Ala Val Val Ser Pro Gly Pro Cys Thr Phe Gly Thr Val Ser
65 70 75 80

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

Gly Gly Gly Arg Asn Pro Leu Gln Leu Pro Phe Asn Phe Thr Trp Pro
100 105 110

Gly Thr Phe Ser Leu Ile Ile Glu Ala Trp His Ala Pro Gly Asp Asp
115 120 125

Leu Arg Pro Glu Ala Leu Pro Pro Asp Ala Leu Ile Ser Lys Ile Ala
130 135 140

Ile Gln Gly Ser Leu Ala Val Gly Gln Asn Trp Leu Leu Asp Glu Gln

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

Ser Pro Cys Phe Asn Gly Gly Ser Cys Arg Glu Arg Asn Gln Gly Ala
370 375 380

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

Lys Lys Val Asp Arg Cys Thr Ser Asn Pro Cys Ala Asn Gly Gly Gln
405 410 415

Cys Leu Asn Arg Gly Pro Ser Arg Met Cys Arg Cys Arg Pro Gly Phe
420 425 430

Thr Gly Thr Tyr Cys Glu Leu His Val Ser Asp Cys Ala Arg Asn Pro
435 440 445

Cys Ala His Gly Gly Thr Cys His Asp Leu Glu Asn Gly Leu Met Cys
450 455 460

Thr Cys Pro Ala Gly Phe Ser Gly Arg Arg Cys Glu Val Arg Thr Ser
465 470 475 480

Ile Asp Ala Cys Ala Ser Ser Pro Cys Phe Asn Arg Ala Thr Cys Tyr
485 490 495

Thr Asp Leu Ser Thr Asp Thr Phe Val Cys Asn Cys Pro Tyr Gly Phe
500 505 510

Val Gly Ser Arg Cys Glu Phe Pro Val Gly Leu Pro Pro Ser Phe Pro
515 520 525

Trp Val Ala Val Ser Leu Gly Val Gly Leu Ala Val Leu Leu Val Leu
530 535 540

Leu Gly Met Val Ala Val Ala Val Arg Gln Leu Arg Leu Arg Arg Pro
545 550 555 560

Asp Asp Gly Ser Arg Glu Ala Met Asn Asn Leu Ser Asp Phe Gln Lys
565 570 575

Asp Asn Leu Ile Pro Ala Ala Gln Leu Lys Asn Thr Asn Gln Lys Lys

580

585

590

Glu Leu Glu Val Asp Cys Gly Leu Asp Lys Ser Asn Cys Gly Lys Gln
 595 600 605

Gln Asn His Thr Leu Asp Tyr Asn Leu Ala Pro Gly Pro Leu Gly Arg
 610 615 620

Gly Thr Met Pro Gly Lys Phe Pro His Ser Asp Lys Ser Leu Gly Glu
 625 630 635 640

Lys Ala Pro Leu Arg Leu His Ser Glu Lys Pro Glu Cys Arg Ile Ser
 645 650 655

Ala Ile Cys Ser Pro Arg Asp Ser Met Tyr Gln Ser Val Cys Leu Ile
 660 665 670

Ser Glu Glu Arg Asn Glu Cys Val Ile Ala Thr Glu Val
 675 680 685

<210> 285
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 285

Gly Gly Gly Gly
 1

<210> 286
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 286

Gly Gly Gly Gly Ser
 1 5

<210> 287
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 287

Gly Gly Gly Gly Gln
1 5

<210> 288
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 288

Ser Gly Gly Gly Gly Ser
1 5

<210> 289
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 289

Pro Gly Gly Gly Gly Ser
1 5

<210> 290
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 290

Pro Gly Gly Asp Gly Ser

1

5

<210> 291
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 291

Gly Gly Gly Gly Ser Gly Gly Gly Ser
1 5

<210> 292
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 292

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 293
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 293

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 294
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 294

His His His His His His
1 5

<210> 295
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 295

Arg Asp Trp Asp Phe Asp Val Phe Gly Gly Gly Thr Pro Val Gly Gly
1 5 10 15

<210> 296
<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> 296

Gln Arg Phe Val Thr Gly His Phe Gly Gly Leu Xaa Pro Ala Asn Gly
1 5 10 15

<210> 297
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 297

Gln Arg Phe Val Thr Gly His Phe Gly Gly Leu Tyr Pro Ala Asn Gly
1 5 10 15

<210> 298

<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 298

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

<210> 299
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 299

Thr Gly His Phe Gly Gly Leu His Pro
1 5

<210> 300
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 300

Gln Arg Phe Cys Thr Gly His Phe Gly Gly Leu His Pro Cys Asn Gly
1 5 10 15

<210> 301
<211> 585
<212> PRT
<213> Homo sapiens

<400> 301

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> 302
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 302

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> 303
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 303

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> 304
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 304

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> 305
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 305

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 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> 306
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 306

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> 307
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 307

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> 308
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 308

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> 309
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 309

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> 310
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 310

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> 311

<211> 585

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 311

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 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> 312
<211> 585
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 312

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> 313
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 313

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> 314
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 314

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> 315
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 315

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> 316
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 316

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> 317
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 317

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> 318
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 318

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> 319
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 319

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> 320
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 320

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> 321
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 321

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> 322
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 322

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> 323
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 323

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> 324
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 324

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 His Leu Val
565 570 575

Ala Ala Ser Lys Ala Ala Leu Gly Leu
580 585

<210> 325
<211> 585
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 325

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> 326
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 326

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> 327
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 327

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> 328
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 328

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> 329
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 329

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> 330
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 330

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> 331
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 331

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> 332
 <211> 333
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 332

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> 333

<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 333

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> 334
<211> 338
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 334

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> 335
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 335

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> 336
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 336

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> 337
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 337

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> 338
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 338

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> 339
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 339

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> 340
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 340

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> 341
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 341

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> 342
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 342

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
 1 5 10

<210> 343
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 343

Gly Thr Lys Phe Leu Ala Pro
 1 5

<210> 344
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 344

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 345
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 345

Ile Tyr Ala Met Asn
1 5

<210> 346
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 346

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Ser

<210> 347
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 347

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Phe Phe Ala Tyr
1 5 10

<210> 348

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 348

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> 349

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 349

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> 350

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 350

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> 351
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 351

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 352
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 352

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 353
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 353

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 354
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 354

Lys Tyr Ala Met Asn
1 5

<210> 355
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 355

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 356
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 356

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10

<210> 357
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 357

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> 358
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 358

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> 359
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 359

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> 360
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 360

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 361
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 361

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 362
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 362

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 363
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 363

Ser Tyr Ala Met Asn
1 5

<210> 364
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 364

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 365
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 365

His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Phe Trp Ala Tyr
1 5 10

<210> 366

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 366

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> 367

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 367

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> 368

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 368

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> 369

<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 369

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 370
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 370

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 371
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 371

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 372
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 372

Arg Tyr Ala Met Asn
1 5

<210> 373
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 373

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 374
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 374

His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Tyr Phe Ala Tyr
1 5 10

<210> 375
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 375

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> 376
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 376

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> 377
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 377

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 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> 378
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 378

Arg Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 379
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 379

Ala Thr Asp Met Arg Pro Ser
1 5

<210> 380
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 380

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 381
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 381

Val Tyr Ala Met Asn
1 5

<210> 382
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 382

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Lys

<210> 383
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 383

His Gly Asn Phe Gly Asn Ser Tyr Leu Ser Trp Trp Ala Tyr
1 5 10

<210> 384
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 384

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> 385
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 385

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> 386

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 386

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> 387
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 387

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 388

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 388

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 389

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 389

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 390

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 390

Lys Tyr Ala Met Asn
1 5

<210> 391

<211> 19

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 391

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Ser

<210> 392
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 392

His Gly Asn Phe Gly Asn Ser Tyr Thr Ser Tyr Tyr Ala Tyr
1 5 10

<210> 393
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 393

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> 394
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 394

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> 395
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 395

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> 396
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 396

Arg Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 397
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 397

Ala Thr Asp Met Arg Pro Ser
1 5

<210> 398
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 398

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 399

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 399

Gly Tyr Ala Met Asn
1 5

<210> 400

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 400

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Glu

<210> 401

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 401

His Arg Asn Phe Gly Asn Ser Tyr Leu Ser Trp Phe Ala Tyr
1 5 10

<210> 402
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 402

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> 403
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 403

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> 404
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 404

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> 405

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 405

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Tyr Tyr Pro Asn
1 5 10

<210> 406

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 406

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 407

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 407

Ala Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 408

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 408

Val Tyr Ala Met Asn
1 5

<210> 409

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 409

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Lys

<210> 410

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 410

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Trp Trp Ala Tyr
1 5 10

<210> 411

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 411

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> 412
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 412

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> 413
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 413

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> 414
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 414

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
1 5 10

<210> 415
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 415

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 416
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 416

Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 417

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 417

Ser Tyr Ala Met Asn
1 5

<210> 418

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 418

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 419

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 419

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Trp Ala Tyr
1 5 10

<210> 420
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 420

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> 421
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 421

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> 422
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 422

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> 423
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 423

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
1 5 10

<210> 424

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 424

Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 425

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 425

Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 426

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 426

Lys Tyr Ala Met Asn
1 5

<210> 427

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 427

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 428

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 428

His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10

<210> 429

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 429

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> 430
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 430

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> 431
<211> 249

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 431

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> 432
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 432

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> 433
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 433

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> 434
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 434

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 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> 435
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 435

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 Ile Ser Ser Tyr
 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
 35 40 45

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

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

Leu Val Thr Val Ser Ser
 115

<210> 436
 <211> 108

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 436

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Asn Asn Asn
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg 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 Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 437
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 437

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 Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
35 40 45

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys

<210> 438
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 438

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 Ile Ser Ser Tyr
 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
 35 40 45

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
 130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
 145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
 165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

<210> 439
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 439

Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 440
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 440

Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 441

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 441

Arg Ser Ser Gln Ser Leu Val Tyr Arg Glu Gly Asn Thr Tyr Leu Ser
1 5 10 15

<210> 442

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 442

Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Ala Asn Thr Tyr Leu Ser
1 5 10 15

<210> 443

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 443

Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Gln Thr Tyr Leu Ser
1 5 10 15

<210> 444

<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 444

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

<210> 445
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 445

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 446
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 446

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 447
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 447

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 448
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 448

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 449
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 449

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120

<210> 450
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 450

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 451
<211> 123
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 451

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 452

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 452

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 453
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 453

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 454
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 454

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 455
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 455

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 456
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 456

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Glu Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 457
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 457

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Ala Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 458
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 458

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Gln Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 459
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 459

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Asn Ala Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 460

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 460

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly 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

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 461
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 461

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Glu Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly 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

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 462
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 462

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Ala Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly 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

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 463
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 463

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 464
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 464

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Glu Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 465
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 465

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Ala Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 466
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 466

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Gln Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 467
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 467

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Asn Ala Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Gly Gly 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

Thr His Trp Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 468
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 468

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly 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

Thr His Trp Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 469
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 469

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Glu Gly Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly 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

Thr His Trp Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 470

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 470

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg
20 25 30

Asp Ala Asn Thr Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly 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

Thr His Trp Pro Pro Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 471
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 471

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 472
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 472

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 Asn Tyr
20 25 30

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

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 473
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 473

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Gln Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 474
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 474

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Asn Ala Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 475
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 475

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
 130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
 145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
 180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
 225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 245 250

<210> 476
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 476

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
 130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 477
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 477

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 478
<211> 250
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 478

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 479
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 479

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 480
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 480

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 481
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 481

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Ala Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
245 250

<210> 482
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 482

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 483
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 483

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
 130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
 145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
 180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
 195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
 225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
 245 250

<210> 484
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 484

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
 130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Ala Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 485
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 485

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Gln Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 486
<211> 250
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 486

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Asn Ala Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
 225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
 245 250

<210> 487
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 487

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 488
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 488

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 489
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 489

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
 130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
 145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 490
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 490

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 491
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 491

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 492
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 492

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 493
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 493

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Ala Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
245 250

<210> 494
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 494

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
 225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
 245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
 275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 495
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 495

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Ala Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
 500 505

<210> 496

<211> 505

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 496

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Gln Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 497
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 497

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Asn Ala Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 498
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 498

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 499
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 499

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 500
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 500

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 501
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 501

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

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320 325

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 502
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 502

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 503
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 503

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
 225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
 245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
 275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 504
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 504

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Ala Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 505

<211> 505

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 505

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 506
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 506

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 507
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 507

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Ala Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
 500 505

<210> 508
 <211> 505
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 508

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Gln Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 509
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 509

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Gly Asn Ala Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 510
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 510

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

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320 325

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 511
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 511

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 512
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 512

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 513
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 513

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
 500 505

<210> 514
 <211> 505

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 514

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 515
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 515

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Glu Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
 305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
500 505

<210> 516
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 516

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Ala Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val Tyr Arg Asp Ala Asn Thr Tyr Leu
165 170 175

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
 385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
 405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
 420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
 435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
 450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu
 500 505

<210> 517
 <211> 984
 <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 Ile Ser Ser Tyr
 20 25 30

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

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
660 665 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
675 680 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
690 695 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705 710 715 720

Leu Ser Leu Ser Pro Gly Lys 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> 518
 <211> 982
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 518

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 Ile Ser Ser Tyr
 20 25 30

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

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
 325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
 340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
660 665 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
675 680 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
690 695 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705 710 715 720

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser 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 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
755 760 765

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
770 775 780

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
785 790 795 800

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
805 810 815

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
820 825 830

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
835 840 845

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
850 855 860

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
865 870 875 880

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
885 890 895

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
900 905 910

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
915 920 925

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
930 935 940

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
945 950 955 960

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
965 970 975

Ser Leu Ser Pro Gly Lys
980

<210> 519
<211> 984
<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 Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
35 40 45

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
 355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
 565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
660 665 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
675 680 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
690 695 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705 710 715 720

Leu Ser Leu Ser Pro Gly Lys 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> 520

<211> 982

<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 Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
35 40 45

Gly Tyr Val Tyr Tyr Ser Gly Thr 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

Ser Ile Ala Val Thr Gly Phe Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Arg Val Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
660 665 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
675 680 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
690 695 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705 710 715 720

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser 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 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
755 760 765

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
770 775 780

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
785 790 795 800

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
805 810 815

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
820 825 830

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
835 840 845

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
850 855 860

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
865 870 875 880

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
885 890 895

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
900 905 910

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
915 920 925

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
930 935 940

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
945 950 955 960

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
965 970 975

Ser Leu Ser Pro Gly Lys
980

<210> 521
<211> 984
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 521

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
660 665 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
675 680 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
690 695 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705 710 715 720

Leu Ser Leu Ser Pro Gly Lys 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> 522
<211> 982
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 522

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 Ala Ser Ile Ser Ser Phe
20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
660 665 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
675 680 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
690 695 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705 710 715 720

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser 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 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
755 760 765

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
770 775 780

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
785 790 795 800

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
805 810 815

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
820 825 830

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
835 840 845

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
850 855 860

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
865 870 875 880

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
885 890 895

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
900 905 910

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
915 920 925

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 930 935 940

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 945 950 955 960

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 965 970 975

Ser Leu Ser Pro Gly Lys
 980

<210> 523
 <211> 984
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 523

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 Ala Ser Ile Ser Ser Phe
 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

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

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
 565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
 580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 660 665 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 675 680 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 690 695 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 705 710 715 720

Leu Ser Leu Ser Pro Gly Lys 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> 524
<211> 982
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 524

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 Ala Ser Ile Ser Ser Phe
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

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

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
 385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
 405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
 420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
 435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
 450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
 465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 485 490 495

Gly Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 500 505 510

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 515 520 525

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 530 535 540

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 545 550 555 560

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
 565 570 575

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
 580 585 590

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
595 600 605

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
610 615 620

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
625 630 635 640

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
645 650 655

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
660 665 670

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
675 680 685

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
690 695 700

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
705 710 715 720

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser 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 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
755 760 765

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
770 775 780

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
785 790 795 800

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
805 810 815

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
820 825 830

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
835 840 845

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
850 855 860

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
865 870 875 880

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
885 890 895

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
900 905 910

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
915 920 925

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
930 935 940

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
945 950 955 960

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
965 970 975

Ser Leu Ser Pro Gly Lys
980

<210> 525
<211> 993
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 525

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 Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr
500 505 510

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
515 520 525

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
530 535 540

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
545 550 555 560

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
565 570 575

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val
580 585 590

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
595 600 605

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
610 615 620

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
625 630 635 640

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
645 650 655

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
660 665 670

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
675 680 685

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
690 695 700

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
705 710 715 720

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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 Gly Gly Gly Gly Ser Asp Lys
755 760 765

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
770 775 780

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
785 790 795 800

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
805 810 815

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
820 825 830

Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys
835 840 845

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
850 855 860

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
865 870 875 880

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
885 890 895

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
900 905 910

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
915 920 925

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
930 935 940

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
945 950 955 960

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
965 970 975

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
980 985 990

Lys

<210> 526
<211> 991
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 526

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 Asn Tyr
20 25 30

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

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
 465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
 485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr
 500 505 510

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 515 520 525

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 530 535 540

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 545 550 555 560

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 565 570 575

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val
 580 585 590

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 595 600 605

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 610 615 620

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 625 630 635 640

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 645 650 655

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 660 665 670

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
675 680 685

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
690 695 700

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
705 710 715 720

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro 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 Gly Gly Gly Gly Ser Asp Lys Thr His
755 760 765

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
770 775 780

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
785 790 795 800

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
805 810 815

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
820 825 830

Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser
835 840 845

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
850 855 860

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
865 870 875 880

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
885 890 895

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 900 905 910

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 915 920 925

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 930 935 940

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 945 950 955 960

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 965 970 975

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 980 985 990

<210> 527
 <211> 993
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 527

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr
500 505 510

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
515 520 525

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
530 535 540

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
545 550 555 560

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
565 570 575

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val
580 585 590

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
595 600 605

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
610 615 620

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
625 630 635 640

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
645 650 655

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
660 665 670

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
675 680 685

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
690 695 700

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
705 710 715 720

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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 Gly Gly Gly Gly Ser Asp Lys
755 760 765

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
770 775 780

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
785 790 795 800

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
805 810 815

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
820 825 830

Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys
835 840 845

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
850 855 860

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
865 870 875 880

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
885 890 895

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
900 905 910

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
915 920 925

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
930 935 940

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 945 950 955 960

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 965 970 975

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 980 985 990

Lys

<210> 528
 <211> 991
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 528

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 Asn Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Leu Cys Leu Glu Trp Met
 35 40 45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Val Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Asn Ser Ala Phe Tyr Ser Tyr Tyr Asp Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Thr Leu Gly Gln Pro Ala Ser Ile Ser
145 150 155 160

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

Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
180 185 190

Lys Val Ser Asn Trp Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Gly
195 200 205

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

Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr
225 230 235 240

Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Gly Gly Ser
245 250 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
260 265 270

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
275 280 285

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
290 295 300

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
305 310 315 320

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
325 330 335

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
385 390 395 400

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
405 410 415

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
420 425 430

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
435 440 445

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
450 455 460

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
465 470 475 480

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
485 490 495

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Asp Lys Thr
500 505 510

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
515 520 525

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
530 535 540

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
545 550 555 560

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
565 570 575

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val
580 585 590

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
595 600 605

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
610 615 620

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
625 630 635 640

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
645 650 655

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
660 665 670

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
675 680 685

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
690 695 700

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
705 710 715 720

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro 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 Gly Gly Gly Gly Ser Asp Lys Thr His
755 760 765

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
770 775 780

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
785 790 795 800

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
805 810 815

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
820 825 830

Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser
835 840 845

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
850 855 860

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
865 870 875 880

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
885 890 895

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
900 905 910

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
915 920 925

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
930 935 940

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
945 950 955 960

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
965 970 975

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
980 985 990

<210> 529
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 529

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 Ala Ser Ile Ser Ser Phe
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
35 40 45

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

Leu Val Thr Val Ser Ser
115

<210> 530
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 530

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 Asn Lys 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 Asp Arg Ser Pro
85 90 95

Leu Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105

<210> 531

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 531

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 Ala Ser Ile Ser Ser Phe
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

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

Lys

<210> 532

<211> 496

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 532

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 Ala Ser Ile Ser Ser Phe
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Thr 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 Ile Ala Val Ala Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

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

Lys Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
245 250 255

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
260 265 270

Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
290 295 300

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
305 310 315 320

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
325 330 335

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
340 345 350

Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val
355 360 365

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
370 375 380

Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser
385 390 395 400

Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val
405 410 415

Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala
420 425 430

Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro
435 440 445

Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu
450 455 460

Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp
465 470 475 480

Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
485 490 495

<210> 533
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 533

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> 534
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 534

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> 535
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 535

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> 536
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 536

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> 537
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 537

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> 538
<211> 225
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 538

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> 539
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 539

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> 540
 <211> 225
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 540

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> 541
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 541

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> 542
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 542

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 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> 543
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 543

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> 544
 <211> 480
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 544

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> 545
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 545

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> 546
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 546

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
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<210> 547
 <211> 484
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic peptide

<400> 547

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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> 548

<211> 480

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 548

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> 549
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 549

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1 5 10 15

Gly Gly Gly Ser
20

<210> 550
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 550

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> 551
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 551

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> 552
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 552

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> 553
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 553

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> 554
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 554

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 Ser Tyr
20 25 30

Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Ser 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

Ser Ile Ala Val Arg Gly Phe Phe 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
130 135 140

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
145 150 155 160

Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile
180 185 190

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Gly Thr Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Arg 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 His His His His His His
500

Claims

1. A bispecific antibody construct comprising a first binding domain which binds to human DLL3 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, wherein the first binding domain binds to an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 260.
2. The antibody construct according to claim 1, wherein the first binding domain further binds to macaque DLL3, preferably to *Macaca fascicularis* DLL3.
3. The antibody construct according to claim 1 or 2, wherein the second binding domain binds to human CD3 epsilon and to *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus* CD3 epsilon.
4. 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.
5. The antibody construct according to any one of the preceding claims, wherein the first binding domain binds to an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 258.
6. The antibody construct according to claim 5, 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 selected from the group consisting of:
 - a) CDR-H1 as depicted in SEQ ID NO: 31, CDR-H2 as depicted in SEQ ID NO: 32, CDR-H3 as depicted in SEQ ID NO: 33, CDR-L1 as depicted in SEQ ID NO: 34, CDR-L2 as depicted in SEQ ID NO: 35 and CDR-L3 as depicted in SEQ ID NO: 36;
 - b) CDR-H1 as depicted in SEQ ID NO: 41, CDR-H2 as depicted in SEQ ID NO: 42, CDR-H3 as depicted in SEQ ID NO: 43, CDR-L1 as depicted in SEQ ID NO: 44, CDR-L2 as depicted in SEQ ID NO: 45 and CDR-L3 as depicted in SEQ ID NO: 46;
 - c) CDR-H1 as depicted in SEQ ID NO: 51, CDR-H2 as depicted in SEQ ID NO: 52, CDR-H3 as depicted in SEQ ID NO: 53, CDR-L1 as depicted in SEQ ID NO: 54, CDR-L2 as depicted in SEQ ID NO: 55 and CDR-L3 as depicted in SEQ ID NO: 56;

- d) CDR-H1 as depicted in SEQ ID NO: 61, CDR-H2 as depicted in SEQ ID NO: 62, CDR-H3 as depicted in SEQ ID NO: 63, CDR-L1 as depicted in SEQ ID NO: 64, CDR-L2 as depicted in SEQ ID NO: 65 and CDR-L3 as depicted in SEQ ID NO: 66;
 - e) CDR-H1 as depicted in SEQ ID NO: 71, CDR-H2 as depicted in SEQ ID NO: 72, CDR-H3 as depicted in SEQ ID NO: 73, CDR-L1 as depicted in SEQ ID NO: 74, CDR-L2 as depicted in SEQ ID NO: 75 and CDR-L3 as depicted in SEQ ID NO: 76;
 - f) CDR-H1 as depicted in SEQ ID NO: 81, CDR-H2 as depicted in SEQ ID NO: 82, CDR-H3 as depicted in SEQ ID NO: 83, CDR-L1 as depicted in SEQ ID NO: 84, CDR-L2 as depicted in SEQ ID NO: 85 and CDR-L3 as depicted in SEQ ID NO: 86;
 - g) CDR-H1 as depicted in SEQ ID NO: 91, CDR-H2 as depicted in SEQ ID NO: 92, CDR-H3 as depicted in SEQ ID NO: 93, CDR-L1 as depicted in SEQ ID NO: 94, CDR-L2 as depicted in SEQ ID NO: 95 and CDR-L3 as depicted in SEQ ID NO: 96;
 - h) CDR-H1 as depicted in SEQ ID NO: 101, CDR-H2 as depicted in SEQ ID NO: 102, CDR-H3 as depicted in SEQ ID NO: 103, CDR-L1 as depicted in SEQ ID NO: 104, CDR-L2 as depicted in SEQ ID NO: 105 and CDR-L3 as depicted in SEQ ID NO: 106; and
 - i) CDR-H1 as depicted in SEQ ID NO: 111, CDR-H2 as depicted in SEQ ID NO: 112, CDR-H3 as depicted in SEQ ID NO: 113, CDR-L1 as depicted in SEQ ID NO: 114, CDR-L2 as depicted in SEQ ID NO: 115 and CDR-L3 as depicted in SEQ ID NO: 116.
7. The antibody construct according to claim 5 or 6, wherein the first binding domain comprises a VH region selected from the group consisting of those depicted in 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: 435 and SEQ ID NO: 529.
8. The antibody construct according to any one of claims 5 to 7, wherein the first binding domain comprises a VL region selected from the group consisting of those depicted in 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: 436 and SEQ ID NO: 530.
9. The antibody construct according to any one of claims 5 to 8, 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: 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: 435+436; and SEQ ID NOs: 529+530 .

10. The antibody construct according to any one of claims 5 to 9, wherein the first binding domain comprises a polypeptide selected from the group consisting of those depicted in 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: 437 and SEQ ID NO: 531.
11. The antibody construct according to any one of claims 5 to 10, comprising a polypeptide selected from the group consisting of those depicted in 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: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 438 and SEQ ID NO: 532.
12. The antibody construct according to any one of claims 1 to 4, wherein the first binding domain binds to an epitope of DLL3 which is comprised within the region as depicted in SEQ ID NO: 259.
13. The antibody construct according to claim 12, 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 selected from the group consisting of:
 - a) CDR-H1 as depicted in SEQ ID NO: 121, CDR-H2 as depicted in SEQ ID NO: 122, CDR-H3 as depicted in SEQ ID NO: 123, CDR-L1 as depicted in SEQ ID NO: 124, CDR-L2 as depicted in SEQ ID NO: 125 and CDR-L3 as depicted in SEQ ID NO: 126;
 - b) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 134, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;
 - c) CDR-H1 as depicted in SEQ ID NO: 141, CDR-H2 as depicted in SEQ ID NO: 142, CDR-H3 as depicted in SEQ ID NO: 143, CDR-L1 as depicted in SEQ ID

NO: 144, CDR-L2 as depicted in SEQ ID NO: 145 and CDR-L3 as depicted in SEQ ID NO: 146;

d) CDR-H1 as depicted in SEQ ID NO: 151, CDR-H2 as depicted in SEQ ID NO: 152, CDR-H3 as depicted in SEQ ID NO: 153, CDR-L1 as depicted in SEQ ID NO: 154, CDR-L2 as depicted in SEQ ID NO: 155 and CDR-L3 as depicted in SEQ ID NO: 156;

e) CDR-H1 as depicted in SEQ ID NO: 161, CDR-H2 as depicted in SEQ ID NO: 162, CDR-H3 as depicted in SEQ ID NO: 163, CDR-L1 as depicted in SEQ ID NO: 164, CDR-L2 as depicted in SEQ ID NO: 165 and CDR-L3 as depicted in SEQ ID NO: 166;

f) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 439, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 134, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;

g) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 440, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 134, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;

h) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 441, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;

i) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 442, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;

j) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 443, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;

k) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 132, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 444, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136;

- l) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 439, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 441, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136; and
- m) CDR-H1 as depicted in SEQ ID NO: 131, CDR-H2 as depicted in SEQ ID NO: 440, CDR-H3 as depicted in SEQ ID NO: 133, CDR-L1 as depicted in SEQ ID NO: 442, CDR-L2 as depicted in SEQ ID NO: 135 and CDR-L3 as depicted in SEQ ID NO: 136.
14. The antibody construct according to claim 12 or 13, wherein the first binding domain comprises a VH region selected from the group consisting of those depicted in SEQ ID NO: 127, SEQ ID NO: 137, SEQ ID NO: 147, SEQ ID NO: 157, SEQ ID NO: 167, SEQ ID NO: 445, SEQ ID NO: 446, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 454, and SEQ ID NO: 455.
15. The antibody construct according to any one of claims 12 to 14, wherein the first binding domain comprises a VL region selected from the group consisting of those depicted in SEQ ID NO: 128, SEQ ID NO: 138, SEQ ID NO: 148, SEQ ID NO: 158, SEQ ID NO: 168, SEQ ID NO: 456, SEQ ID NO: 457, SEQ ID NO: 458, SEQ ID NO: 459, SEQ ID NO: 460, SEQ ID NO: 461, SEQ ID NO: 462, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, and SEQ ID NO: 470.
16. The antibody construct according to any one of claims 12 to 15, 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: 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 137+456; SEQ ID NOs 137+457; SEQ ID NOs 137+458; SEQ ID NOs 137+459; SEQ ID NOs 137+460; SEQ ID NOs 445+138; SEQ ID NOs 446+138; SEQ ID NOs 447+138; SEQ ID NOs 445+460; SEQ ID NOs 448+461; SEQ ID NOs 449+462; SEQ ID NOs 450+463; SEQ ID NOs 450+464; SEQ ID NOs 450+465; SEQ ID NOs 450+466; SEQ ID NOs 450+467; SEQ ID NOs 450+468; SEQ ID NOs 451+463; SEQ ID NOs 452+463; SEQ ID NOs 453+463; SEQ ID NOs 451+468; SEQ ID NOs 454+469; and SEQ ID NOs 455+470.

17. The antibody construct according to any one of claims 12 to 16, wherein the first binding domain comprises a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 129, SEQ ID NO: 139, SEQ ID NO: 149, SEQ ID NO: 159, SEQ ID NO: 169, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 492, and SEQ ID NO: 493.
18. The antibody construct according to any one of claims 12 to 17, comprising a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 130, SEQ ID NO: 140, SEQ ID NO: 150, SEQ ID NO: 160, SEQ ID NO: 170; SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 505, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 513, SEQ ID NO: 514, SEQ ID NO: 515, and SEQ ID NO: 516.
19. The antibody construct according to any one of claims 5-11, comprising or consisting of a polypeptide selected from the group consisting of those depicted in SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524.
20. A polynucleotide encoding an antibody construct as defined in any one of the preceding claims.
21. A vector comprising a polynucleotide as defined in claim 20.
22. A host cell transformed or transfected with the polynucleotide as defined in claim 20 or with the vector as defined in claim 21.

23. A process for the production of an antibody construct according to any one of claims 1 to 19, said process comprising culturing a host cell as defined in claim 22 under conditions allowing the expression of said antibody construct and recovering the produced antibody construct from the culture.
24. A pharmaceutical composition comprising an antibody construct according to any one of claims 1 to 18, or produced according to the process of claim 23.
25. The antibody construct according to any one of claims 1 to 19, or produced according to the process of claim 23, for use in the prevention, treatment or amelioration of a tumor or cancer disease or a metastatic cancer disease.
26. A method for the treatment or amelioration of a tumor or cancer disease or 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 19, or produced according to the process of claim 23.
27. The method according to claim 26 or the antibody construct according to claim 24, wherein the tumor or cancer disease is selected from the group consisting of lung cancer, preferably SCLC, breast, cervical, colon, colorectal, endometrial, head and neck, liver, ovarian, pancreatic, prostate, skin, gastric, testis, thyroid, adrenal, renal, bladder, uterine, esophageal, urothelial and brain tumor or cancer, lymphoma, carcinoma, and sarcoma, and a metastatic cancer disease derived from any of the foregoing.
28. A kit comprising an antibody construct according to any one of claims 1 to 19, an antibody construct produced according to the process of claim 23, a polynucleotide as defined in claim 20, a vector as defined in claim 21, and/or a host cell as defined in claim 22.